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Docket No.: 787CIP2B

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Jc840 U.S. PTO

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

Jc836 U.S. PTO
09/620325
07/19/00

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren,
Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman,
Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T.
Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

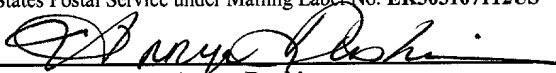
- ☒ This is a new application for a
- ☒ Utility patent.
- ☐ Design patent.
- ☒ This is a continuation-in-part application of prior application no. 09/560,875 filed April 27, 2000, Attorney Docket No. 787CIP, which is a continuation-in-part application of prior application no. 09/496,914 filed February 03, 2000, Attorney Docket No. 787.

2. Application Papers Enclosed

- 1 Title Page
- 138 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
- 4 Page(s) of Claims
- 1 Page(s) of Abstract
- 0 Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal
- 1357 Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **July 19, 2000**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. **EK305107112US**


Anya Dushine

3. Oath or Declaration

- ☐ Enclosed
 - ☐ Executed by (check all applicable boxes)
 - ☐ Inventor(s)
 - ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
 - ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
 - ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- ☒ Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- ☒ Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- ☒ Statement Under 37 CFR § 1.821
- ☒ Paper copy of sequence listing identical to computer copy (1357 pages)
- ☐ Microfiche computer program
- ☒ Verified statement claiming small entity status under 37 CFR 1.9 and 1.27
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- ☒ Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. Filing Fee Calculation (37 CFR 1.16)

A. ☒ Utility Application

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$345.00		\$690.00
TOTAL	28-20	= 8	X 9 =	\$72.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 39 =	\$0.00	X 78 =	\$0.00
<input checked="" type="checkbox"/> First Presentation of Multiple Dependent Claim			+ 130 =	\$130.00	+ 260 =	\$0.00
FILING FEE:				\$547.00	OR	\$0.00

B. ☐ Design Application (\$155.00/\$310.00) Filing Fee: \$ _____

C. ☐ Plant Application (\$240.00/\$480.00) Filing Fee: \$ _____

D. Other fees

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ _____

☐ Other \$ _____

TOTAL FEES \$ 547.00

7. Method of Payments of Fees

- ☐ Enclosed check
- ☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

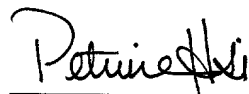
Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Petrina S. Hsi at the address below.

Respectfully submitted,

Date: July 19, 2000

By:



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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) or Patentee(s): Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren, Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T. Drmanac

Application No. or Patent No.: Not Yet Assigned

Filed or Issued: Herewith

For: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR § 1.9(f) AND 1.27(c)) - SMALL BUSINESS CONCERN**

I hereby declare that I am

- ☐ The owner of the small business concern identified below:
- ☒ An official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: HYSEQ, INC.
ADDRESS: 670 Almanor Avenue
Sunnyvale, CA 94085

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR § 121.12, and reproduced in 37 CFR § 1.9(d), for purposes of paying reduced fees under § 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to, and remain with, the small business concern identified above with regard to the invention, entitled NOVEL NUCLEIC ACIDS AND POLYPEPTIDES by inventors, Y. Tom Tang, et al. described in

- ☒ The specification filed herewith.
- ☐ Application Serial No. [], filed [Date].
- ☐ Patent No. [], issued [Date].

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below¹ and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR § 1.9(c), or by any concern which would not qualify as a small business concern under 37 CFR § 1.9(d) or a nonprofit organization under 37 CFR § 1.9(e).

Full Name: _____

Address: _____

() Individual () Small Business Concern () Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate (37 CFR § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of person signing: Mark E. Gitter

Title of person
other than owner: Chief Financial Officer

Address of person signing: HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085

Signature: _____

Date: _____

7-18-00

¹NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR § 1.27)

Our Ref. No.: 787CIP2B

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

Express Mail Label No.: EK305107112US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. CROSS REFERENCE TO RELATED APPLICATIONS

5 This application is a continuation-in-part application of U.S. Application Serial No. 09/560,875, filed April 27, 2000, which in turn is a continuation-in-part application of U.S. Application Serial No. 09/496,914, filed February 03, 2000, both of which are incorporated herein by reference in their entirety.

10 2. BACKGROUND OF THE INVENTION

2.1 TECHNICAL FIELD

15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2.2 BACKGROUND

20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as
25 signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the

case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 - 419 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanosine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 - 419 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 - 419. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 - 419 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 - 419. The sequence information can be a segment of any one of SEQ ID NO: 1 - 419 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 - 419.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-419 or novel segments or parts of the nucleic acids of the invention are used as primers in

expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-419 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as

5 expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in the SEQ ID NO: 1-419; a polynucleotide comprising any of the full length protein coding sequences of the SEQ ID NO: 1-419; and a polynucleotide comprising any of the nucleotide
10 sequences of the mature protein coding sequences of the SEQ ID NO: 1-419. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in the SEQ ID NO: 1-419; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the
15 Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

20 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the SEQ ID NO: 1-419; or (b)
25 polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The
30 polypeptides of the invention may be wholly or partially chemically synthesized but are

preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an
5 acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable
10 culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a
15 variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell
20 or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art
25 and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that
30 specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies,

are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides

and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have the closest homology (set forth in Table 1). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived

The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of
5 nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating
10 sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides
15 or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide
20 linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment",
25 "portion," or "segment" or "probe" or "primer" are used interchangeable and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17
nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less
30 than about 200 nucleotides, more preferably less than about 100 nucleotides, more

preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-419.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-419. The sequence information can be a segment of any one of SEQ ID NOs: 1-419 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-419. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosome. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used.

The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater

than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

5 The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

10 The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

15 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

20 The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

25 The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

30

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be

selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

5 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated
10 biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

 The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present
15 with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

20 The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free
25 of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

 The term "recombinant expression vehicle or vector" refers to a plasmid or
30 phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence.

An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.*

Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell.

5 Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 10 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium 15 pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which 20 does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of 25 residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further 30 variation of this embodiment, by no more than 20% (80% sequence identity) and in a

further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic

acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each,
5 unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide
10 comprising the nucleotide sequences of the SEQ ID NO: 1 - 419; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 - 419; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 419. The polynucleotides of the present invention also include, but are not limited to, a
15 polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of the SEQ ID NO: 1 - 419; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above;
20 or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 419. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable
25 immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The

polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of the SEQ ID NO: 1 - 419 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of the SEQ ID NO: 1 - 419 or a portion thereof as a probe. Alternatively, the polynucleotides of the SEQ ID NO: 1 - 419 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of the SEQ ID NO: 1 - 419, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably

greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 419, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 419 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 419, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide

which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence

5 variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid

10 sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*,

15 hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as

20 intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed

25 protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on

30 either side of the site of being changed. In general, the techniques of site-directed

mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-419, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 419 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 419 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors

are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

5 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are
10 exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

15 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from
20 retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion
30 of translated protein into the periplasmic space or extracellular medium. Optionally,

the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain
5 nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

10 Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous
15 promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which
20 encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a
25 lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be
30 used in conventional manners to produce the gene product encoded by the isolated

fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more

salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be
5 disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,
10 *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in
15 order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the
20 regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment
25 regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or

modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-419 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 419 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 419 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-419 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-419 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-419.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by

expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms,
5 part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the
10 nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present
15 invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing
20 primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically
25 active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or
30 protein. As used herein, a cell is said to be altered to express a desired polypeptide or

protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules

include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-419.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule.

Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological

activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion

proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak
5 (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be
10 employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted,
15 inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the
20 polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are
25 used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE 30 IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984);

- 5 Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-
10 Manning et al, ISMB-97, vol 4, pp. 202-209, herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).
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4.5 GENE THERAPY

- Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to
20 restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer
25 methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of
30 the present invention can also be accomplished with extrachromosomal substrates

(transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter

DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes

exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous

recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express
5 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare
10 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or
15 other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap
20 assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for
25 high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of
30 course, to isolate correlative receptors or ligands. Proteins involved in these binding

interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

- 5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.
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4.7.2 NUTRITIONAL USES

- Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.
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4.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

- A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of
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therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco.

5 Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M.

Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte

10 Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J.

Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990;

Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I.

Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

15 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell

stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in

Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons,

Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D.

In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8,

20 John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and

Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E.

In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12,

25 John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211,

1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad.

Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin

6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.

6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci.

30 U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F.,

Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.

5 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M.

10 Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells,

gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of

differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one

of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone

marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic

5 lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al.,
10 Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc.,
15 New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay,
20 Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In
25 Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.7.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments.

The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses,

herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

10 Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-
15 Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The
20 therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

25 Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited
30 by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and

5 persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing

10 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that
15 destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of
20 repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ

transplant rejection or GVHD can be assessed using animal models that are predictive

25 of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine
30 models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York,

1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient,

transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J.

Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in
10 Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan,
15 A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

20 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of
Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
25 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

 Assays for lymphocyte survival/apoptosis (which will identify, among others,
30 proteins that prevent apoptosis after superantigen induction and proteins that regulate

lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for

movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a

precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

5 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced
10 tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and
15 polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain
20 cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

25 Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser
30 therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the

5 polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, 10 Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide 15 acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, 20 Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these 25 individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar 30 (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-

Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA

84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor
5 for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands.

10 The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of
15 colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.7.13 DRUG SCREENING

20 This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host
25 cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being

tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the

“hit” to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s).

As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

5 The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion
10 of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

15 **4.7.15 ANTI-INFLAMMATORY ACTIVITY**

 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting
20 chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion
25 injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and
30 hypersensitivity to an antigenic substance or material. Compositions of this invention

may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.7.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.7.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration,

and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

5 Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, 10 the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, 15 traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide 20 sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of 25 the protein, e.g., by an antibody specific to the variant sequence.

4.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The 30 experimental model system is adjuvant induced arthritis in rats, and the protocol is

described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the

invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF,

Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical

condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.

Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present

invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For

transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

- 5 Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or
- 10 dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as
- 15 the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or
- 20 pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

- Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in
- 25 admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such

administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described

previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological

stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without

limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by
5 reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of
10 protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and
15 at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which
20 are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for
25 delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the
30 invention. Preferably for bone and/or cartilage formation, the composition would

include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent

useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby
5 providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming
10 growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical
15 composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other
20 clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays,
25 histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including,
30 without limitation, in the form of viral vectors or naked DNA). Cells may also be

cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

5 **4.9.3 EFFECTIVE DOSAGE**

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing
10 symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating
15 concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately
20 determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for
25 determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in
30 formulating a range of dosage for use in human. The dosage of such compounds lies

preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

5 4.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining
10 region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments,
15 including Fab, Fab', F(ab')₂, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also
20 interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see
25 Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the
30 invention, antibodies of the invention that recognize fragments are those which can

distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

5 Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

10 Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further
15 provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such
20 antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L.
25 Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where
30 abnormal expression of the protein is involved. In the case of cancerous cells or

leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or α -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known

in the art (Campbell, A.M., Monoclonal Antibody Technology: Laboratory
Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers,
Amsterdam, The Netherlands (1984)). Techniques described for the production of
single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain
5 antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the
immunized animal and is screened for the presence of antibodies with the desired
specificity using one of the above-described procedures. The present invention further
provides the above-described antibodies in delectably labeled form. Antibodies can be
10 delectably labeled through the use of radioisotopes, affinity labels (such as biotin,
avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase,
etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc.
Procedures for accomplishing such labeling are well-known in the art, for example, see
(Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al.,
15 Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding,
J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*,
and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of
interest is expressed. The antibodies may also be used directly in therapies or other
20 diagnostics. The present invention further provides the above-described antibodies
immobilized on a solid support. Examples of such solid supports include plastics such
as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic
resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies
to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of
25 Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford,
England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press,
N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in*
vitro, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the
proteins of the present invention.

4.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 419 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any

of the nucleotide sequences of the SEQ ID NOs: 1 - 419 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting

search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991))

or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991);
Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca
Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA
transcription from DNA, while antisense RNA hybridization blocks translation of an
5 mRNA molecule into polypeptide. Both techniques have been demonstrated to be
effective in model systems. Information contained in the sequences of the present
invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.13 DIAGNOSTIC ASSAYS AND KITS

10 The present invention further provides methods to identify the presence or
expression of one of the ORFs of the present invention, or homolog thereof, in a test
sample, using a nucleic acid probe or antibodies of the present invention, optionally
conjugated or otherwise associated with a suitable label.

15 In general, methods for detecting a polynucleotide of the invention can comprise
contacting a sample with a compound that binds to and forms a complex with the
polynucleotide for a period sufficient to form the complex, and detecting the complex,
so that if a complex is detected, a polynucleotide of the invention is detected in the
sample. Such methods can also comprise contacting a sample under stringent
hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the
20 invention under such conditions, and amplifying annealed polynucleotides, so that if a
polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

25 In general, methods for detecting a polypeptide of the invention can comprise
contacting a sample with a compound that binds to and forms a complex with the
polypeptide for a period sufficient to form the complex, and detecting the complex, so
that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of
the antibodies or one or more of the nucleic acid probes of the present invention and
assaying for binding of the nucleic acid probes or antibodies to components within the
test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly

5 available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention.

Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: *Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

10 The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

20 In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

25 In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are

not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 419, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while

antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

5 Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.16 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 419. Because the
15 corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NOs: 1 - 419 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188
20 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

25 Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively
30 labeled nucleotides. The nucleotide sequences may be used to construct hybridization

probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads
5 may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently
10 bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups ($>NH$) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA
15 (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred.
20 The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and
25 then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well)
30 standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These

methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may

represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12
5 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid
10 molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other
15 embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are
20 within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

25 All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the

assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genepet release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 419.

Table 1 shows the various tissue sources of SEQ ID NO: 1-419.

The nearest neighbor results for SEQ ID NO: 1-419 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-419 from Genpept (and contains the translated amino acid sequences for which the nucleic acid sequence encodes). The nearest neighbor results for SEQ ID NO: 1-419 are shown in Table 2 below.

TABLE 1

TISSUE ORIGIN	RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	23 45 52 55 59 61 65-66 69 72 75-76 80 105 123 130 133-134 137 147 149 157-158 179 198 202 207 212-213 233 246 253-254 259 263 272-273 275 295 303 327 352 364 389 391-392 406
adult brain	GIBCO	ABD003	3 7 14 19 22-23 26 29 31-32 37 43-45 48 50-51 55 58-59 62 65 69-70 74 77 79-80 85-86 91 105 111 113 115-116 123 133 135 144-145 149-150 155 157-158 168 179 186 191 198 210-211 213 221 224 227-228 230-233 236-237 239 242-243 246 248 252 259 261 263-265 268-275 281-283 286 288 303 311 316-317 321 329 332 334 342-343 346 352 377 379 385 389 395-396 400
adult brain	Clontech	ABR001	7 29 32 44-45 52 69 77-78 80 110 191 222 233 236 257-258 262 271 297-298 341 343 368 385 389 393 401 407
adult brain	Clontech	ABR006	3 10-12 23 33 39 43 45 80-81 83-84 94 117 198 272 300 385 387-389 398 413-414 417
adult brain	Clontech	ABR008	1 3 5-7 12 15 18-23 25 28-30 32-35 37-43 47-48 51-52 54 58- 61 63 67-70 72-73 75-76 79 82- 86 92 94-99 101 105-106 109 111 113 120 128 131-132 134 137 139-147 154 156 159 165 168-171 173 176-181 184 187-188 191-194 197 200 202 204 210-211 215 218 220 224 230-233 238-239 243 247-248 252-259 262-263 265-266 268-269 272-273 275 281-286 294 296 298-301 303-305 308 310 312-314 317-318 321 325 327 342 346-352 354-355 361 364 368 370 377 381-383 385 387-388 391-393 398 400-403 406-408 410 414 416-417 419
adult brain	Clontech	ABR011	85
adult brain	BioChain	ABR012	344
adult brain	Invitrogen	ABR013	74 141-143 385
adult brain	Invitrogen	ABR014	43 48 417
adult brain	Invitrogen	ABR015	391-392 417
adult brain	Invitrogen	ABR016	23 45 48 54 337 395-396
adult brain	Invitrogen	ABT004	20 23 37 40 43 48 50 58 60 78 85-86 105 111 126 137 145 147 159 161 164 188 191 194 198 208 212 223 229 237 239 252-256 263 271-272 275 291 295 299 334 368

TABLE 1

			376 381 385 388-389 393 398 401 406 419
adipocytes	Stratagene	ADP001	10-11 20 23 37 43 50 52 54 60 69 86 102 115-116 119 123 127 145 156-158 166 179 181-182 234 238 243 253-254 259 261 268-272 281-282 284 290 294-295 314 346 382 399 414 418
adrenal gland	Clontech	ADR002	10-11 13 21 25-26 31 33 50-51 54-55 65 69 80 86 93 95 97 106 111 133 149 156 166 173 181-182 188 194 203 210-211 213 238 248 253-254 257-258 286 294 298 302 311 317 327 346 356 383 393 398 405 412 418
adult heart	GIBCO	AHR001	1 7 10-12 19-20 29 31-32 37 43- 45 47 50 52 54-55 59-65 72 74- 76 79-80 85 101-102 113-114 119-123 130-133 136-137 139 141-143 145 148-149 154-155 157-158 163 172 178-179 182 196-197 202 207 212-214 222 227-228 236-238 240 243 248 252-254 257-259 261-264 268-270 272-273 277-279 288-289 294-296 300 305 311 314 325 335-336 341 344 346 350 352 361 364 366 368 385 390 398 400-401 403-406 412 414 418
adult kidney	GIBCO	AKD001	1 3-4 7 10-12 14 19-20 22 25-27 29 31-32 37 44-48 50-52 54-55 58-62 65 67-69 74-77 79-80 89 91 101-103 111 113-114 119 121- 123 126 128 130 132-134 136-138 141-144 147-149 153 155 159 166 171 174 178-179 181-182 188 191-192 196 200-201 207 209-213 218-219 223-224 227-228 230-233 235-240 244-246 252-259 261-264 268-272 275 277-279 281-282 285-287 290 294-295 301 305 309 311 317-318 329-330 332 334 341-344 346 350 352 361 364 368 370 373-375 377 382-385 391-394 400-401 404-406 414 418
adult kidney	Invitrogen	AKT002	4 12 21 29 32 45 48 51 67-68 75-76 80 97 103 110 120-123 137-138 144 147 153 155 157-158 169-170 179 186 188-190 194 196 212 232-233 242 264 268-269 272 274-275 284 308 341 343 346 352 357 366 385 398 405-406 414 419
adult lung	GIBCO	ALG001	2 10-11 37 50 59 69-70 75-76 80 114 118 123 133 147 149 155 157-158 166 179 181 223 242 246 264 270-271 274 277-279 289 311

TABLE 1

			332 334 337 342 370 384 394
lymph node	Clontech	ALN001	43 54 60 69 71 108 113 123 134 152 155-156 181 212 222 232 270 274 281-282 294 322 337 350 366 368 380 400
young liver	GIBCO	ALV001	7 14 17 25 49 59-61 80 123 130- 131 134 145 149 153-154 166 169-171 173 179 181-182 196 200 212 231 233 261-262 272 275 286 295 344 361 364 368 373 405 408 414
adult liver	Invitrogen	ALV002	3 13 17 21 25 47-48 51 75-76 88 91 100 107 114 123 131 134 139 155 164 174 176 194 196 201 217 220 223-225 232 237 244-245 255-256 259 261 272 281-282 285-286 288 310 317 343 346 352 376 379 398 404 416
adult ovary	Invitrogen	AOV001	3-7 10-12 14 17 19-21 23 25 28- 29 31-32 37 43-45 47-48 50-51 54-55 58-61 65 67-70 72 74-82 87 91-92 98-101 103 111 113 115-116 118-120 123 128 131-133 137 139 141-145 147 149-153 155-158 160 164-167 169-173 178-179 181-182 186 188-191 194 200 204 207 209-214 218 220 222-223 227-228 231-233 235-240 242-243 246 248 251-256 259 261-262 264-265 268-279 284-288 290 294-295 298-301 303 305 307 309 311 317 321-323 325 327 332 334 337 341 344 346 350-352 354-355 366 370 374-375 377 382-385 391-397 400-403 405-406 408 412 414 418
adult placenta	Clontech	APL001	29 32 100 123 128 149 227-228 247 295 301 382
placenta	Invitrogen	APL002	20 23 43 48 110 139 232 238 253-258 261 271 352 398
adult spleen	GIBCO	ASP001	12 43 52 54-55 59-61 64 80 108 113 121-123 131 137 149 155 159 163 166 181 186 191 210-212 239 243 253-254 261 264 270 272 287 294-295 308 311 315 327 329 332 334-335 337 342 344-345 350 352 368 373 376 382 400-401
adult testis	GIBCO	ATS001	1 10-11 14 29 32 37 44 50 54-55 61 79-80 90 118-119 123 128 144-145 149 155 169-170 182 192 194 197 209 212 224 232 239-240 243 259 267-269 271 274-275 289 294-295 350 352 361 364 398 400-401 418
Genomic DNA from BAC 63I18	Research Genetics (CITB	BAC001	164

TABLE 1

	BAC Library)		
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	291
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC003	291
adult bladder	Invitrogen	BLD001	43 80 91 137 146 154 167 201 238-239 272 287 317 329 368 391-392
bone marrow	Clontech	BMD001	1-3 7 12 14 16 26 31 37 43-46 49 54 57 59-61 67-70 74-77 80 82 84 91 98-99 102 104 108 113 117-119 123 127-128 130 133 139 145 153 155 157-158 160 168-170 179 181 188 202 207-208 210-212 222 230 232 236 242 247 250 259 261 264-265 268-270 274 276-279 286 289 293-295 300 311 317 325 335 352 364 366 370 384 387 393 395-396 398 414
bone marrow	Clontech	BMD002	1-4 7 10-11 13 16 19 21 36 43- 44 48 52 54 58 60 98-99 108 110 117 123 137-138 173 179 181 230-232 242 253-254 262 268-269 272-273 281-283 292 294 314 316 347 370 383 387 393 398 405 408 414
bone marrow	Clontech	BMD007	419
adult colon	Invitrogen	CLN001	12 26 33 101 104 108 119 179 232 253-254 270 300 340 376 381 404 414
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL016	7 393 413
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL021	117 176
adult cervix	BioChain	CVX001	3 7 12 17 29 31-33 38 43 45 48 50 54-56 59 65 67-70 77 79-80 86 91 102-103 108 113 118 120- 122 125 129 133 141-144 149 153 155-158 165-166 175 179 181 194

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 1

			199-200 212-214 218 227-228 235-236 240 259 262 264 270 272 274 279 281-282 285-288 293 295 301 309-311 317-318 327 332 335 342-343 346 353 356 361 366 374-375 377 381 385 395-396 400 403 405 408 410 414 416
diaphragm	BioChain	DIA002	80 212
endothelial cells	Strategene	EDT001	1 3-4 7 10-12 14 16 20-21 24 28-29 32 38 43-44 47-52 54-55 58-61 74-77 86 91-92 97 103 113 115-116 123 128 130 139 141-147 149 152 155-158 160 166 169-170 172-173 179 181 186 189-191 207 210-212 214 218-219 223 231-233 236 238-239 246 253-259 261-262 264 268-273 276 279 281-282 284-288 294-295 298 301 303 305 312 314-315 335 341 343-346 349 351-352 361 365 368 370 373-375 377 380 382 393 398 401-403 405 414 418
Genomic clones from the short arm of chromosome 8	DNA from Genetic Research	EPM001	164 291
esophagus	BioChain	ESO002	20 123
fetal brain	Clontech	FBR001	82 95 152
fetal brain	Clontech	FBR004	33 81 134 150 198 304 400 407 414
fetal brain	Clontech	FBR006	3-6 12 16-20 23 37 40 43-44 48 51 54-55 59 63 69 75-76 85-86 91 93 103 105-106 109 111 113 119 129 134 141-143 156 159 165 173 177 179-181 188-191 198 202-203 210-211 230-232 238-239 253-259 262 266 268-270 272-273 275 283 287 293-294 298-300 304-306 314-315 319-322 325 330 344 368-369 383 388 393 405 407 414
fetal brain	Clontech	FBRS03	166 288 344 391-392
fetal brain	Invitrogen	FBT002	16 23 31 43 48 50 52 61 64 69 81 86 123 131 134 144 156 162 166 176 178-179 188-191 197 201 229 237-238 251 255-256 263 268-269 272-273 275 285 294-295 299 301 303 332 342 346 352 365 368 395-396 398 401-402 406
fetal heart	Invitrogen	FHR001	43 80 294
fetal kidney	Clontech	FKD001	7 45 67-69 123 133 155 157-158 166 169-170 181 196 202 207 216 218 237 246 259 261 264 270 273 277-278 294 332 387 398
fetal kidney	Clontech	FKD002	123 379
fetal kidney	Invitrogen	FKD007	81

TABLE 1

fetal lung	Clontech	FLG001	3 43 45 55 111 132-133 259 270 404
fetal lung	Invitrogen	FLG003	17 23 31 43 47 75-76 80-81 91 134 185 204-206 237 255-256 272 275 287 294-295 314 330-331 377 406
fetal lung	Clontech	FLG004	43 317
fetal liver- spleen	Soares	FLS001	1 3-8 10-14 16-17 20-23 25-29 31-32 37-38 43-45 47-48 50-60 62-63 65 67-70 74 77-79 81-82 86 88 91-93 98-99 101 105-106 110-119 121-123 127-128 130-131 133-134 136 139-143 146-148 153-156 160 163-164 166-170 172-173 175 178 181 186 189-190 196 204 207-208 212 225 227-228 230-246 249-250 252-254 257-259 261-264 268-275 277-279 281-282 285-287 290 294-295 299 301 307-309 316-318 325 327-328 332 334 337 339 341 344 346-352 364 366 368 370 372-379 382 385-386 391-393 398 401-402 404-406 410 412 414
normalized fetal liver- spleen	Soares	FLS002	1 3-4 7 10-14 16-17 20 22-23 25-26 31 37 43-45 47-48 50 54- 55 58-60 62 67-70 78 80 88-89 91-93 100-101 106 111-112 115- 117 119 123 126-128 130 132-133 136-137 140 144 148 153 157-158 165 168-170 173 175-177 179 181 186 189-190 192 194-196 199-200 202 204 209 213 217 224-225 227-228 230-242 246 248 251 253-254 259 261-262 264-265 268-269 272-273 279 281-282 285 288 290 292 294 296 299-300 307 311-312 318-320 322-328 332 334 337-338 341-343 346 348 350 361 364 366 368 370-372 376-380 382 384-387 391-392 394 398-399 402-403 406 412 414 419
fetal liver- spleen	Soares	FLS003	19 22-23 50 253-254 290 295 383 385 391-392 401 405
fetal liver	Invitrogen	FLV001	7 20 23 31 43 51 60-61 67-68 77 79 91 102 166 217-218 230 232 234 237 239 252-254 257-259 268-269 275 285 290 294-296 298 317-318 322 332 368 370 373 379 398 401 404
fetal liver	Clontech	FLV002	67-68 283
fetal liver	Clontech	FLV004	4 16 23 25 196 268-269 272 298 370 394
fetal muscle	Invitrogen	FMS001	23 52 55 58 106 110 134 154 166 177 179 189-190 193 198 203 207 229-230 233 253-254 259 290

TABLE 1

			294-295 307 317 352 368 383 390 404
fetal muscle	Invitrogen	FMS002	10-11 80 123 154 231 290 295 319-320
fetal skin	Invitrogen	FSK001	3-4 7 10-11 15 18 20-21 23 30-31 33 35 43 50 52 54 62 64 77 80 86 89 109 115-116 121-122 126 130 132 144 148 153 166 171 181 185-186 188-190 194 205-207 218 224 226-228 230 234-235 237-239 242-243 253-254 257-259 263 268-269 272 275 285 288 290 294-295 299-300 317 326-327 329 333-334 342 352 358-360 362-368 377 381-383 391-393 398 401 405 418
fetal skin	Invitrogen	FSK002	3 16 49 54 123 138 169-170 196 207 210-211 235 246 383 393 401 408
fetal spleen	BioChain	FSP001	212
umbilical cord	BioChain	FUC001	12 16 21 23 28-29 32-33 41-43 46 48 51 54-55 59 74-76 78-79 98-99 123 125 133 146 148 150 153-154 159 164 166 181-182 188 198 200 207 212 218 222 224 227-228 231 236-237 248 253-254 259 261 268-270 272 277-278 285-288 290 294-295 311 316-317 327 343-344 346-347 352 366 368-370 373 377 379 382 391-392 399-400 402 412 414 418
fetal brain	GIBCO	HFB001	1 3 7 12 14 19-21 23 31 43-45 47 50 52 54-55 58-61 63 65 74-76 80-81 86 91 94 102 105 111 115-116 118-119 121-123 128 132 137 139 141-146 149-150 153 155-159 169-170 173 179 186 188 194 198 201 207 209-211 213 218 229 232-233 236-237 246-247 253-259 261-263 265 268-275 277-279 281-282 284 286 289 293 295 299 301 309 311 314 329 332 341-342 346 349-350 364-365 368 377 379 384 388 398 400-402 405 407 414 418
macrophage	Invitrogen	HMP001	186 259 334 414
infant brain	Soares	IB2002	3 7 10-11 14-15 17 19-20 22-23 31 37 43-45 51 54-55 60-61 64-65 69 73-74 77 80 85-86 89-90 93-94 102 105 109 114 123 128 131-132 137 144-145 147 150 152-153 155-159 164-166 169-170 173-174 178 180-181 183-184 186 188-191 193-194 198 210-211 218 224 227-228 230-233 236-237 239 242 246-247 251-259 261 263-264

TABLE 1

			267-269 271 273 275 280-283 285-286 288 293 295-296 300 303-304 306 314 316-317 329-330 342 346 348-351 361 364 373-375 377 383 385 388 393 398-401 407 418-419
infant brain	Soares	IB2003	3-4 7 10-12 31 37 39 43 45 48 51 69 74 80 91 111 123 131 133 137 144-145 159 169-171 173 178 189-190 198 212 232 236 238-239 246 251-254 257-258 263 268-269 271-272 283 299 303 332 373-375 377 388-389 399 404 407
infant brain	Soares	IBM002	25 43 70 89 137 186 242 257-258 286 393
infant brain	Soares	IBS001	3 15 37 137 191 231 238 271 299 317 385 393
lung fibroblast	Strategene	LFB001	1 21 45 47 61 63 86 102 113 119 130 141-143 157-158 181 188 231 234 268-270 272 279 284 295 341 344 398 405 414
lung tumor	Invitrogen	LGT002	1 3-4 12 14 20 29 31-32 37 43- 44 47-51 54-55 59-60 62 65 67- 68 75-76 88 91 101-102 107-108 110-111 113-114 119-120 123 127 132-133 139 144-145 148 159 171 173 177 185-186 189-190 192 197 205-207 209-214 220-221 223 230 232 237-238 242 248 253-256 259 261 263-264 268-273 276-280 284-285 287 292 294-296 301 314 317 322 332 341-342 344 346 352-353 361 370 376-377 383 386-387 391-393 398 400 402 405-406 414
lymphocytes	ATCC	LPC001	21 26 37 47-48 59 86 91 102 119 123 130 144 149 155 159 178 181 186 191 207 220 229 255-256 261 271 279 288 295 300 311 319-320 329 332 350 361 366 381 383 387 402 418
leukocyte	GIBCO	LUC001	2-3 7-8 10-14 17 20-21 24 37-38 43-44 46-50 52 54 56 58-61 70 74-76 81 86 91 97-99 101 106 109-110 117-120 123 125 128-131 133 141-143 145-147 149 155-159 165-166 169-170 173 178-179 181 186 189-193 200 202-203 207 209-214 218 227-228 230-233 236-237 239 242 246-248 253-254 257-259 261-275 277-279 281-282 285-286 293-295 300 307 310-311 314 316-318 322 325 330 332 337-342 344 349-350 352 361 364 366 368 370 374-377 381 383 391-393 400-402 408 414 418

TABLE 1

leukocyte	Clontech	LUC003	21 43 60-61 92 117-119 179 181 186 200 218 230-231 264 270 274 277-278 294 308 350 414
melanoma from cell line ATCC # CRL 1424	Clontech	MEL004	1 10-11 16 37 44 51 59 67-68 78 86 103 113-114 130 145 149 152 156 173 181 188 209-211 222 231-232 237 239 250 263-264 268-272 274 295 310 316-317 325 368 377 401 405 414
mammary gland	Invitrogen	MMG001	3 9 12 16 20 23 29 31-32 34 37 43-44 47 50-52 56 58 60-61 67- 69 75-76 79 84 86 91 98-102 108 110 114-117 119 123 126-127 129 132 134 137 147 149 152-153 156 164 168 171 173 178-181 187-190 193 196 204 209 212 214 218 223-224 229-230 232 234 237-239 243 248 252-261 263-264 266-269 271-273 275 285 287-288 290 294-296 298-299 303 310 316-317 327 329 332 341-342 344 346 349 354-356 366 368 370 381 383 385 391-392 394-396 398 402 404 406 416
induced neuron cells	Stratagene	NTD001	10-11 20-21 24 37 59 63 67-68 89 120 133 144 165 173 178-179 242 261 279 294 303 398 401 405 414
retinoid acid induced neuronal cells	Stratagene	NTR001	34 89 123 277-278 295 401
neuronal cells	Stratagene	NTU001	10-11 16 28 43 48 50 59 69 75- 76 123 128 156 179 229 232-233 261 268-269 287 295 311 385 393 418
pituitary gland	Clontech	PIT004	3 7 22-23 26 75-76 111 141-143 286
placenta	Clontech	PLA003	224
prostate	Clontech	PRT001	62 64 91 98-99 102 129 133 139 148-149 152 154-155 172 186 192 213 233 253-254 262 270 274 295 303 350 364 382 414 418
rectum	Invitrogen	REC001	3 33 43 50 69 74 91 95 108 132 134 169-170 181 194 208 230-231 234 242 253-258 261 263 266 270 285 288 298 308 317 336-337 394
salivary gland	Clontech	SAL001	12 26 44 47 49 51 54-55 59 79 91 108 111 123 132 134 212-213 229 237-238 250 253-254 295 311 352 381 383 390 394 401
saliva gland	Clontech	SALS03	37 261
skin fibroblast	ATCC	SFB001	166
skin fibroblast	ATCC	SFB002	341
small	Clontech	SIN001	12 22 24 31 37-38 41-43 46 49

TABLE 1

intestine			86 115-116 120 133 149 166 169-170 174 196 209 230-231 238 250 253-254 263 275 295 364 384 386-387 410 414
skeletal muscle	Clontech	SKM001	59 75-76 123 154 238 271 274 311 345 366 390
spinal cord	Clontech	SPC001	23 26 29 32 37 43 47 55 58-59 80 98-99 102 104 115-116 119-120 133-135 137 144 146 149 152 157-158 173 186 188 207 231 236 255-256 262 270 274 281-282 284 309 316 364 368 382 389 393-394 414
adult spleen	Clontech	SPLc01	14 52 80 110 207 261 368
stomach	Clontech	STO001	31 47 74 80 102 110 132 145 149 176 179 230 294 310 316 322 401 418
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP002	33 45 48 110 370 388 398 400-401 414
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP005	16 347 383
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP008	163 402
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP009	43 370
thalamus	Clontech	THA002	23 33 49 51 69 73 84-86 95 115-116 134 152 155 176 191 198 221 263 266 273 275 284 295-296 311 329 389
thymus	Clontech	THM001	3 7 14 16 21 27 37-38 44 47 60-61 69 72 84 101 149 157-158 166 173 181 186 200 207 209 218 227-228 232 236 249 259 262 273 295 337 368 374-376 381 393 419
thymus	Clontech	THMc02	3-4 7-8 12-13 16-17 21-22 31 36-38 44 49 51 60 63 75-76 86 89 91 98-99 103 106 111 113 118 123 128 130 134 139-140 155 157-158 160 166 171 175 177 181 191 200 203 210-211 213 215-219 230-232 235 239 248 250-251 253-259 262 264-265 270-272 276

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 1

			279 281-282 292 296 298 308 322 325 330 337 339-346 350 366 370 373 381 393 399 402 413-415
thyroid gland	Clontech	THR001	3 7 22 26 30-31 36 43 47 50-51 54-55 58-61 65 71 74-76 78-80 89 98-102 111 115-117 123 127- 128 130-133 139 141-145 149-150 154-155 166-167 171-174 181 186 189-190 194 200 207 209 212-213 222 230 233 237-239 243 248 250 257-258 261 268-272 276-279 284 286 293-295 311-312 317-322 327 335 339 341-344 349 352 368 377 383 393 395-396 400 403 405 412 414 418-419
trachea	Clontech	TRC001	1 62 75-76 115-116 149 151 153 230 236 261 264 284 294 341 344 364 377 391-392
uterus	Clontech	UTR001	33 43 48-49 52 55 60 74 80 83 86 89 111 123 134 139 157-158 175 181 229 268-270 287 294-295 325 414

TABLE 2

SEQ ID NO	CORRESPONDING SEQ ID NO. IN U.S.S.N. 09/560,875	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	44	AL137294	Homo sapiens hypothetical protein	469	95
2	50	AJ271684	Homo sapiens myeloid DAP12-associating lectin	1013	100
3	93	AL133589	Homo sapiens hypothetical protein	2707	99
4	224	U51730	Murine leukemia virus reverse transcriptase	316	43
5	318	AB033027	Homo sapiens KIAA1201 protein	3847	100
6	318	AB033027	Homo sapiens KIAA1201 protein	3809	99
7	795	AF161432	Homo sapiens HSPC314	1059	93
8	857	AB029488	Homo sapiens C11orf21	758	99
9	924	AJ251024	Homo sapiens putative odorant binding protein ag	1239	100
10	944	AK001284	Homo sapiens unnamed protein product	2410	97
11	944	AK001284	Homo sapiens unnamed protein product	2410	97
12	967	AE003799	Drosophila melanogaster CG5323 gene product	288	40
13	1055	AF197927	Homo sapiens AF5q31 protein	3992	99
14	1091	D28500	Homo sapiens mitochondrial isoleucine tRNA synthetase	4286	98
15	1225	X97868	Homo sapiens arylsulphatase	3141	98
16	1257	AL162048	Homo sapiens hypothetical protein	1532	100
17	1289	AL137657	Homo sapiens hypothetical protein	586	100
18	1292	AL137662	Homo sapiens hypothetical protein	1339	99
19	1455	M15888	Bos taurus endozepine-related protein precursor	2425	85
20	1488	X66363	Homo sapiens serine/threonine protein kinase	2562	100
21	1666	AE003606	Drosophila melanogaster CG1078 gene product	412	30
22	1811	AF100772	Homo sapiens tenascin-M1	11535	99
23	1885	AF090934	Homo sapiens PRO0518	382	100
24	1911	AB021643	Homo sapiens	2761	99

TABLE 2

			gonadotropin inducible transcription repressor-3		
25	1935	Z83123	Caenorhabditis elegans T04A11.2	315	50
26	1971	AF070666	Homo sapiens Kruppel-associated box protein	466	97
27	1989	AK000137	Homo sapiens unnamed protein product	925	99
28	2041	A58331	Homo sapiens unnamed protein product	1126	61
29	2178	AF227906	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 2 precursor	7820	99
30	2237	AF118566	Mus musculus hematopoietic zinc finger protein	1769	92
31	2279	AK000619	Homo sapiens unnamed protein product	810	100
32	2338	AF227906	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 2 precursor	7820	99
33	2351	AF117946	Homo sapiens Link guanine nucleotide exchange factor II	2363	100
34	2405	AB032997	Homo sapiens KIAA1171 protein	2946	99
35	2531	AB032971	Homo sapiens KIAA1145 protein	2290	100
36	2584	AE003453	Drosophila melanogaster CG15670 gene product	352	37
37	2608	AF177388	Homo sapiens cancer-amplified transcriptional coactivator ASC-2	10748	99
38	2655	AJ002744	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7	3469	96
39	2656	AF097366	Homo sapiens cone sodium-calcium potassium exchanger	3166	100
40	2866	AB032958	Homo sapiens KIAA1132 protein	9116	100
41	3015	AB018299	Homo sapiens KIAA0756 protein	4445	99
42	3015	AB018299	Homo sapiens KIAA0756 protein	4408	98
43	3043	X13916	Homo sapiens LDL-receptor related precursor (AA -19 to 4525)	4292	99
44	3986	AF151083	Homo sapiens HSPC249	444	98

TABLE 2

45	4647	AB017026	Mus musculus oxysterol-binding protein	2173	98
46	4659	D87077	Homo sapiens KIAA0240	5024	100
47	5032	AK001862	Homo sapiens unnamed protein product	954	100
48	5244	AB033010	Homo sapiens KIAA1184 protein	2024	100
49	5268	D86971	Homo sapiens no similarities to reported gene products	840	45
50	5281	AE001691	Thermotoga maritima conserved hypothetical protein	307	40
51	5282	AF174602	Homo sapiens F-box protein Fbx22	391	93
52	6147	Z50853	Homo sapiens CLPP	615	100
53	6178	M20153	Rattus norvegicus cytochrome c oxidase subunit VIc	81	55
54	6184	X03475	Rattus norvegicus ribosomal protein L35a (aa 1-110)	576	99
55	6187	AB029025	Homo sapiens KIAA1102 protein	4394	100
56	6190	U20239	Mus musculus fibrosin	288	76
57	6191	AF125101	Homo sapiens HSPC040 protein	70	100
58	6194	AB018333	Homo sapiens KIAA0790 protein	6546	100
59	6196	X54326	Homo sapiens glutaminyl-tRNA synthetase	7577	99
60	6201	X61585	Bos taurus polynucleotide adenylyltransferase	3715	97
61	6208	AB040921	Homo sapiens KIAA1488 protein	4418	99
62	6214	AC006370	Homo sapiens testis-specific basic protein Y 1	87	50
63	6217	AE003585	Drosophila melanogaster CG17652 gene product	400	40
64	6220	AJ245922	Homo sapiens alpha-tubulin 8	2370	100
65	6221	AB029001	Homo sapiens KIAA1078 protein	4418	100
66	6222	Z97653	Homo sapiens c380A1.2.1 (novel protein (isoform 1))	1567	100
67	6223	AJ404326	Homo sapiens SR+89	1871	99
68	6223	AJ404326	Homo sapiens SR+89	902	64
69	6226	AF134726	Homo sapiens G9A	5334	99
70	6227	AE003538	Drosophila melanogaster CG10191	358	44

TABLE 2

			gene product		
71	6229	M15530	Homo sapiens B-cell growth factor	89	40
72	6248	S67970	Homo sapiens ZNF75=KRAB zinc finger	951	76
73	6260	L28035	Mus musculus protein kinase C gamma	3768	98
74	6264	U16359	Rattus norvegicus nitric oxide synthase	91	58
75	6269	AK000566	Homo sapiens unnamed protein product	1053	100
76	6269	AK000566	Homo sapiens unnamed protein product	537	100
77	6275	X61118	Homo sapiens TTG-2a/RBTN-2a	876	100
78	6276	Z96932	Homo sapiens nuclear autoantigen fo 14 kDa	496	83
79	6280	AJ277291	Homo sapiens HELG protein	678	72
80	6287	X82157	Homo sapiens hevin	3525	99
81	6290	AC007192	Homo sapiens P85B_HUMAN; PTDINS-3-KINASE P85-BETA	3825	99
82	6293	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1713	51
83	6305	AF084464	Rattus norvegicus GTP-binding protein REM2	141	30
84	6308	AL049795	Homo sapiens dJ622L5.2 (novel protein)	1756	98
85	6309	D00189	Rattus norvegicus Na+,K+-ATPase alpha-subunit	4269	99
86	6312	U33460	Homo sapiens DNA-directed RNA polymerase I, largest subunit	8777	98
87	6314	D87076	Homo sapiens similar to human bromodomain protein BR140 (JC2069)	3067	100
88	6316	L43912	Macaca mulatta mannose-binding protein A	589	93
89	6336	AB018341	Homo sapiens KIAA0798 protein	1224	52
90	6341	U70976	Homo sapiens arrestin	2068	99
91	6343	U80931	Caenorhabditis elegans strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases	1049	46
92	6346	AE003435	Drosophila melanogaster CG3016 gene product	240	36
93	6357	AB037860	Homo sapiens KIAA1439	2670	99

TABLE 2

			protein		
94	6359	AL354615	Homo sapiens hypothetical protein	2418	100
95	6367	AE003789	Drosophila melanogaster CG15234 gene product	66	40
96	6383	AC006729	Caenorhabditis elegans Hypothetical protein Y24D9A.e	120	31
97	6385	AF070530	Homo sapiens unknown	2227	99
98	6396	AJ133352	Homo sapiens ZNF237 protein	2006	100
99	6396	AJ133352	Homo sapiens ZNF237 protein	1025	96
100	6403	AF170708	Homo sapiens T-box protein TBX3	3700	99
101	6405	AK002080	Homo sapiens unnamed protein product	1546	99
102	6414	L32977	Homo sapiens Rieske Fe-S protein	1239	93
103	6418	AL080125	Homo sapiens hypothetical protein	1652	56
104	6422	AJ271671	Homo sapiens IRT1 protein	432	36
105	6425	AB006631	Homo sapiens The human homolog of mouse Cux-2	6559	100
106	6436	AF067165	Homo sapiens zinc finger protein 3	977	64
107	6471	AF038169	Homo sapiens unknown	154	38
108	6474	X57817	Homo sapiens immunoglobulin lambda light chain	947	79
109	6482	U97002	Caenorhabditis elegans similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1	583	37
110	6504	AL031282	Homo sapiens dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins)	1041	99
111	6510	M93134	Friend murine leukemia virus pol protein	289	45
112	6515	AF055473	Homo sapiens GAGE-8	232	47
113	6529	X07383	Sus scrofa	60	38

TABLE 2

			preproendothelin (AA - 19 to 184)		
114	6535	S79410	Mus musculus nuclear localization signal binding protein	99	42
115	6536	AB020710	Homo sapiens KIAA0903 protein	4919	100
116	6536	AB020710	Homo sapiens KIAA0903 protein	3334	75
117	6541	AE003492	Drosophila melanogaster CG1998 gene product	799	47
118	6542	D38552	Homo sapiens The ha1539 protein is related to cyclophilin.	2995	100
119	6547	AF272981	Homo sapiens cytosolic aminopeptidase P	3305	100
120	6548	AJ224747	Homo sapiens C-terminal variant of hINADL including 2 amino acid exchanges and an insertion of 28 amino acids in frame.	7969	100
121	6552	AL080063	Homo sapiens hypothetical protein	1354	100
122	6552	AL080063	Homo sapiens hypothetical protein	998	98
123	6555	X63526	Homo sapiens homologue to elongation factor 1-gamma from A.salina	2273	99
124	6560	X15940	Homo sapiens ribosomal protein L31 (AA 1-125)	644	100
125	6566	M60832	Homo sapiens alpha-2 type VIII collagen	3581	99
126	6576	AF039697	Homo sapiens antigen NY-CO-31	1213	97
127	6584	AF156929	Sus scrofa inflammatory response protein 6	1588	83
128	6588	AF264717	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2	5610	99
129	6589	AF044578	Homo sapiens putative DNA polymerase; POL4P	2478	94
130	6590	X89750	Homo sapiens TGIF protein	1413	100
131	6597	M93107	Homo sapiens (R)-3-hydroxybutyrate dehydrogenase	1663	96
132	6600	AB018314	Homo sapiens KIAA0771 protein	4930	99
133	6602	AF151538	Homo sapiens deoxycytidyl transferase; Rev1p	4281	99

TABLE 2

134	6604	AB020716	Homo sapiens KIAA0909 protein	6344	99
135	6605	AJ243874	Homo sapiens oligophrenin-4	3682	100
136	6608	Z11737	Homo sapiens flavin-containing monooxygenase 4	2969	100
137	6610	AB002318	Homo sapiens KIAA0320	4639	99
138	6614	AJ245600	Homo sapiens hypothetical protein	2616	99
139	6623	AK001447	Homo sapiens unnamed protein product	1024	100
140	6629	AB006624	Homo sapiens KIAA0286	2246	99
141	6631	X90530	Homo sapiens ragB	1926	99
142	6631	X90530	Homo sapiens ragB	1405	99
143	6631	X90530	Homo sapiens ragB	1893	96
144	6632	AL022394	Homo sapiens dJ511B24.3 (KIAA0395 (probable Zinc Finger Homeobox protein))	4990	99
145	6633	Y11395	Homo sapiens seventransmembrane-domain protein	2168	100
146	6634	AJ010119	Homo sapiens Ribosomal protein kinase B (RSK-B)	4001	100
147	6635	AL080157	Homo sapiens hypothetical protein	2278	100
148	6639	X54131	Homo sapiens protein-tyrosine phosphatase	10465	99
149	6649	AK001972	Homo sapiens unnamed protein product	1665	100
150	6651	AC004142	Homo sapiens similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906)	3676	100
151	6655	AL117544	Homo sapiens hypothetical protein	1226	100
152	6658	AF203032	Homo sapiens neurofilament protein	5115	99
153	6667	AL034417	Homo sapiens bK215D11.2 (similar to rat gene 33)	2476	100
154	6672	X69090	Homo sapiens 190kD protein	7546	99
155	6682	AB032957	Homo sapiens KIAA1131 protein	5395	100
156	6683	AK000486	Homo sapiens unnamed protein product	801	100
157	6687	U39045	Rattus norvegicus cytoplasmic dynein	3241	97

TABLE 2

			intermediate chain 2B		
158	6687	AF063231	Mus musculus cytoplasmic dynein intermediate chain 2	3159	97
159	6688	AF202893	Mus musculus Kif21b	4336	95
160	6696	Y13115	Homo sapiens serine/threonine protein kinase	5071	99
161	6701	AB030207	Homo sapiens G gamma subunit	364	100
162	6707	AL133030	Homo sapiens hypothetical protein	6174	99
163	6712	AB037883	Homo sapiens Gb3/CD77 synthase	1916	99
164	6714	D90868	Escherichia coli similar to	1489	100
165	6720	X98834	Homo sapiens zinc finger protein Hsa12	5290	100
166	6721	D80007	Homo sapiens similar to hypothetical protein YM9959.11C of S.cerevisiae.	9568	100
167	6722	AF019926	Mus musculus protein kinase	1694	90
168	6736	M34513	Homo sapiens omega protein	317	91
169	6740	Y08612	Homo sapiens 88kDa nuclear pore complex protein	2313	99
170	6740	Y08612	Homo sapiens 88kDa nuclear pore complex protein	1561	99
171	6760	AB018310	Homo sapiens KIAA0767 protein	2968	100
172	6775	AF186249	Homo sapiens six transmembrane epithelial antigen of prostate	1790	100
173	6784	AB029012	Homo sapiens KIAA1089 protein	4933	100
174	6793	AB026893	Homo sapiens vascular cadherin-2	5962	100
175	6795	X74331	Homo sapiens DNA primase (p58 subunit)	1720	100
176	6796	AC002391	Arabidopsis thaliana hypothetical protein	72	30
177	6807	AC007228	Homo sapiens R31665_2	1488	48
178	6808	X14830	Homo sapiens acetylcholine receptor beta-subunit preprotein	2639	100
179	6810	U80446	Caenorhabditis elegans coded for by C. elegans cDNA yk172e6.3; coded for by C. elegans cDNA	420	40

TABLE 2

			yk158f7.3; coded for by C. elegans cDNA yk158f7.5; coded for by C. elegans cDNA yk172e6.5		
180	6815	AB002360	Homo sapiens KIAA0362	5766	99
181	6819	Z82215	Homo sapiens dJ6802.2 (myosin, heavy polypeptide 9, non- muscle)	9828	100
182	6821	AC004010	Homo sapiens similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	2723	100
183	6827	AJ269537	Homo sapiens chondroitin-4- sulfotransferase	557	40
184	6829	X99688	Homo sapiens TYL	3326	99
185	6830	U90305	Homo sapiens iroquois- class homeodomain protein IRX-3	1022	99
186	6835	AF180473	Homo sapiens Not2p	2267	100
187	6848	AB029009	Homo sapiens KIAA1086 protein	4798	99
188	6849	AF023453	Homo sapiens actin- related protein 3-beta	2219	100
189	6851	AB020699	Homo sapiens KIAA0892 protein	3222	100
190	6851	AC003030	Homo sapiens R29828_1	2294	100
191	6863	AB020630	Homo sapiens KIAA0823 protein	2159	100
192	6869	AK001387	Homo sapiens unnamed protein product	1255	99
193	6874	D63484	Homo sapiens The KIAA0150 gene product is novel.	4940	99
194	6887	Y07595	Homo sapiens transcription factor TFIIH	2373	100
195	6890	AF143321	Homo sapiens unknown	918	95
196	6894	X83618	Homo sapiens hydroxymethylglutaryl- CoA synthase	2647	100
197	6899	AF134726	Homo sapiens NG37	4359	99
198	6900	AB035356	Homo sapiens neurexin I-alpha protein	6948	99
199	6903	Z68005	Caenorhabditis elegans F59F3.4	67	37
200	6910	AB018323	Homo sapiens KIAA0780 protein	5220	99
201	6913	AB043634	Homo sapiens PAR-6A	885	100
202	6918	AP000693	Homo sapiens partial CDS	4875	99
203	6923	AF002223	Homo sapiens	3490	100

TABLE 2

			myotubularin related 1		
204	6926	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	1611	100
205	6929	AB002355	Homo sapiens KIAA0357	10119	100
206	6929	AF257737	Homo sapiens ciliary dynein heavy chain 9	11126	99
207	6932	X65873	Homo sapiens kinesin heavy chain	4860	100
208	6941	AL080159	Homo sapiens hypothetical protein	1942	100
209	6951	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	2782	99
210	6954	X71125	Homo sapiens glutaminyl-peptide cyclotransferase	1914	100
211	6954	X71125	Homo sapiens glutaminyl-peptide cyclotransferase	1456	97
212	6956	X54304	Homo sapiens myosin regulatory light chain	897	100
213	6957	AB007883	Homo sapiens KIAA0423	8621	99
214	6960	AK000432	Homo sapiens unnamed protein product	1622	100
215	6966	AF039563	Mus musculus retinoblastoma binding protein	792	94
216	6968	AL117352	Homo sapiens dJ876B10.2 (novel protein (ortholog of rat EXO84))	3713	99
217	6969	AF228603	Homo sapiens pleckstrin 2	1841	100
218	6970	AL117455	Homo sapiens hypothetical protein	4598	100
219	6971	AK002077	Homo sapiens unnamed protein product	989	100
220	6989	AF156271	Homo sapiens RING finger protein terf	476	40
221	6990	AC005551	Homo sapiens R26529_2, partial CDS	1020	100
222	6994	AL080129	Homo sapiens hypothetical protein	3789	99
223	6996	AE003603	Drosophila melanogaster CG1172 gene product	512	54
224	6997	AB002379	Homo sapiens KIAA0381	4437	99
225	7009	U03399	Homo sapiens T-complex protein 10A	846	77
226	7016	AB014091	Xenopus laevis alpha-1-antiprotease	850	42
227	7023	AB029040	Homo sapiens KIAA1117 protein	7032	99
228	7023	AL121716	Homo sapiens	6329	99

TABLE 2

			dJ202D23.2 (novel protein)		
229	7035	X92715	Homo sapiens KRAB /C2H2 zinc finger protein	3102	97
230	7038	X54637	Homo sapiens protein tyrosine kinase	5564	98
231	7039	AB007925	Homo sapiens KIAA0456 protein	5491	99
232	7040	AJ251245	Rattus norvegicus SECIS binding protein 2	3086	72
233	7041	AF113125	Homo sapiens E-1 enzyme	581	100
234	7044	M19529	Sus scrofa follistatin A	1906	98
235	7059	AB040902	Homo sapiens KIAA1469 protein	3403	100
236	7060	D87685	Homo sapiens similar to human transcription factor TFIIS (S34159).	8083	99
237	7063	AB029334	Halocynthia roretzi HrPET-1	638	35
238	7067	AK001603	Homo sapiens unnamed protein product	2079	99
239	7070	D86973	Homo sapiens similar to Yeast translation activator GCN1 (P1:A48126)	12033	99
240	7071	AL034452	Homo sapiens dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
241	7079	AF088219	Homo sapiens lysozyme homolog	307	42
242	7085	AF007872	Homo sapiens torsinB	1277	98
243	7148	U94586	Homo sapiens NADH:ubiquinone oxidoreductase MLRQ subunit	277	66
244	7156	U28486	Mus musculus proline-rich acidic protein	313	48
245	7156	U28486	Mus musculus proline-rich acidic protein	297	47
246	7171	AF022770	Mus musculus peripheral benzodiazepine receptor associated protein; PBR associated protein; PAP7	2078	91
247	7241	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006),	2685	99

TABLE 2

			AA823760 (NID:g2893628), AA215791 (NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)		
248	7265	AB037756	Homo sapiens KIAA1335 protein	3590	99
249	7268	AF070447	Homo sapiens barrier- to-autointegration factor	290	90
250	7308	AB020719	Homo sapiens KIAA0912 protein	6488	100
251	7336	X79828	Mus musculus NK10	202	53
252	7347	AB004109	Cricetulus griseus phosphatidylserine synthase II	2262	92
253	7405	AB028972	Homo sapiens KIAA1049 protein	2866	99
254	7405	AB028972	Homo sapiens KIAA1049 protein	2754	97
255	7412	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	2850	100
256	7412	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	2530	100
257	7436	X82260	Homo sapiens RanGAP1	2929	100
258	7436	X82260	Homo sapiens RanGAP1	1843	97
259	7454	AF160909	Drosophila melanogaster BcDNA.LD03471	943	59
260	7476	AF225324	Centrocercus urophasianus gag polyprotein	94	33
261	7598	X74801	Homo sapiens gamma subunit of CCT chaperonin	2745	99
262	7619	AL031427	Homo sapiens dJ167A19.1 (novel protein)	1608	100
263	7644	AF258614	Canis familiaris vacuolar proton-ATPase subunit ATP6H	345	72
264	7648	X16396	Homo sapiens precursor polypeptide (AA -29 to 315)	1749	100
265	7659	AK000281	Homo sapiens unnamed protein product	1814	99
266	7661	AB011128	Homo sapiens KIAA0556	5761	99

TABLE 2

			protein		
267	7669	AL050284	Homo sapiens hypothetical protein	2857	100
268	7686	D26068	Homo sapiens KIAA0038	1208	100
269	7686	AF045555	Homo sapiens wbscr1 alternative spliced product	1318	100
270	7694	U22229	Felis catus ribosomal protein L41	128	100
271	7697	Y17169	Homo sapiens A6 related protein	1819	100
272	7733	Y12065	Homo sapiens hNop56	2956	99
273	7734	AF177758	Homo sapiens ubiquitin specific protease 16	2998	100
274	7744	AB020681	Homo sapiens KIAA0874 protein	3090	100
275	7751	AL050297	Homo sapiens hypothetical protein	1227	99
276	7756	AC007204	Homo sapiens BC273239_1	3398	99
277	7761	Z68747	Homo sapiens imogen 38	2024	99
278	7761	Z68747	Homo sapiens imogen 38	1958	97
279	7776	AK001467	Homo sapiens unnamed protein product	3416	99
280	7783	AF095687	Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x	409	100
281	7800	AF119664	Homo sapiens transcriptional regulator protein HCNGP	1574	100
282	7800	AF119664	Homo sapiens transcriptional regulator protein HCNGP	1150	89
283	7801	Y17849	Homo sapiens ganglioside-induced differentiation associated protein 1	1839	98
284	7811	X55740	Homo sapiens 5'-nucleotidase	3012	100
285	7817	AF039688	Homo sapiens antigen NY-CO-3	931	100
286	7821	AL050282	Homo sapiens hypothetical protein	2424	100
287	7822	AB007836	Homo sapiens Hic-5	2544	100
288	7841	AB002301	Homo sapiens KIAA0303	11166	100
289	7847	U32305	Caenorhabditis elegans B0336.11 gene product	233	26
290	7880	AF078844	Homo sapiens hqp0376 protein	416	81
291	7910	U28377	Escherichia coli ORF_f239; was ORF_f191 and ORF_f194 before	1198	100

TABLE 2

			splice		
292	7925	AL122047	Homo sapiens hypothetical protein	404	100
293	7936	AL080123	Homo sapiens hypothetical protein	3321	99
294	7945	U58682	Homo sapiens ribosomal protein S28	340	100
295	7948	X57432	Rattus rattus ribosomal protein S2	1520	98
296	7963	AB002348	Homo sapiens KIAA0350 protein	5186	99
297	7984	AC000098	Arabidopsis thaliana YUP8H12.9	37	46
298	7985	AF110645	Homo sapiens candidate tumor suppressor p33 ING1 homolog	843	69
299	8014	AB011168	Homo sapiens KIAA0596 protein	6279	99
300	8025	AJ237839	Homo sapiens hypothetical protein	11699	99
301	8029	AP001633	Oryza sativa ESTs AU083470 (E11568), C20136 (E11568) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence; unknown protein (AC003028)	424	43
302	8043	AL163201	Homo sapiens tensin, putative protein-tyrosine phosphatase, EC 3.1.3.48	74	35
303	8164	AC002550	Homo sapiens Unknown gene product	858	99
304	8175	U26592	Homo sapiens diabetes mellitus type I autoantigen	253	66
305	8250	X60155	Homo sapiens zinc finger 41	4349	100
306	8253	X53330	Platynereis dumerilii H4 protein (AA 1 - 103)	523	100
307	8255	AC003682	Homo sapiens R27945_2	2558	100
308	8258	X80473	Mus musculus rab19	596	56
309	8270	J02649	Rattus norvegicus unknown protein	201	95
310	8271	AC006014	Homo sapiens similar to RFP transforming protein; similar to P14373 (PID:g132517)	1331	99
311	8272	X92972	Homo sapiens protein phosphatase 6	1666	100
312	8279	L35269	Homo sapiens zinc	2803	99

TABLE 2

			finger protein		
313	8284	AC003682	Homo sapiens F18547_1	3184	96
314	8285	X79204	Homo sapiens ataxin-1	4195	99
315	8304	X17620	Homo sapiens Nm23 protein	965	99
316	8309	AB029004	Homo sapiens KIAA1081 protein	2362	100
317	8320	Z56281	Homo sapiens interferon regulatory factor 3	2331	100
318	8331	Z73906	Caenorhabditis elegans Similarity to B.subtilis YQJC protein (TR:G1303954)-cDNA EST EMBL:T01187 comes from this gene	470	70
319	8332	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	8819	99
320	8332	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	8589	97
321	8335	AF153450	Manduca sexta juvenile hormone esterase binding protein	225	32
322	8337	AF227198	Homo sapiens CDC2-related protein kinase 7	7231	99
323	8353	X99586	Homo sapiens SMT3C protein	441	87
324	8355	Y18198	Homo sapiens ONECUT-2 transcription factor (OC-2)	2592	100
325	8358	AK001550	Homo sapiens unnamed protein product	3654	99
326	8361	AF139471	Homo sapiens putative calcium-activated potassium channel regulatory subunit	1385	100
327	8369	AL110479	Caenorhabditis elegans predicted using Genefinder-cDNA EST yk524f8.5 comes from this gene-cDNA EST yk631e2.5 comes from this gene-cDNA EST EMBL:C08367 comes from this gene-cDNA EST yk524f8.3 comes from this gene	709	48
328	8385	AF007826	Homo sapiens bax epsilon	133	66
329	8397	AE003544	Drosophila melanogaster CG11712 gene product	514	47
330	8414	AE003536	Drosophila melanogaster CG17365	267	35

TABLE 2

			gene product		
331	8431	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	8569	99
332	8433	AF203687	Homo sapiens prolactin regulatory element-binding protein	2181	100
333	8444	M27685	Mus musculus ultra-high sulphur keratin	650	59
334	8446	U04968	Cricetulus griseus nucleotide excision repair protein	3712	97
335	8460	AF188181	Homo sapiens G-protein gamma 12 subunit	356	100
336	8478	AF117587	Manduca sexta unknown	255	74
337	8490	X67699	Homo sapiens CDw52 antigen	297	100
338	8505	AF022789	Homo sapiens ubiquitin hydrolyzing enzyme I	1892	100
339	8523	AJ001006	Mus musculus EMeg32 protein	938	96
340	8530	U31332	Homo sapiens DP prostanoid receptor	1467	100
341	8533	AF019661	Mus musculus zeta proteasome chain; PSMA5	1214	100
342	8534	AF156557	Homo sapiens stomatin related protein	2036	100
343	8536	AK000438	Homo sapiens unnamed protein product	593	100
344	8537	AF161512	Homo sapiens HSPC163	738	100
345	8543	AL031115	Homo sapiens ZXDA, ZXDB (zinc finger X-linked protein)	4298	100
346	8546	L40410	Homo sapiens thyroid receptor interactor	806	100
347	8553	AC004542	Homo sapiens OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308)	2533	99
348	8556	AB002298	Homo sapiens KIAA0300	8265	99
349	8561	AE003691	Drosophila melanogaster CG5276 gene product	875	53
350	8562	AK000051	Homo sapiens unnamed protein product	1613	100
351	8569	U10362	Homo sapiens GP36b glycoprotein	790	57
352	8587	AL133506	Unknown /prediction=(method:"genscan", version:"1.0", score:"109.13"); /prediction=(method:	825	48
353	8597	X61001	Gallus gallus lysozyme	422	42

TABLE 2

354	8610	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	1190	100
355	8610	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	937	95
356	8615	AJ242832	Homo sapiens calpain	3756	100
357	8622	S52624	Homo sapiens orf 5' of PAF receptor	185	100
358	8626	AF005081	Homo sapiens skin-specific protein	652	100
359	8628	Y16793	Homo sapiens keratin, type I	2232	100
360	8629	AF005080	Homo sapiens skin-specific protein	438	73
361	8630	AK001429	Homo sapiens unnamed protein product	682	99
362	8632	AF005080	Homo sapiens skin-specific protein	375	62
363	8634	Y16132	Homo sapiens CDT6	1874	100
364	8643	D64048	Rattus norvegicus phosphatidylinositol 3-kinase p45 subunit	2347	97
365	8644	X63422	Homo sapiens H(+)-transporting ATP synthase	209	100
366	8645	M73837	Homo sapiens modulator recognition factor 2	1284	100
367	8646	X52563	Bos taurus permability increasing protein	383	29
368	8657	X82385	Homo sapiens RNA polymerase II subunit	429	95
369	8661	AJ245586	Homo sapiens KRAB protein domain	396	98
370	8670	AF223466	Homo sapiens HT015 protein	1311	97
371	8692	AF250878	Salmonella typhi plasmid maintenance protein	50	40
372	8698	AF117383	Homo sapiens placental protein 13; PP13	746	100
373	8762	AK000192	Homo sapiens unnamed protein product	1446	99
374	8768	AK001715	Homo sapiens unnamed protein product	715	99
375	8768	AL163815	Arabidopsis thaliana putative protein	302	67
376	8799	AL031685	Homo sapiens dJ963K23.2 (novel protein)	343	48
377	8806	AB023191	Homo sapiens KIAA0974 protein	2953	100
378	8809	AL031778	Homo sapiens dJ34B21.1 (novel BZRP	920	100

TABLE 2

			(benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)		
379	8814	AL021939	Homo sapiens dJ352A20.2 (aldehyde dehydrogenase family protein)	1764	100
380	8822	AB037784	Homo sapiens KIAA1363 protein	1895	98
381	8833	Y08565	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	3331	99
382	8835	AB037755	Homo sapiens KIAA1334 protein	1655	100
383	8877	AB037811	Homo sapiens KIAA1390 protein	1563	99
384	8886	AK000767	Homo sapiens unnamed protein product	2470	100
385	9003	AF178432	Homo sapiens SH3 protein	3302	100
386	9157	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	893	95
387	9175	AF015454	Xenopus laevis ER1	1716	80
388	9205	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit	2352	99
389	9260	X89480	Sus scrofa transmembrane protein	601	80
390	9295	AB027003	Mus musculus protein phosphatase	378	84
391	9307	AF112200	Homo sapiens NADH-oxidoreductase B18 subunit	739	100
392	9307	AF112200	Homo sapiens NADH-oxidoreductase B18 subunit	613	88
393	9312	AL133565	Homo sapiens hypothetical protein	6331	100
394	9347	AE003511	Drosophila melanogaster CG14194 gene product	825	48
395	9370	L27479	Homo sapiens X123	1237	99
396	9370	L27479	Homo sapiens X123	1206	97
397	9382	AF182066	Mus musculus Bv8 variant 3 precursor	293	51
398	9591	AJ001019	Homo sapiens ring finger protein	1292	99
399	9650	X68453	Sus scrofa tubulin-	1882	94

TABLE 2

			tyrosine ligase		
400	9655	AK001723	Homo sapiens unnamed protein product	624	56
401	9663	AF151069	Homo sapiens HSPC235	1694	96
402	9715	AF043695	Caenorhabditis elegans Similar to mitochondrial carrier protein	556	43
403	9755	AK000149	Homo sapiens unnamed protein product	2589	99
404	9766	AF130979	Homo sapiens SH3 domain-containing protein 6511	2249	99
405	9771	AL008635	Homo sapiens dJ510H16.2 (high-mobility group protein 2-like 1)	3026	99
406	9784	AL137593	Homo sapiens hypothetical protein	1124	100
407	9925	AF111179	Rattus norvegicus G-septin alpha	1739	98
408	9970	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	2371	95
409	9997	Z19585	Homo sapiens thrombospondin-4	4239	100
410	10008	AB033053	Homo sapiens KIAA1227 protein	1857	100
411	10010	AC005534	Homo sapiens supported by human ESTs AA412402 (NID:g2070990) NH44021 (NID:g1182549), mouse EST AA065933 (NID:g1562789), and genscan	756	100
412	10023	AF090326	Mus musculus AE-1 binding protein AEBP2	1540	97
413	10043	U39412	Homo sapiens alpha SNAP	879	81
414	10093	AC003007	Homo sapiens Unknown gene product (partial)	649	96
415	10172	U66372	Bos taurus ribosomal protein S29	230	73
416	10184	AB032910	Hylobates muelleri dopamine receptor D4	83	46
417	10205	AF225903	Homo sapiens D1 dopamine receptor interacting protein calcyon	1152	100
418	10246	AE003486	Drosophila melanogaster CG1749 gene product	1291	65
419	10298	X92666	Bos taurus cysteine string protein	1085	98

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 - 419, a mature protein coding portion of SEQ ID NO: 1 - 419, an active domain of SEQ ID NO:1 - 419, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 - 419.

5

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

10

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

15

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

20

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

25

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

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16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-419, a mature protein coding portion of SEQ ID NO: 1-419, an active domain of SEQ ID NO: 1-419, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-419, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

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21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

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22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 - 419.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

15

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

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26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

ABSTRACT OF THE INVENTION

The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

5

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren, Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T. Drmanac

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

 X is attached hereto.

 was filed on [date] as Application Serial Number []
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS
09/560,875	April 27, 2000	Pending
09/496,914	February 03, 2000	Pending

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Petrina S. Hsi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Xue, Aidong J.
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Gly Gly His Leu Arg Met Ile Lys Arg Val Gln Asn Leu Leu Gly His		
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Tyr Leu Ile His Gly Phe Arg Val Arg Pro Glu Pro Asn Gly Asp Leu		
93 98 103 108		
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Asp Leu Glu Ala Met Val Ala Val Phe Gly Ser Lys Gly Leu Arg Val		
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Val Lys Ile Ser Trp Gly Gln Gly His Phe Trp Glu Leu Trp Arg Ser		
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Gly Leu Trp Asn Met Ser Asp Trp Ile Trp Asp Ala Arg Trp Leu Glu		
141 146 151 156		
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Gly Asn Ile Ala Leu Ala Leu Gly His Asn Ser Val Val Leu Tyr Asp		
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Pro Val Val Gly Cys Ile Leu Gln Glu Val Pro Cys Thr Asp Arg Cys		
173 178 183 188		
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Leu Leu Ala Thr Ala	Ser Glu Asp Arg Ser	Val Arg Ile Trp Lys	Val	
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Gly Asp Leu Arg Val	Pro Gly Gly Arg Val	Gln Asn Ile Gly His	Cys	
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Phe Gly His Ser Ala	Arg Val Trp Gln Val	Lys Leu Leu Glu Asn	Tyr	
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317	322	327	332	
gcc ata gct gcc cat	gag agg cag gcc tgg	gtg atc act ggg ggt	gat	1057
Ala Ile Ala Ala His	Glu Arg Gln Ala Trp	Val Ile Thr Gly Gly	Asp	
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Asp Ser Gly Ile Arg	Leu Trp His Leu Val	Gly Arg Gly Tyr Arg	Gly	
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Leu Lys Ala Val Thr	Leu Ala Gly Ser Trp	Arg Leu Leu Ala Val	Thr	
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Asp Thr Gly Ala Leu	Tyr Leu Tyr Asp Val	Glu Val Lys Cys Trp	Glu	
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Gln Leu Leu Glu Asp	Lys His Phe Gln Ser	Tyr Cys Leu Leu Glu	Ala	
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gct cct ggt ccc gag	ggc ttc gga ttg tgt	gct atg gcc aat ggg	gaa	1345
Ala Pro Gly Pro Glu	Gly Phe Gly Leu Cys	Ala Met Ala Asn Gly	Glu	
429	434	439	444	

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Gly Arg Val Lys Val Val Pro Ile Asn Thr Pro Thr Ala Ala Val Asp	
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Gln Thr Leu Phe Pro Gly Lys Val His Ser Leu Ser Trp Ala Leu Arg	
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Gly Tyr Glu Glu Leu Leu Leu Leu Ala Ser Gly Pro Gly Gly Val Val	
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Val Pro Asp Gly Ser Met Val Ile Leu Gly Phe His Ala Asn Glu Phe	
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Val Val Trp Asn Pro Arg Ser His Glu Lys Leu His Ile Ile Asn Cys	
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Glu Tyr Gly Val Pro Ser Phe Met Gln Pro Asp Asp Leu Glu Pro Gly	
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Ser Glu Gly Pro Asp Leu Thr Asp Ile Val Ile Thr Cys Ser Glu Asp	
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Thr Thr Val Cys Val Leu Ala Leu Pro Thr Thr Thr Gly Ser Ala His	
717 722 727 732	
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Phe Ser Ile Met Val Thr Pro Asp Pro Ser Thr Pro Ser Arg Leu Ala	
781 786 791 796	
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Cys His Val Met His Leu Ser Ser His Arg Leu Asp Glu Tyr Trp Asp	
797 802 807 812	
cgg caa cgc aat cgg cat cgg atg gtt aag gta gac cca gag acc agg	2497
Arg Gln Arg Asn Arg His Arg Met Val Lys Val Asp Pro Glu Thr Arg	
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Tyr Met Ser Leu Ala Val Cys Glu Leu Asp Gln Pro Gly Leu Gly Pro	
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Leu Val Ala Ala Ala Cys Ser Asp Gly Ala Val Arg Leu Phe Leu Leu	
845 850 855 860	
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Gln Asp Ser Gly Arg Ile Leu Gln Leu Leu Ala Glu Thr Phe His His	
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Lys Arg Cys Val Leu Lys Val His Ser Phe Thr His Glu Ala Pro Asn	
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Asn Trp Tyr Asp *	
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Met Asn Cys Thr Leu Lys
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Asn Thr Leu Thr Lys Leu Ile Leu Glu Thr Gly Val Asn Cys Val Ser
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Leu Leu Pro Leu Ala Leu Leu Arg Val Arg Cys Thr Pro Tyr Trp Ala
23 28 33 38
ggg ttc tta cct ttt gaa atc atg tat ggg agg gcg ctg cct atc ttg 498
Gly Phe Leu Pro Phe Glu Ile Met Tyr Gly Arg Ala Leu Pro Ile Leu
39 44 49 54
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Pro Lys Leu Arg Asp Ala Gln Leu Ala Lys Ile Ser Gln Thr Asn Leu
55 60 65 70
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Leu Gln Tyr Leu Gln Ser Pro Gln Gln Val Gln Asp Ile Ile Leu Pro
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87 92 97 102

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Cys His Ser Phe Pro Pro Gly Asp Leu Leu Phe Val Lys Lys Phe Gln	
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Arg Glu Gly Leu Pro Pro Ala Trp Lys Arg Pro His Thr Val Ile Thr	
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Met Pro Thr Ala Leu Lys Val Asp Gly Ile Pro Ala Trp Ile His His	
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151 156 161 166	
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Arg Ala Gly Ser Gly Pro Leu Lys Leu His Leu Ser Trp Val Lys Pro	
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Leu Asp *	
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Met Lys Gly
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Phe Lys Leu Ser Cys Thr Ala Ser Asn Ser Asn Arg Ser Thr Pro Ala
4 9 14 19

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Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn
20 25 30 35

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Gln Asp Gly Asp Thr Met Val Glu Lys Gly Ser Asp His Ser Ser Asp
36 41 46 51

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Lys Ser Pro Ser Thr Pro Glu Gln Gly Val Gln Arg Ser Cys Ser Ser
52 57 62 67

cag tcc ggc cgg agc ggc ggc aag aat tcc aag aaa agc cag agt tgg 595
Gln Ser Gly Arg Ser Gly Gly Lys Asn Ser Lys Lys Ser Gln Ser Trp
68 73 78 83

tat aat gtg tta agc ccc acc tac aag cag aga aat gaa gac ttc aga 643
Tyr Asn Val Leu Ser Pro Thr Tyr Lys Gln Arg Asn Glu Asp Phe Arg
84 89 94 99

aag ctc ttt aag cag ctt cca gac acg gag cgc ctc att gtt gat tac 691
Lys Leu Phe Lys Gln Leu Pro Asp Thr Glu Arg Leu Ile Val Asp Tyr
100 105 110 115

tca tgt gca ctc caa aga gac att ctc ctt cag ggc cga ctc tac ctc 739
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116 121 126 131

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132 137 142 147

ctg ctg aca gtc cgt ttg aaa gac atc tgt tcc atg act aaa gaa aaa 835
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148 153 158 163

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Lys	His	Phe	Phe	Thr	Ser	Phe	Gly	Ala	Arg	Asp	Arg	Thr	Tyr	Met	Met	
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Met	Phe	Arg	Leu	Trp	Gln	Asn	Ala	Leu	Leu	Glu	Lys	Pro	Leu	Cys	Pro	
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Pro Asn Gly Phe His Leu Gln Ser Val Ser Lys Leu Leu Leu Val Ile							
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Met Lys Gly

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Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn	
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Gln Asp Gly Asp Thr Met Val Glu Lys Gly Ser Asp His Ser Ser Asp	
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Lys Ser Pro Ser Thr Pro Glu Gln Gly Val Gln Arg Ser Cys Ser Ser	
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Gln Ser Gly Arg Ser Gly Gly Lys Asn Ser Lys Lys Ser Gln Ser Trp	
68 73 78 83	
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Tyr Asn Val Leu Ser Pro Thr Tyr Lys Gln Arg Asn Glu Asp Phe Arg	
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Ser Cys Ala Leu Gln Arg Asp Ile Leu Leu Gln Gly Arg Leu Tyr Leu	
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Thr Met Gly Tyr Cys Glu Glu Ile Pro Val Glu Glu Asn Glu Val Asn				
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Ile Met Gly Glu Lys Ile Glu Met Ile Ala Pro Val Asn Ser Pro Ser				
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Lys Lys Lys Glu Gln Ser Glu Val Ser Val Ser Pro Arg Ala Ser Lys	
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Gly Arg Arg His Glu Ser Lys Asp Lys Ser Ser Lys Lys His Lys Ser	
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118 123 128 133	
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374	389
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390	405
gct cag tat gaa atg gca aga tca caa acc cac aca caa aga gga atg	1423
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Arg Pro Gly Arg Arg Ser Ala Val Pro Arg Trp Pro His Leu Ser Ser
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Pro Ser Arg Asp Gln Glu Ala Pro Gly Ser Met Met Pro Pro Ala Ala
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Ala Gln Pro Ser Ala His Gly Ala Leu Val Pro Pro Ala Thr Ala His
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Glu Pro Val Asp His Pro Ala Leu His Trp Leu Ala Cys Cys Cys Cys
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125          130

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                                         Met Lys Thr Leu Phe Leu
                                         1

ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc ttc acc ctg gag gag      160
Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu Glu Glu
  7                      12                      17                      22

gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc gat aag      208
Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val Asp Lys
  23                      28                      33                      38

gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg aag gtg      256
Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val Lys Val
  39                      44                      49                      54

aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc atg agg      304
Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe Met Arg
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gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg gag gag      352
Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu
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cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac ctg cag      400
Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr Leu Gln
  87                      92                      97                      102

gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac cag cgc      448
Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp Gln Arg
  103                      108                      113                      118

cgt ggg ggc ctg cgc tac atg gga aag ctt gtg gca tct gct ccc tgc      496
Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Ala Ser Ala Pro Cys
  119                      124                      129                      134

agg gcc gtg ccg ctg tcc cca cgt cgg ctc acc tgg cca cct cac ctg      544
Arg Ala Val Pro Leu Ser Pro Arg Arg Leu Thr Trp Pro Pro His Leu
  135                      140                      145                      150

cag gta gga atc cta ata cca acc tgg agg ccc tgg aag aat tta aga      592
Gln Val Gly Ile Leu Ile Pro Thr Trp Arg Pro Trp Lys Asn Leu Arg
  151                      156                      161                      166

aat tgg tgc agc aca agg gac tct cgg agg agg aca ttt tca tgc ccc      640
Asn Trp Cys Ser Thr Arg Asp Ser Arg Arg Arg Thr Phe Ser Cys Pro

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167	172	177	182	
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Cys Arg Arg Glu Ala	Ala Phe Ser Asn Thr	Arg Gln Pro Pro Gly Leu		
183	188	193	198	
cac ctc cag agc cca	ccc tac cac cag aca	cag agc ccg gac cac ctg		736
His Leu Gln Ser Pro	Pro Tyr His Gln Thr	Gln Ser Pro Asp His Leu		
199	204	209	214	
gac cta ccc tcc agc	cat gac cct tcc ctg	ctc cca ccc acc tga		781
Asp Leu Pro Ser Ser	His Asp Pro Ser Leu	Leu Pro Pro Thr *		
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Met Arg Gln Lys Arg Lys Gly Asp Leu	Ser Pro Ala Glu Leu Met Met		
1	5	10	15
ctg act ata gga gat gtt att aaa	caa ctg att gaa gcc cac gag cag		153
Leu Thr Ile Gly Asp Val Ile Lys Gln	Leu Ile Glu Ala His Glu Gln		
17	22	27	32
ggg aaa gac atc gat cta aat aag	gtg aaa acc aag aca gct gcc aaa		201
Gly Lys Asp Ile Asp Leu Asn Lys Val	Lys Thr Lys Thr Ala Ala Lys		
33	38	43	48
tat ggc ctt tct gcc cag ccc cgc	ctg gtg gat atc att gct gcc gtc		249
Tyr Gly Leu Ser Ala Gln Pro Arg Leu	Val Asp Ile Ile Ala Ala Val		
49	54	59	64
cct cct cag tat cgc aag gtc ttg	atg ccc aag tta aag gcg aaa ccc		297
Pro Pro Gln Tyr Arg Lys Val Leu Met	Pro Lys Leu Lys Ala Lys Pro		
65	70	75	80
atc aga act gct agt ggg att gct	gtc gtg gct gtg atg tgc aaa ccc		345
Ile Arg Thr Ala Ser Gly Ile Ala Val	Val Ala Val Met Cys Lys Pro		
81	86	91	96
cac aga tgt cca cac atc agt ttt	aca gga aat ata tgt gta tac tgc		393
His Arg Cys Pro His Ile Ser Phe Thr	Gly Asn Ile Cys Val Tyr Cys		
97	102	107	112

cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act	441
Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr	
113 118 123 128	
ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct	489
Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro	
129 134 139 144	
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Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His	
145 150 155 160	
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc	585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala	
161 166 171 176	
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc	633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala	
177 182 187 192	
tta tca gga cat act tcc aac aat att tac gag gca gtc aag tat tct	681
Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser	
193 198 203 208	
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca	729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
209 214 219 224	
gat tac tgc atg aag cga cat tta agt gac atg ttg acc tat ggc tgc	777
Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys	
225 230 235 240	
aca agg ctg gag att ggg gtg cag agt gtt tat gaa gat gtg gct aga	825
Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg	
241 246 251 256	
gac acc aac agg ggc cac act gtg aag gca gtg tgt gag tca ttt cac	873
Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
257 262 267 272	
ctg gcc aaa gat tcc ggt ttt aaa gtg gtg gcc cat atg atg cct gac	921
Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp	
273 278 283 288	
ctg cca aac gtg gga cta gaa aga gac att gaa cag ttc aca gag ttt	969
Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe	
289 294 299 304	
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Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr	
305 310 315 320	
ctg gtg att cgt ggg acc ggg ctt tat gag ctt tgg aaa tca gga aga	1065
Leu Val Ile Arg Gly Thr Gly Leu Tyr Glu Leu Trp Lys Ser Gly Arg	
321 326 331 336	
gat aag agt tac tct cct agt gac ctg gtt gaa ttg gtg gct cgg atc	1113

Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
337 342 347 352	
cta gcc ctc gtg cct cca tgg act cga gtg tac cga gta cag agg gat	1161
Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	
353 358 363 368	
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Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg	
369 374 379 384	
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Glu Leu Ala Leu Ala Arg Met Lys Asp Leu Gly Ile Gln Cys Arg Asp	
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Val Arg Thr Arg Glu Val Gly Ile Gln Glu Ile His His Lys Val Arg	
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Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly	
417 422 427 432	
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Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro Asp Gln Asp Ile Leu Ile	
433 438 443 448	
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449 454 459 464	
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Leu Gly Gly Gly Val Ser Ile Val Arg Glu Leu His Val Tyr Gly Ser	
465 470 475 480	
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Val Val Pro Val Ser Ser Arg Asp Pro Thr Lys Phe Gln His Gln Gly	
481 486 491 496	
ttt ggc atg ctg ctg atg gag gaa gca gaa aga ata gct aga gaa gaa	1593
Phe Gly Met Leu Leu Met Glu Glu Ala Glu Arg Ile Ala Arg Glu Glu	
497 502 507 512	
cat ggg tct ggg aaa atc gct gtg ata tca gga gtg gat gtc ctg ggg	1641
His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Asp Val Leu Gly	
513 518 523 528	
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Gln Arg Gln Arg Gly Gly His His Arg Ser Cys Ser Leu *	
529 534 539	
gcaaggggtc ggcaccagga attattatag aaagatcggc tacagattac aaggcccgtg	1750
catggtgaag atgctgaaat aatggccaca ccagtccact cttctgcagt atcctccctg	1810
gcagaacacg gagaatcagg atttcttaaa tactcaacag agaggctgag cagagcaa	1870

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Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Glu Leu Met Met
1 5 10 15

ctg act ata gga gat gtt att aaa caa ctg att gaa gcc cac gag cag 153
Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
17 22 27 32

ggg aaa gac atc gat cta aat aag gtg aaa acc aag aca gct gcc aaa 201
Gly Lys Asp Ile Asp Leu Asn Lys Val Lys Thr Lys Thr Ala Ala Lys
33 38 43 48

tat ggc ctt tct gcc cag ccc cgc ctg gtg gat atc att gct gcc gtc 249
Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
49 54 59 64

cct cct cag tat cgc aag gtc ttg atg ccc aag tta aag gcg aaa ccc 297
Pro Pro Gln Tyr Arg Lys Val Leu Met Pro Lys Leu Lys Ala Lys Pro
65 70 75 80

atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc 345
Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro
81 86 91 96

cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc 393
His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys
97 102 107 112

cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act 441
Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr
113 118 123 128

ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct 489

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Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro	
129 134 139 144	
ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat	537
Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His	
145 150 155 160	
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc	585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala	
161 166 171 176	
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc	633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala	
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Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser	
193 198 203 208	
gag aga agc ctc aca aag tgt att gga att act att gaa acc aga cca	729
Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
209 214 219 224	
gat tac tgc atg aag cga cat tta agt gac atg ttg acc tat ggc tgc	777
Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys	
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Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg	
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Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
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Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp	
273 278 283 288	
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Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe	
289 294 299 304	
ttt gag aac cct gct ttt cgt ccc gat ggg ctg aaa ctc tat cct acc	1017
Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr	
305 310 315 320	
ctg gtg att cgt ggg acc ggg ctt tat gag ctt tgg aaa tca gga aga	1065
Leu Val Ile Arg Gly Thr Gly Leu Tyr Glu Leu Trp Lys Ser Gly Arg	
321 326 331 336	
gat aag agt tac tct cct agt gac ctg gtt gaa ttg gtg gct cgg atc	1113
Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
337 342 347 352	
cta gcc ctc gtg cct cca tgg act cga gtg tac cga gta cag agg gat	1161
Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	

353	358	363	368	
att cca atg cct tta gtt agc tca gga gta		gag cat ggt aac ctg aga		1209
Ile Pro Met Pro Leu Val Ser Ser Gly Val		Glu His Gly Asn Leu Arg		
369	374	379	384	
gag ctg gca ctt gca aga atg aaa gac ctc		gga ata cag tgt cga gat		1257
Glu Leu Ala Leu Ala Arg Met Lys Asp Leu		Gly Ile Gln Cys Arg Asp		
385	390	395	400	
gtg aga acc aga gaa gtt gga atc caa gaa		att cat cac aaa gta cgg		1305
Val Arg Thr Arg Glu Val Gly Ile Gln Glu		Ile His His Lys Val Arg		
401	406	411	416	
cca tac cag gtt gaa ttg gta agg aga gat		tat gtt gca aat ggt ggc		1353
Pro Tyr Gln Val Glu Leu Val Arg Arg Asp		Tyr Val Ala Asn Gly Gly		
417	422	427	432	
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Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro		Asp Gln Asp Ile Leu Ile		
433	438	443	448	
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Gly Leu Leu Arg Leu Arg Lys Cys Ser Glu		Glu Thr Phe Arg Phe Glu		
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Leu Gly Gly Gly Val Ser Ile Val Arg Glu		Leu His Val Tyr Gly Ser		
465	470	475	480	
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Val Val Pro Val Ser Ser Arg Asp Pro Thr		Lys Phe Gln His Gln Gly		
481	486	491	496	
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Phe Gly Met Leu Leu Met Glu Glu Ala Glu		Arg Ile Ala Arg Glu Glu		
497	502	507	512	
cat ggg tct ggg aaa atc gct gtg ata tca		ggg gtc ggc acc agg aat		1641
His Gly Ser Gly Lys Ile Ala Val Ile Ser		Gly Val Gly Thr Arg Asn		
513	518	523	528	
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Tyr Tyr Arg Lys Ile Gly Tyr Arg Leu Gln		Gly Pro Tyr Met Val Lys		
529	534	539	544	
atg ctg aaa taa tgg ccacaccagt ccactcttct		gcagtatcct ccctggcaga		1744
Met Leu Lys *				
545				
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ataaaaactga ttgtcattcg aaaaaaaaaa aa 2076

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Met Ala Glu Leu Gln Gln Leu Arg Val Gln Glu Ala Val
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gag tcc atg gtg aag agt ctg gaa aga gag aac atc cgg aag atg cag 157
Glu Ser Met Val Lys Ser Leu Glu Arg Glu Asn Ile Arg Lys Met Gln
14 19 24 29

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Gly Leu Met Phe Arg Cys Ser Ala Ser Cys Cys Glu Asp Ser Gln Ala
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tcc atg aag cag gtg cac cag tgc atc gag cgc tgc cat gtg cct ctg 253
Ser Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu
46 51 56 61

gct caa gcc cag gct ttg gtc acc agt gag ctg gag aag ttc cag gac 301
Ala Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp
62 67 72 77

cgc ctg gcc cgg tgc acc atg cat tgc aac gac aaa gcc aaa gat tca 349
Arg Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser
78 83 88 93

ata gat gct ggg agt aag gag ctt cag gtg aag cag cag ctg gac agt 397
Ile Asp Ala Gly Ser Lys Glu Leu Gln Val Lys Gln Gln Leu Asp Ser
94 99 104 109

tgt gtg acc aag tgt gtg gat gac cac atg cac ctc atc cca act atg 445
Cys Val Thr Lys Cys Val Asp Asp His Met His Leu Ile Pro Thr Met
110 115 120 125

acc aag aag atg aag gag gct ctc tta tca att gga aaa taa aagtatt 494
Thr Lys Lys Met Lys Glu Ala Leu Leu Ser Ile Gly Lys *
126 131 136

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Met Asn Arg Glu Asp Arg Asn Val Leu Arg Met Lys Glu Arg Glu Arg	
1 5 10 15	
cggaatcag gaa att cag cag ggc gaa gac gcc ttc cca cct agc tct	155
Arg Asn Gln Glu Ile Gln Gln Gly Glu Asp Ala Phe Pro Pro Ser Ser	
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tgc tac ggc aat gac acc atg agg acg cct cac atc gac cgc ctt gcc 251
Cys Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala
47 52 57 62

agg gaa ggc gtg cga ctg act cag cac atc tct gcc gcc tcc ctc tgc 299
Arg Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
63 68 73 78

agc cca agc cgg tcc gcg ttc ttg acg gga aga tac ccc atc cga tca 347
Ser Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser
79 84 89 94

ggg atg gtt tct agt ggt aat aga cgt gtc atc caa aat ctt gca gtc 395
Gly Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val
95 100 105 110

ccc gca ggc ctc cct ctt aat gag aca aca ctt gca gcc ttg cta aag 443
Pro Ala Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Ala Leu Leu Lys
111 116 121 126

aag caa gga tac agc acg ggg ctt ata ggc aaa tgg cac caa ggc ttg 491
Lys Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu
127 132 137 142

aac tgc gac tcc cga agt gac cag tgc cac cat cca tat aat tat ggg 539
Asn Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly
143 148 153 158

ttt gac tac tac tat ggc atg ccg ttc act ctc gtt gac agc tgc tgg 587
Phe Asp Tyr Tyr Tyr Gly Met Pro Phe Thr Leu Val Asp Ser Cys Trp
159 164 169 174

ccg gac ccc tct cgt aac acg gaa tta gcc ttt gag agt cag ctc tgg 635
Pro Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp
175 180 185 190

ctc tgt gtg cag cta gtt gcc att gcc atc ctc acc cta acc ttt ggg 683
Leu Cys Val Gln Leu Val Ala Ile Ala Ile Leu Thr Leu Thr Phe Gly
191 196 201 206

aag ctg agc ggc tgg gtc tct gtt ccc tgg ctc ctg atc ttc tcc atg	731
Lys Leu Ser Gly Trp Val Ser Val Pro Trp Leu Leu Ile Phe Ser Met	
207 212 217 222	
att ctg ttt att ttc ctc ttg ggc tat gct tgg ttc tcc agc cac acg	779
Ile Leu Phe Ile Phe Leu Leu Gly Tyr Ala Trp Phe Ser Ser His Thr	
223 228 233 238	
tcc cct tta tac tgg gac tgc ctc ctc atg cgg ggg cac gag atc acg	827
Ser Pro Leu Tyr Trp Asp Cys Leu Leu Met Arg Gly His Glu Ile Thr	
239 244 249 254	
gag cag ccc atg aag gct gaa cga gct gga tcc att atg gtg aag gaa	875
Glu Gln Pro Met Lys Ala Glu Arg Ala Gly Ser Ile Met Val Lys Glu	
255 260 265 270	
gcg att tcc ttt tta gaa agg cac agt aag gaa act ttc ctt ctc ttt	923
Ala Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe	
271 276 281 286	
ttc tcc ttt ctt cac gtg cac aca cct ctc ccc acc acg gac gat ttc	971
Phe Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe	
287 292 297 302	
act ggc acc agc aag cat ggc ttg tat ggg gat aat gtg gaa gag atg	1019
Thr Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met	
303 308 313 318	
gac tcc atg gtg ggc aag att ctt gat gct atc gat gat ttt ggc cta	1067
Asp Ser Met Val Gly Lys Ile Leu Asp Ala Ile Asp Asp Phe Gly Leu	
319 324 329 334	
agg aac aac acc ctt gtc tac ttt aca tca gat cac gga ggg cat ttg	1115
Arg Asn Asn Thr Leu Val Tyr Phe Thr Ser Asp His Gly Gly His Leu	
335 340 345 350	
gaa gct agg cga ggg cat gcc caa ctt ggt gga tgg aat gga ata tac	1163
Glu Ala Arg Arg Gly His Ala Gln Leu Gly Gly Trp Asn Gly Ile Tyr	
351 356 361 366	
aaa ggt gga aaa ggc atg ggg ggc tgg gaa ggt gga atc cgc gtc cca	1211
Lys Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro	
367 372 377 382	
gga att gtc cga tgg cct gga aag gta cca gct gga cgg ttg att aag	1259
Gly Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys	
383 388 393 398	
gaa cct aca agt tta atg gat att tta cca act gtc gca tca gtg tca	1307
Glu Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser	
399 404 409 414	
gga gga agt ctc cct cag gac agg gtc att gac ggc cga gac ctc atg	1355
Gly Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met	
415 420 425 430	
ccc ttg ctg cag ggc aac gtc agg cac tcg gag cat gaa ttt ctt ttc	1403

<222> (9) .. (2255)

<400> 16

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Met Leu Gly Thr Leu Arg Ala Met Glu Gly Glu Asp Val Glu	
1 5 10	
gac gac cag ctg ctg cag aag ctc agg gcc agt cgc cgc cgc ttc cag	98
Asp Asp Gln Leu Leu Gln Lys Leu Arg Ala Ser Arg Arg Arg Phe Gln	
15 20 25 30	
agg cgc atg cag cgg ctg ata gag aag tac aac cag ccc ttc gag gac	146
Arg Arg Met Gln Arg Leu Ile Glu Lys Tyr Asn Gln Pro Phe Glu Asp	
31 36 41 46	
acc ccg gtg gtg caa atg gcc acg ctg acc tac gag acg cca cag gga	194
Thr Pro Val Val Gln Met Ala Thr Leu Thr Tyr Glu Thr Pro Gln Gly	
47 52 57 62	
ttg aga att tgg ggt gga aga cta ata aag gaa aga aac gaa gga gag	242
Leu Arg Ile Trp Gly Gly Arg Leu Ile Lys Glu Arg Asn Glu Gly Glu	
63 68 73 78	
atc cag gac tcc tcc atg aag ccc gcg gac agg aca gat ggc tcc gtg	290
Ile Gln Asp Ser Ser Met Lys Pro Ala Asp Arg Thr Asp Gly Ser Val	
79 84 89 94	
caa gct gca gcc tgg ggt cct gag ctt ccc tcg cac cgc aca gtc ctg	338
Gln Ala Ala Ala Trp Gly Pro Glu Leu Pro Ser His Arg Thr Val Leu	
95 100 105 110	
gga gcc gat tca aaa agc ggt gag gtc gat gcc acg tca gac cag gaa	386
Gly Ala Asp Ser Lys Ser Gly Glu Val Asp Ala Thr Ser Asp Gln Glu	
111 116 121 126	
gag tca gtt gct tgg gcc tta gca cct gca gtg cct caa agc cct ttg	434
Glu Ser Val Ala Trp Ala Leu Ala Pro Ala Val Pro Gln Ser Pro Leu	
127 132 137 142	
aaa aat gaa tta aga agg aaa tac ttg acc caa gtg gat ata ctg cta	482
Lys Asn Glu Leu Arg Arg Lys Tyr Leu Thr Gln Val Asp Ile Leu Leu	
143 148 153 158	
caa ggt gca gag tat ttt gag tgt gca ggt aac aga gct gga agg gat	530
Gln Gly Ala Glu Tyr Phe Glu Cys Ala Gly Asn Arg Ala Gly Arg Asp	
159 164 169 174	
gta cgt gtg act ccg ctg cct tca ctg gcc tca cct gcc gtg cct gcc	578
Val Arg Val Thr Pro Leu Pro Ser Leu Ala Ser Pro Ala Val Pro Ala	
175 180 185 190	
ccc gga tac tgc agt cgt atc tcc aga aag agt cct ggt gac cca gcg	626
Pro Gly Tyr Cys Ser Arg Ile Ser Arg Lys Ser Pro Gly Asp Pro Ala	
191 196 201 206	
aaa cca gct tca tct ccc aga gaa tgg gat cct ttg cat cct tcc tcc	674
Lys Pro Ala Ser Ser Pro Arg Glu Trp Asp Pro Leu His Pro Ser Ser	

207	212	217	222	
aca gac atg gcc tta gta cct aga aat gac agc ctc tcc cta caa gag				722
Thr Asp Met Ala Leu Val Pro Arg Asn Asp Ser Leu Ser Leu Gln Glu				
223	228	233	238	
acc agt agc agc agc ttc tta agc agc cag ccc ttt gaa gat gat gac				770
Thr Ser Ser Ser Ser Phe Leu Ser Ser Gln Pro Phe Glu Asp Asp Asp				
239	244	249	254	
att tgc aat gtg acc atc agt gac ctg tac gca ggg atg ctg cac tcc				818
Ile Cys Asn Val Thr Ile Ser Asp Leu Tyr Ala Gly Met Leu His Ser				
255	260	265	270	
atg agc cgg ctg ttg agc aca aag cca tca agc atc atc tcc acc aaa				866
Met Ser Arg Leu Leu Ser Thr Lys Pro Ser Ser Ile Ile Ser Thr Lys				
271	276	281	286	
acg ttc atc atg caa aac tgg aac tgc agg agg agg cac aga tat aag				914
Thr Phe Ile Met Gln Asn Trp Asn Cys Arg Arg Arg His Arg Tyr Lys				
287	292	297	302	
agc agg atg aac aaa aca tat tgc aaa gga gcc aga cgt tct cag agg				962
Ser Arg Met Asn Lys Thr Tyr Cys Lys Gly Ala Arg Arg Ser Gln Arg				
303	308	313	318	
agc tcc aag gag aac ttc ata ccc tgc tct gag cct gtg aaa ggg aca				1010
Ser Ser Lys Glu Asn Phe Ile Pro Cys Ser Glu Pro Val Lys Gly Thr				
319	324	329	334	
ggg gca tta aga gat tgc aag aac gta tta gat gtt tct tgc cgt aag				1058
Gly Ala Leu Arg Asp Cys Lys Asn Val Leu Asp Val Ser Cys Arg Lys				
335	340	345	350	
aca ggt tta aaa ttg gaa aaa gct ttt ctt gaa gtc aac aga ccc caa				1106
Thr Gly Leu Lys Leu Glu Lys Ala Phe Leu Glu Val Asn Arg Pro Gln				
351	356	361	366	
atc cat aag tta gat cca agt tgg aag gag cgc aaa gtg aca ccc tcg				1154
Ile His Lys Leu Asp Pro Ser Trp Lys Glu Arg Lys Val Thr Pro Ser				
367	372	377	382	
aag tat tct tcc ttg att tac ttc gac tcc agt gca aca tat aat ctt				1202
Lys Tyr Ser Ser Leu Ile Tyr Phe Asp Ser Ser Ala Thr Tyr Asn Leu				
383	388	393	398	
gat gag gaa aat aga ttt agg aca tta aaa tgg tta att tct cct gta				1250
Asp Glu Glu Asn Arg Phe Arg Thr Leu Lys Trp Leu Ile Ser Pro Val				
399	404	409	414	
aaa ata gtt tcc aga cca aca ata cga cag ggc cat gga gag aac cgt				1298
Lys Ile Val Ser Arg Pro Thr Ile Arg Gln Gly His Gly Glu Asn Arg				
415	420	425	430	
cag agg gag att gaa atc cga ttt gat cag ctt cat cgg gaa tat tgc				1346
Gln Arg Glu Ile Glu Ile Arg Phe Asp Gln Leu His Arg Glu Tyr Cys				
431	436	441	446	

ctg agt ccc agg aac cag cct cgc cgg atg tgc ctc ccg gac tcc tgg	1394
Leu Ser Pro Arg Asn Gln Pro Arg Arg Met Cys Leu Pro Asp Ser Trp	
447 452 457 462	
gcc atg aac atg tac aga ggg ggt cct gcg agt cct ggt ggc ctt cag	1442
Ala Met Asn Met Tyr Arg Gly Gly Pro Ala Ser Pro Gly Gly Leu Gln	
463 468 473 478	
ggc tta gaa acc cgc agg ctg agt tta cct tcc agc aaa gca aaa gca	1490
Gly Leu Glu Thr Arg Arg Leu Ser Leu Pro Ser Ser Lys Ala Lys Ala	
479 484 489 494	
aaa agt tta agt gag gct ttt gaa aac cta ggc aaa aga tct ctg gaa	1538
Lys Ser Leu Ser Glu Ala Phe Glu Asn Leu Gly Lys Arg Ser Leu Glu	
495 500 505 510	
gca ggt agg tgc ctg ccc aag agc gat tca tct tca tca ctt cca aag	1586
Ala Gly Arg Cys Leu Pro Lys Ser Asp Ser Ser Ser Ser Leu Pro Lys	
511 516 521 526	
acc aac ccc aca cac agc gca act cgc ccg cag cag aca tct gac ctt	1634
Thr Asn Pro Thr His Ser Ala Thr Arg Pro Gln Gln Thr Ser Asp Leu	
527 532 537 542	
cac gtt cag gga aat agt tct gga ata ttt aga aag tca gtg tca ccc	1682
His Val Gln Gly Asn Ser Ser Gly Ile Phe Arg Lys Ser Val Ser Pro	
543 548 553 558	
agc aaa act ctt tca gtc cca gat aaa gaa gtg cca ggc cac gga agg	1730
Ser Lys Thr Leu Ser Val Pro Asp Lys Glu Val Pro Gly His Gly Arg	
559 564 569 574	
aat cgt tac gat gaa att aaa gaa gaa ttt gac aag ctt cat caa aag	1778
Asn Arg Tyr Asp Glu Ile Lys Glu Glu Phe Asp Lys Leu His Gln Lys	
575 580 585 590	
tat tgc ctc aaa tct cct ggg cag atg aca gtg cct tta tgt att gga	1826
Tyr Cys Leu Lys Ser Pro Gly Gln Met Thr Val Pro Leu Cys Ile Gly	
591 596 601 606	
gtg tct aca gat aaa gca agt atg gaa gtt cga tat caa aca gaa ggc	1874
Val Ser Thr Asp Lys Ala Ser Met Glu Val Arg Tyr Gln Thr Glu Gly	
607 612 617 622	
ttc tta gga aaa tta aat cca gac cct cac ttc cag ggt ttc cag aag	1922
Phe Leu Gly Lys Leu Asn Pro Asp Pro His Phe Gln Gly Phe Gln Lys	
623 628 633 638	
ttg cca tca tca ccc ctg ggg tgc aga aaa agt cta ctg ggc tca act	1970
Leu Pro Ser Ser Pro Leu Gly Cys Arg Lys Ser Leu Leu Gly Ser Thr	
639 644 649 654	
gca att gag gct cct tca tct aca tgt gtt gct cgt gcc atc acg agg	2018
Ala Ile Glu Ala Pro Ser Ser Thr Cys Val Ala Arg Ala Ile Thr Arg	
655 660 665 670	

gat ggc acg agg gac cat cag ttc cct gca aaa aga ccc agg cta tca	2066
Asp Gly Thr Arg Asp His Gln Phe Pro Ala Lys Arg Pro Arg Leu Ser	
671 676 681 686	
gaa ccc cag ggc tcc gga cgc cag ggc aat tcc ctg ggt gcc tca gat	2114
Glu Pro Gln Gly Ser Gly Arg Gln Gly Asn Ser Leu Gly Ala Ser Asp	
687 692 697 702	
ggg gtg gac aac acc gtc aga ccg gga gac cag ggc agc tct tca cag	2162
Gly Val Asp Asn Thr Val Arg Pro Gly Asp Gln Gly Ser Ser Ser Gln	
703 708 713 718	
ccc aac tca gaa gag aga gga gag aac acg tct tac agg atg gaa gag	2210
Pro Asn Ser Glu Glu Arg Gly Glu Asn Thr Ser Tyr Arg Met Glu Glu	
719 724 729 734	
aaa agt gat ttc atg cta gaa aaa ttg gaa act aaa agt gtg tag cta	2258
Lys Ser Asp Phe Met Leu Glu Lys Leu Glu Thr Lys Ser Val *	
735 740 745	
ggttatttcg gagtgttatt tatcttccca cttgctctct gtttgtattt ttgttttgtt	2318
tttgattcct gagactgtga ggacttggtt gacttctctg cccttaaagt aaatattagt	2378
gaaatttggtt ccatcagaga taacctogag ttcttggtgt agaaattatg tgaataaagt	2438
tgctcaatta gaattttaaa aaaaaaaaaa a	2469

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 <211> 1201
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (59)..(700)

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atg gac ccg gcg ctg gca gcc caa atg agc gag gct gtg gcc gaa aag	106	
Met Asp Pro Ala Leu Ala Ala Gln Met Ser Glu Ala Val Ala Glu Lys		
1 5 10 15		
atg ctc cag tac cgg cgg gac aca gca ggc tgg aag att tgc cgg gaa	154	
Met Leu Gln Tyr Arg Arg Asp Thr Ala Gly Trp Lys Ile Cys Arg Glu		
17 22 27 32		
ggc aat gga gtt tca gtt tcc tgg agg cca tct gtg gag ttt cca ggg	202	
Gly Asn Gly Val Ser Val Ser Trp Arg Pro Ser Val Glu Phe Pro Gly		
33 38 43 48		
aac ctg tac cga gga gaa ggc att gta tat ggg aca cta gag gag gtg	250	
Asn Leu Tyr Arg Gly Glu Gly Ile Val Tyr Gly Thr Leu Glu Glu Val		
49 54 59 64		

tgg gac tgt gtg aag cca gct gtt gga ggc cta cga gtg aag tgg gat	298
Trp Asp Cys Val Lys Pro Ala Val Gly Gly Leu Arg Val Lys Trp Asp	
65 70 75 80	
gag aat gtg acc ggt ttt gaa att atc caa agc atc act gac acc ctg	346
Glu Asn Val Thr Gly Phe Glu Ile Ile Gln Ser Ile Thr Asp Thr Leu	
81 86 91 96	
tgt gta agc aga acc tcc act ccc tcc gct gcc atg aag ctc att tct	394
Cys Val Ser Arg Thr Ser Thr Pro Ser Ala Ala Met Lys Leu Ile Ser	
97 102 107 112	
ccc aga gat ttt gtg gac ttg gtg cta gtc aag aga tat gag gat ggg	442
Pro Arg Asp Phe Val Asp Leu Val Leu Val Lys Arg Tyr Glu Asp Gly	
113 118 123 128	
acc atc agt tcc aac gcc acc cat gtg gag cat ccg tta tgt ccc ccg	490
Thr Ile Ser Ser Asn Ala Thr His Val Glu His Pro Leu Cys Pro Pro	
129 134 139 144	
aag cca ggt ttt gtg aga gga ttt aac cat cct tgt ggt tgc ttc tgt	538
Lys Pro Gly Phe Val Arg Gly Phe Asn His Pro Cys Gly Cys Phe Cys	
145 150 155 160	
gaa cct ctt cca ggg gaa ccc acc aag acc aac ctg gtc aca ttc ttc	586
Glu Pro Leu Pro Gly Glu Pro Thr Lys Thr Asn Leu Val Thr Phe Phe	
161 166 171 176	
cat acc gac ctc agc ggt tac ctc cca cag aac gtg gtg gac tcc ttc	634
His Thr Asp Leu Ser Gly Tyr Leu Pro Gln Asn Val Val Asp Ser Phe	
177 182 187 192	
ttc ccc cgc agc atg acc cgg ttt tat gcc aac ctt cag aaa gca gtg	682
Phe Pro Arg Ser Met Thr Arg Phe Tyr Ala Asn Leu Gln Lys Ala Val	
193 198 203 208	
aag caa ttc cat gag taa tgctat cgttacttct tggcaaagaa ctcccgtgac	736
Lys Gln Phe His Glu *	
209 214	
tcatcgagga gctccagctg ttgggacacc aaggagcctg ggagcacgca gaggcctgtg	796
ttcactctttt ggaacaagct gatggactgc gcatctctga gaatgccaac cagaggcggc	856
agccaccct tctgctcc tgcctcctc agggttggcg tgtgatgagc cattcatgtg	916
ttccaaactc catctgctg ttacccaaac acgcctctcc tggcagggtg gaccaggcc	976
tctaaccatc tgacagagac tcggcctgga caccatgcga tgcactctgg caccaaggct	1036
ttatgtgcc atcactctca gagaccacgt ttccctgact gtcatagaga atcatcatcg	1096
ccactgaaaa ccaggccctg ttgcctttta agcatgtacc gctccctcag tctgtgtgtg	1156
cagcccccca aatatatttt tctgatatag aaaaaaaaaa aaaaa	1201

<210> 18
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (256)..(1329)

<220>
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 <222> (1)..(1501)
 <223> n = a,t,c or g

<400> 18

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ttcgcggcgc acgaggagaa gatccagacc gtgttcgagc agctggtgct ggtggaccac	120
ccgaacatcg tgaagttgca caagtactgg ctggatacct ctgaggcctg cgcgagggtc	180
atcttcatca cagagtacgt gtcatacaggc agcctcaagc aattcctcaa aaagaccaag	240
aagaaccaca aggcc atg aac gcc cgg gcc tgg aag cgc tgg tgc acg cag	291
Met Asn Ala Arg Ala Trp Lys Arg Trp Cys Thr Gln	
1 5 10	
atc ctg tct gcg ctc agc ttc ctg cac gcc tgc acc ccc cca atc atc	339
Ile Leu Ser Ala Leu Ser Phe Leu His Ala Cys Thr Pro Pro Ile Ile	
13 18 23 28	
cac ggg aac ctg acc agc gac acc atc ttc att cag cac aac ggc ctc	387
His Gly Asn Leu Thr Ser Asp Thr Ile Phe Ile Gln His Asn Gly Leu	
29 34 39 44	
atc aag atc ggc tcc gtg tgg cac cga atc ttc tcc aat gca ctt cca	435
Ile Lys Ile Gly Ser Val Trp His Arg Ile Phe Ser Asn Ala Leu Pro	
45 50 55 60	
gat gat ctc cga agc ccc atc cgc gct gag cga gag gaa ctt cgg aac	483
Asp Asp Leu Arg Ser Pro Ile Arg Ala Glu Arg Glu Glu Leu Arg Asn	
61 66 71 76	
ctg cac ttc ttc ccc cca gag tat gga gag gtg gcc gat ggg acc gct	531
Leu His Phe Phe Pro Pro Glu Tyr Gly Glu Val Ala Asp Gly Thr Ala	
77 82 87 92	
gtg gac atc ttc tcc ttt ggg atg tgt gcg ctg gag atg gct gta ctg	579
Val Asp Ile Phe Ser Phe Gly Met Cys Ala Leu Glu Met Ala Val Leu	
93 98 103 108	
gaa atc cag acc aat ggg gac acc cgg gtc aca gag gag gcc att gct	627
Glu Ile Gln Thr Asn Gly Asp Thr Arg Val Thr Glu Glu Ala Ile Ala	
109 114 119 124	

cgc gcc agg cac tcg ctg agt gac ccc aac atg cgg gag ttc atc ctt	675
Arg Ala Arg His Ser Leu Ser Asp Pro Asn Met Arg Glu Phe Ile Leu	
125 130 135 140	
tgc tgc ctg gcc cgg gac cct gcc cgc cgg ccc tct gcc cac agc ctc	723
Cys Cys Leu Ala Arg Asp Pro Ala Arg Arg Pro Ser Ala His Ser Leu	
141 146 151 156	
ctc ttc cac cgc gtg ctc ttc gag gtg cac tcg ctg aag ctc ctg gca	771
Leu Phe His Arg Val Leu Phe Glu Val His Ser Leu Lys Leu Leu Ala	
157 162 167 172	
gcc cac tgc ttc atc cag cac cag tac ctc atg cct gag aat gtg gtg	819
Ala His Cys Phe Ile Gln His Gln Tyr Leu Met Pro Glu Asn Val Val	
173 178 183 188	
gag gag aag acc aag gcc atg gac ctg cac gcg gtc ttg gcg gag ctt	867
Glu Glu Lys Thr Lys Ala Met Asp Leu His Ala Val Leu Ala Glu Leu	
189 194 199 204	
ccc cgg ccc cgc agg ccc ccg ctg cag tgg cgg tac tcg gaa gtc tcc	915
Pro Arg Pro Arg Arg Pro Pro Leu Gln Trp Arg Tyr Ser Glu Val Ser	
205 210 215 220	
ttc atg gag ctg gac aaa ttc ctg gag gat gtc agg aat gga atc tac	963
Phe Met Glu Leu Asp Lys Phe Leu Glu Asp Val Arg Asn Gly Ile Tyr	
221 226 231 236	
cca ctg atg aac ttt gca gcc act cga ccc ctg ggg ctg ccc cgt gtg	1011
Pro Leu Met Asn Phe Ala Ala Thr Arg Pro Leu Gly Leu Pro Arg Val	
237 242 247 252	
ctg gcc cca ccc ccg gag gag gtc caa aag gcc aag acc ccg acg cca	1059
Leu Ala Pro Pro Pro Glu Glu Val Gln Lys Ala Lys Thr Pro Thr Pro	
253 258 263 268	
gag ccc ttt gac tct gag acc aga aag gtc atc cag atg cag tgc aac	1107
Glu Pro Phe Asp Ser Glu Thr Arg Lys Val Ile Gln Met Gln Cys Asn	
269 274 279 284	
ctg gag aga agc gag gac aag gcg cgc tgg cat ctc act ctg ctt ctg	1155
Leu Glu Arg Ser Glu Asp Lys Ala Arg Trp His Leu Thr Leu Leu Leu	
285 290 295 300	
gtg ctg gaa gac cgg ctg cac cgg cag ctg acc tac gac ctg ctc cca	1203
Val Leu Glu Asp Arg Leu His Arg Gln Leu Thr Tyr Asp Leu Leu Pro	
301 306 311 316	
acg gac agc gcc cag gac ctc gcc tcg gag ctc gtg cac tat ggc ttc	1251
Thr Asp Ser Ala Gln Asp Leu Ala Ser Glu Leu Val His Tyr Gly Phe	
317 322 327 332	
ctc cac gag cac gac cgg atg aag ctg gcc gcc ttc ctg gag agc acc	1299
Leu His Glu His Asp Arg Met Lys Leu Ala Ala Phe Leu Glu Ser Thr	
333 338 343 348	

ttc ctc aag tac cgt ggg acc cag gcc tga c ccggagcccc agccccaggg 1350
Phe Leu Lys Tyr Arg Gly Thr Gln Ala *
349 354

gaccatgccg ggggtgctgcc cgggcaggcc atgttgggga gactccagca ccgtggggct 1410

gccctcctcc atgcgcctgg gagcacaaag gccccggtag tgaaggaacc ccccgtctcc 1470

tgagagtggg gctgaccctg ccttgggcgc c 1501

<210> 19
<211> 2510
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (362)..(1966)

<220>
<221> misc_feature
<222> (1)...(2510)
<223> n = a,t,c or g

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cggactccgg cggaatgggg ggtgtggctg ctccgccagg gtccccaggg tgggagagcg 120
gctccgcggc caccgatgcc cggacccccct ctgtcttctg ctagacatgc tcttcctctc 180
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Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln
16 21 26 31

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Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala
32 37 42 47

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Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro
48 53 58 63

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Arg	Tyr	Lys	Trp	Asp	Ala	Trp	Ser	Ser	Leu	Gly	Asp	Met	Thr	Lys	Glu	
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Glu	Ala	Met	Ile	Ala	Tyr	Val	Glu	Glu	Met	Lys	Lys	Ile	Ile	Glu	Thr	
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Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln				
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Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr				
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Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg				
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Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu				
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Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln				
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cac ttg agc gaa gga acc aag ggc cgg cag gtg gga agt gga ggt gat				1654
His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp				
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Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu				
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Gln Ile Ala Leu Val Leu Met Arg Leu Gln Asp Met Gln Asn Val				
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Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys				
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Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg				
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Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala				
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Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln				
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 15 20 25 30

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 Ile Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly Glu
 31 36 41 46

gcc ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc cca 371
 Ala Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro
 47 52 57 62

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Leu Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser	
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Ser Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser	
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Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu	
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Lys Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly	
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Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys	
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Gly Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu	
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				Met	Glu	Gln	Thr	Asp	Cys	Lys						
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Pro	Tyr	Gln	Pro	Leu	Pro	Lys	Val	Lys	His	Glu	Met	Asp	Leu	Ala	Tyr	
8					13					18					23	
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Thr	Ser	Ser	Ser	Asp	Glu	Ser	Glu	Asp	Gly	Arg	Lys	Pro	Arg	Gln	Ser	
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tac	aac	tcc	agg	gag	acc	ctg	cac	gag	tat	aac	cag	gag	ctg	agg	atg	555
Tyr	Asn	Ser	Arg	Glu	Thr	Leu	His	Glu	Tyr	Asn	Gln	Glu	Leu	Arg	Met	
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Gln Glu Met Glu Phe Cys Glu Thr Ser His Thr Leu Cys Ser Gly Tyr	
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Gln Thr Asp Met His Ser Val Ser Arg His Gly Tyr Gln Leu Glu Met	
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Gly Ser Asp Val Asp Thr Glu Thr Glu Gly Ala Ala Ser Pro Asp His	
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Glu Arg Lys Ser Asp Gly Glu Asn Gly Phe Lys Phe Ser Pro Val Cys	
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Cys Asp Met Glu Ala Gln Ala Gly Ser Thr Gln Asp Val Gln Ser Ser	
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Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala Ala Ser Gln Asn	
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Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro Pro Arg Pro Leu	
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Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe Asn Lys Pro Tyr	
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Arg Cys Cys Asn Trp Lys Cys Thr Ala Leu Ser Ala Thr Ala Ile Thr	
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Val Thr Leu Ala Leu Leu Leu Ala Tyr Val Ile Ala Val His Leu Phe	
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Gly Leu Thr Trp Gln Leu Gln Pro Val Glu Gly Glu Leu Tyr Ala Asn	
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Cys	Asn	Gly	Asn	Gly	Glu	Cys	Ile	Ser	Gly	His	Cys	His	Cys	Phe	Pro	
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Cys	Glu	Glu	Gly	Trp	Val	Gly	Pro	Thr	Cys	Glu	Glu	Arg	Ser	Cys	His	
712					717					722					727	
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Ser	His	Cys	Thr	Glu	His	Gly	Gln	Cys	Lys	Asp	Gly	Lys	Cys	Glu	Cys	

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Ala Val Arg Asp Gly Cys Pro Gly Leu Cys Phe Gly Asn Gly Arg Cys				
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Gln Gln Ser Asn Cys Tyr Ile Ser Pro Leu Cys Gln Gly Ser Pro Asp				
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Pro Leu Asp Leu Ile Gln Gln Ser Gln Thr Leu Phe Ser Gln His Thr				
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Ser Arg Leu Phe Tyr Asp Arg Ile Lys Phe Leu Ile Gly Lys Asp Ser				
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Thr His Val Ile Pro Pro Glu Val Ser Phe Asp Ser Arg Arg Ala Cys				
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Val Asn Val Ser Phe Leu His His Ser Asp Tyr Gly Phe Thr Ile Ser				
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Arg Gln Asp Gly Ser Phe Asp Leu Val Ala Ile Gly Gly Ile Ser Val				
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984 989 994 999	
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Cys Pro Glu Arg Gly Thr Ile Val Pro Glu Leu Gln Val Val Gln Glu	
1000 1005 1010 1015	
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Glu Ile Pro Ile Pro Ser Ser Phe Val Arg Leu Ser Tyr Leu Ser Ser	
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Arg Thr Pro Gly Tyr Lys Thr Leu Leu Arg Ile Leu Leu Thr His Ser	
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Thr Ser Asn Arg Glu Asn Val Leu Met Ser Thr Asn Leu Thr Ala Thr				
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Ser Thr Ile Tyr Ile Leu Lys Gln Glu Asn Thr Gln Ser Thr Tyr Arg				
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Cys Asp Ser Cys Glu Lys	Cys Leu Thr Ser Val	Ser Glu Tyr Ile Ser	
140	145	150	155
agt gat gga agc tat	gca aga atg aaa gct	gat gaa tgt agt gga tgt	652
Ser Asp Gly Ser Tyr	Ala Arg Met Lys Ala	Asp Glu Cys Ser Gly Cys	
156	161	166	171
ggg aaa tca ctc ctc	cat att aag ctt gag	aaa act cat cca gga gat	700
Gly Lys Ser Leu Leu	His Ile Lys Leu Glu	Lys Thr His Pro Gly Asp	
172	177	182	187
caa gct tat gaa ttt	aat caa aat ggg gaa	cct tat act cta aat gaa	748
Gln Ala Tyr Glu Phe	Asn Gln Asn Gly Glu	Pro Tyr Thr Leu Asn Glu	
188	193	198	203
gaa agt ctt tat cag	aaa att cgt att ttg	gag aaa cct ttt gaa tat	796
Glu Ser Leu Tyr Gln	Lys Ile Arg Ile Leu	Glu Lys Pro Phe Glu Tyr	
204	209	214	219
att gaa tgc cag aaa	gcc ttc caa aag gac	act gtt ttt gtt aat cac	844
Ile Glu Cys Gln Lys	Ala Phe Gln Lys Asp	Thr Val Phe Val Asn His	
220	225	230	235
atg gaa gaa aag ccc	tat aag tgg aat gga	tct gaa ata gcc ttt ctc	892
Met Glu Glu Lys Pro	Tyr Lys Trp Asn Gly	Ser Glu Ile Ala Phe Leu	
236	241	246	251
cag atg tcg gac ctc	act gta cat cag aca	tct cat atg gaa atg aag	940
Gln Met Ser Asp Leu	Thr Val His Gln Thr	Ser His Met Glu Met Lys	
252	257	262	267
ccc tat gaa tgc agt	gaa tgt ggg aaa tcc	ttc tgt aaa aag tca aaa	988
Pro Tyr Glu Cys Ser	Glu Cys Gly Lys Ser	Phe Cys Lys Lys Ser Lys	
268	273	278	283
ttt att ata cat cag	agg act cac aca gga	gag aaa cct tac gaa tgt	1036
Phe Ile Ile His Gln	Arg Thr His Thr Gly	Glu Lys Pro Tyr Glu Cys	
284	289	294	299
aat cag tgt ggg aaa	tcc ttc tgc cag aag	gga acc ctt act gtg cat	1084
Asn Gln Cys Gly Lys	Ser Phe Cys Gln Lys	Gly Thr Leu Thr Val His	
300	305	310	315
cag aga aca cac aca	ggg gag aag ccc tat	gaa tgt aat gaa tgt ggg	1132
Gln Arg Thr His Thr	Gly Glu Lys Pro Tyr	Glu Cys Asn Glu Cys Gly	
316	321	326	331
aag aac ttt tac cag	aag tta cac ctc att	cag cat cag aga act cac	1180
Lys Asn Phe Tyr Gln	Lys Leu His Leu Ile	Gln His Gln Arg Thr His	
332	337	342	347
tca gga gag aag ccc	tat gaa tgt agt tat	tgt gga aaa tcc ttt tgc	1228
Ser Gly Glu Lys Pro	Tyr Glu Cys Ser Tyr	Cys Gly Lys Ser Phe Cys	

348	353	358	363	
cag aag aca cac ctc	aca caa cat cag aga	aca cat tca gga gag aga		1276
Gln Lys Thr His Leu	Thr Gln His Gln Arg	Thr His Ser Gly Glu Arg		
364	369	374	379	
cct tat gtt tgt cat	gac tgt ggg aaa acc	ttc tcg cag aag tca gca		1324
Pro Tyr Val Cys His	Asp Cys Gly Lys Thr	Phe Ser Gln Lys Ser Ala		
380	385	390	395	
ctt aat gac cat cag	aaa att cac aca ggt	gtg aaa ctc tac aag tgt		1372
Leu Asn Asp His Gln	Lys Ile His Thr Gly	Val Lys Leu Tyr Lys Cys		
396	401	406	411	
agt gaa tgt ggg aaa	tgc ttc tgc cgc aag	tct act ctc acg acc cac		1420
Ser Glu Cys Gly Lys	Cys Phe Cys Arg Lys	Ser Thr Leu Thr Thr His		
412	417	422	427	
ctg agg acc cac aca	gga gag aaa ccg tat	gaa tgt aat gag tgt gga		1468
Leu Arg Thr His Thr	Gly Glu Lys Pro Tyr	Glu Cys Asn Glu Cys Gly		
428	433	438	443	
aaa gcc ttc tct cgg	atg tca tac ctc act	gta cat tat aga act cat		1516
Lys Ala Phe Ser Arg	Met Ser Tyr Leu Thr	Val His Tyr Arg Thr His		
444	449	454	459	
tca gga gag aaa ccc	tat gag tgt act gaa	tgt gga aaa aaa ttc tac		1564
Ser Gly Glu Lys Pro	Tyr Glu Cys Thr Glu	Cys Gly Lys Lys Phe Tyr		
460	465	470	475	
cac aaa tca gca ttc	aac agc cat cag aga	att cat agg aga ggc aat		1612
His Lys Ser Ala Phe	Asn Ser His Gln Arg	Ile His Arg Arg Gly Asn		
476	481	486	491	
atg aat gta ata gat	gtg gga agg ctt ctc	tga agtcagac ctcattttat		1663
Met Asn Val Ile Asp	Val Gly Arg Leu Leu	*		
492	497	502		
atcagagaac ccttttcagta tagtgaatca gaaactcctg cctgaagtca aacaccttgt				1723
acatcagaga gttcacacag gttagtgtgg acatcccctt gtgtgttgga ctcataatct				1783
gaagactcac agaatggaaa ccatgattat aacaagacca catggtataa caatactaga				1843
ctatagacaa gtaaaaattt ataaatatta agaatgtata tacatgtcac catggattgg				1903
aactgttttg catatcaggg aatatcatagc caaggggaaa tctatcagta taaggaatgt				1963
ggaagacata atccttttgg aactgttaat actaaaagat atgttttctga tacaatagca				2023
aacttgaaaa aaaaaaaaa				2041

<210> 25

<211> 1316

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (192)..(1058)

<400> 25

accggtccgg aattccccggg tcgacgattt cgtgttgagc accttcgtcg ccattggctt 60

tcctccccca gctccagcct ctctcatctt gggaatctgc gtcagaagtc actcgagtc 120

ccgtcagccc agaagacgta aagcaggcta ccagcaattt tgagaacttg caaaaacagc 180

ttgcaaggaa a atg aag ctt cct att ttc ata gca gat gca ttc aca gca 230
Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala
1 5 10

aga gca ttt cgt ggg aat cct gct gct gtt tgc ctc cta gaa aat gaa 278
Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu
14 19 24 29

ttg gat gaa gac atg cat cag aaa att gca agg gag atg aac ctc tct 326
Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser
30 35 40 45

gaa act gct ttt atc cga aaa ctg cac ccg aca gac aac ttt gca caa 374
Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln
46 51 56 61

agt tcc tgc ttt gga ctg aga tgg ttt aca cca gcg agt gag gtc cca 422
Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro
62 67 72 77

ctc tgt ggc cat gcc acc ctg gct tct gca gct gtg ctg ttt cac aaa 470
Leu Cys Gly His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys
78 83 88 93

ata aaa aac atg aat agc acg ctc acg ttt gtc act ctg agt gga gaa 518
Ile Lys Asn Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu
94 99 104 109

cta agg gcc aga cga gca gag gac ggc atc gtc ctg gac ttg cct ctt 566
Leu Arg Ala Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu
110 115 120 125

tat cca gcc cac ccc cag gac ttc cat gaa gta gag gac ttg ata aag 614
Tyr Pro Ala His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys
126 131 136 141

act gcc ata ggc aac aca ctg gtc cag gac atc tgt tat tct cca gat 662
Thr Ala Ile Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp
142 147 152 157

acc caa aag ctc ctc gtc cgc ctc agt gac gtt tac aac agg tcg ttt 710
Thr Gln Lys Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe
158 163 168 173

ctg gag aac ctg aaa gtg aac acg gag aat ctg ctg caa gtt gaa aac	758
Leu Glu Asn Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn	
174 179 184 189	
aca ggg aag gtg aaa ggg ctt att ctt acc ctt aaa gga gag cct ggt	806
Thr Gly Lys Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly	
190 195 200 205	
ggg cag acc caa gca ttt gac ttt tac tca aga tat ttt gca ccg tgg	854
Gly Gln Thr Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp	
206 211 216 221	
gtt ggt gtg gct gaa gac cca gtg aca ggg tct gca cac gct gtt ctc	902
Val Gly Val Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu	
222 227 232 237	
agc agc tac tgg tcc cag cat ctg ggg aag aaa gaa atg cat gct ttt	950
Ser Ser Tyr Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe	
238 243 248 253	
cag tgt tcc cac cga gga gga gag ctg gga att tcc ctt cgt cca gac	998
Gln Cys Ser His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp	
254 259 264 269	
gga agg gtt gac att aga gga ggt gca gct gtt gtt tta gag ggc aca	1046
Gly Arg Val Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr	
270 275 280 285	
ctg aca gcc tag agg tggttatgct gtgacgctgc tgtctctaac caccaagtat	1101
Leu Thr Ala *	
286	
tttctgctta aaaagaaatg taaggggctg ccttttagcaa atgtgcgtag tagtctactt	1161
aatcctcatg ttaaaaaatcg aaaaatgggc caggcgcagt ggctcatgcc tgtaatcgta	1221
gcactttgag aggccaaggt ggggtggatca cctgaggtca ggggttcgac accagcctgg	1281
ccaacatggt gaaacctcgt ctctataaaa aaaaa	1316

<210> 26
 <211> 685
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (172)..(456)

aagctggtac gctgcaggt accggtccgg aattcccggg tcgaccacg cgtccgctgg	60
ctttggtgat tcagccctga cttctcaaaa agcactgcac agaggaggag gcagcagaac	120

cccatttcag cttcttagga ctctgcactt cccagaagg aagaattaaa a atg aat	177
Met Asn	
1	
atg ttc aag gaa gca gtg acc ttc aag gac gtg gct gtg acc ttc acg	225
Met Phe Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Thr Phe Thr	
3 8 13 18	
gag gag gaa ttg ggg ctg ctg ggc cct gcc cag agg aag ctg tac cga	273
Glu Glu Glu Leu Gly Leu Leu Gly Pro Ala Gln Arg Lys Leu Tyr Arg	
19 24 29 34	
gat gtg atg gtg gag aac ttt agg aac ctg ctg tca gtg ggg cat cca	321
Asp Val Met Val Glu Asn Phe Arg Asn Leu Leu Ser Val Gly His Pro	
35 40 45 50	
ccc ttc aaa caa gat gta tca cct ata gaa aga aat gag cag ctt tgg	369
Pro Phe Lys Gln Asp Val Ser Pro Ile Glu Arg Asn Glu Gln Leu Trp	
51 56 61 66	
ata atg acg aca gca acc cga aga cag gga aat tta gat acc tta ctt	417
Ile Met Thr Thr Ala Thr Arg Arg Gln Gly Asn Leu Asp Thr Leu Leu	
67 72 77 82	
gta aaa gct ctt ttg ctc tat gac ctg gct caa act taa acttgattt	466
Val Lys Ala Leu Leu Leu Tyr Asp Leu Ala Gln Thr *	
83 88 93	
gaagttagaa gaaatgttgg aagtcattta tatatgaaga aatgttggaa ggactcatat	526
atgcatacat tccttgagtg actatgaatg actgccgggc agtaacttct gggctgtggg	586
tgtaaactgt gagcactaca aaatgttttt ccttattgat accatattat ggtaggaaag	646
acatggaata aaaaatttag atagtaaaaa aaaaaaaaaa	685

<210> 27
 <211> 917
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160)..(714)

<400> 27	
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ccagtaaggg tttggagtca tcagcaggtt taattttgga ggaactttac aggtttggct	120
ccagcagctg ctgttgccac caccactagt tcaagcacc atg cag ttt acc tca	174
Met Gln Phe Thr Ser	
1	

ata tca aat tct ttg acc tcc act gct gct att ggg ctc tca ttt aca	222
Ile Ser Asn Ser Leu Thr Ser Thr Ala Ala Ile Gly Leu Ser Phe Thr	
6 11 16 21	
act tca acg act acc acc gcc act ttc acc acc aac act act acc aca	270
Thr Ser Thr Thr Thr Thr Ala Thr Phe Thr Thr Asn Thr Thr Thr Thr	
22 27 32 37	
atc acc agt ggc ttt act gtg aac caa aac caa ctg tta tca aga ggg	318
Ile Thr Ser Gly Phe Thr Val Asn Gln Asn Gln Leu Leu Ser Arg Gly	
38 43 48 53	
ttt gaa aac ctt gta cct tat act tca act gtt agt gta gta gca act	366
Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val Val Ala Thr	
54 59 64 69	
cct gtg atg aca tat ggt cat ctg gag ggt ctt ata aat gag tgg aac	414
Pro Val Met Thr Tyr Gly His Leu Glu Gly Leu Ile Asn Glu Trp Asn	
70 75 80 85	
ctt gag ctg gaa gat caa gag aag tac ttt ctt ctc cag gcc act cag	462
Leu Glu Leu Glu Asp Gln Glu Lys Tyr Phe Leu Leu Gln Ala Thr Gln	
86 91 96 101	
gtc aat gct tgg gac cat aca ttg att gag aat ggt gag atg att cgt	510
Val Asn Ala Trp Asp His Thr Leu Ile Glu Asn Gly Glu Met Ile Arg	
102 107 112 117	
att tta cat gga gaa gtg aac aaa gtg aaa ctg gat cag aaa aga ttg	558
Ile Leu His Gly Glu Val Asn Lys Val Lys Leu Asp Gln Lys Arg Leu	
118 123 128 133	
gaa caa gaa ttg gat ttt atc ctg tca cag cag cag gaa cta gaa ttt	606
Glu Gln Glu Leu Asp Phe Ile Leu Ser Gln Gln Gln Glu Leu Glu Phe	
134 139 144 149	
ctg ttg act tat tta gag gag tct acg cgc gac cag agt gga ctt cat	654
Leu Leu Thr Tyr Leu Glu Glu Ser Thr Arg Asp Gln Ser Gly Leu His	
150 155 160 165	
tat ctg cag gat gca gat gag gag cat gtg gag atc tcc acc aga tct	702
Tyr Leu Gln Asp Ala Asp Glu Glu His Val Glu Ile Ser Thr Arg Ser	
166 171 176 181	
gca gaa ttc tga atg cccatatgga ctccctgcag tggattgatc ggaattcagg	757
Ala Glu Phe *	
182	
catgctgcga aggaaggtag aagtggtaac acgggttttt cgaggattat cattcacgag	817
gggtcttttca catcatgttc atcactgttt tttagtgtat tgaccctttt ttcagcttgt	877
cgtttctgga ttattatcta ctaattcttt tgtttatttt	917

gct cct gga atc agc tta gtc aat gaa gct acc ttt ggt tgt tca tgc	857
Ala Pro Gly Ile Ser Leu Val Asn Glu Ala Thr Phe Gly Cys Ser Cys	
118 123 128 133	
aca gat tgc ttc ttt caa aaa tgt tgt cct gct gaa gct gga gtt ctt	905
Thr Asp Cys Phe Phe Gln Lys Cys Cys Pro Ala Glu Ala Gly Val Leu	
134 139 144 149	
ttg gct tat aat aaa aac caa caa att aaa atc cca cct ggt act ccc	953
Leu Ala Tyr Asn Lys Asn Gln Gln Ile Lys Ile Pro Pro Gly Thr Pro	
150 155 160 165	
atc tat gaa tgc aac tca agg tgt cag tgt ggt cct gat tgt ccc aat	1001
Ile Tyr Glu Cys Asn Ser Arg Cys Gln Cys Gly Pro Asp Cys Pro Asn	
166 171 176 181	
agg att gta caa aaa ggc aca cag tat tcg ctt tgc atc ttt cga act	1049
Arg Ile Val Gln Lys Gly Thr Gln Tyr Ser Leu Cys Ile Phe Arg Thr	
182 187 192 197	
agc aat gga cgt ggc tgg ggt gta aag acc ctt gtg aag att aaa aga	1097
Ser Asn Gly Arg Gly Trp Gly Val Lys Thr Leu Val Lys Ile Lys Arg	
198 203 208 213	
atg agt ttt gtc atg gaa tat gtt gga gag gta atc aca agt gaa gaa	1145
Met Ser Phe Val Met Glu Tyr Val Gly Glu Val Ile Thr Ser Glu Glu	
214 219 224 229	
gct gaa aga cga gga cag ttc tat gac aac aag gga atc acg tat ctc	1193
Ala Glu Arg Arg Gly Gln Phe Tyr Asp Asn Lys Gly Ile Thr Tyr Leu	
230 235 240 245	
ttt gat ctg gac tat gag tct gat gaa ttc aca gtg gat gcg gct cga	1241
Phe Asp Leu Asp Tyr Glu Ser Asp Glu Phe Thr Val Asp Ala Ala Arg	
246 251 256 261	
tac ggc aat gtg tct cat ttt gtg aat cac agc tgt gac cca aat ctt	1289
Tyr Gly Asn Val Ser His Phe Val Asn His Ser Cys Asp Pro Asn Leu	
262 267 272 277	
cag gtg ttc aat gtt ttc att gat aac ctc gat act cgt ctt ccc cga	1337
Gln Val Phe Asn Val Phe Ile Asp Asn Leu Asp Thr Arg Leu Pro Arg	
278 283 288 293	
ata gca ttg ttt tcc aca aga acc ata aat gct gga gaa gag ctg act	1385
Ile Ala Leu Phe Ser Thr Arg Thr Ile Asn Ala Gly Glu Glu Leu Thr	
294 299 304 309	
ttt gat tat caa atg aaa ggt tct gga gat ata tct tca gat tct att	1433
Phe Asp Tyr Gln Met Lys Gly Ser Gly Asp Ile Ser Ser Asp Ser Ile	
310 315 320 325	
gac cac agc cca gcc aaa aag agg gtc aga aca gta tgt aaa tgt gga	1481
Asp His Ser Pro Ala Lys Lys Arg Val Arg Thr Val Cys Lys Cys Gly	
326 331 336 341	
gct gtg act tgc aga ggt tac ctc aac tga a ctttttcagg aaatagagct	1532

Ala Val Thr Cys Arg Gly Tyr Leu Asn *
 342 347

gatgattata atattttttt cctaattgtta acatttttta aaatacatat ttgggactct 1592

tattatcaag gttctaccta tggttaattta cgattcatg 1631

<210> 29
 <211> 4884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(4666)

<400> 29

aaggatcctt aattaaatta atcccccccc cccagcgagg aagagccggc cgaagcgtgg 60

cggccacaga ctgtgggtac cgggtccgag ggactcgcgc ttttctctcc gtgcc atg 118
 Met
 1

gcg cca gcg aaa gcc acg aac gtg gtg cgg ctg cta cta ggc tcc aca 166
 Ala Pro Ala Lys Ala Thr Asn Val Val Arg Leu Leu Leu Gly Ser Thr
 2 7 12 17

gcg ctg tgg ctt tcg cag ctc ggc tcc ggg acg gtc gcc gcg tcc aag 214
 Ala Leu Trp Leu Ser Gln Leu Gly Ser Gly Thr Val Ala Ala Ser Lys
 18 23 28 33

tcg gtg act gcc cac ttg gcc gcg aag tgg ccc gag acc ccg ctg ctg 262
 Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu
 34 39 44 49

ctg gag gca agt gaa ttt atg gca gaa gaa agt aat gaa aaa ttt tgg 310
 Leu Glu Ala Ser Glu Phe Met Ala Glu Glu Ser Asn Glu Lys Phe Trp
 50 55 60 65

cag ttt ttg gaa act gtg caa gaa tta gca att tat aag caa aca gaa 358
 Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu
 66 71 76 81

tca gat tat tct tat tac aac tta atc ctg aag aaa gct gga cag ttt 406
 Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln Phe
 82 87 92 97

cta gac aat tta cac atc aac ctt tta aag ttt gct ttc tct ata agg 454
 Leu Asp Asn Leu His Ile Asn Leu Leu Lys Phe Ala Phe Ser Ile Arg
 98 103 108 113

gca tac tcc cca gct att cag atg ttt cag cag att gca gct gat gag 502
 Ala Tyr Ser Pro Ala Ile Gln Met Phe Gln Gln Ile Ala Ala Asp Glu
 114 119 124 129

cca cca cca gat ggt tgt aat gca ttt gtg gtt att cat aag aag cac	550
Pro Pro Pro Asp Gly Cys Asn Ala Phe Val Val Ile His Lys Lys His	
130 135 140 145	
acc tgt aaa att aat gag att aaa aag ctg ctg aag aaa gct gct tca	598
Thr Cys Lys Ile Asn Glu Ile Lys Lys Leu Leu Lys Lys Ala Ala Ser	
146 151 156 161	
agg act aga cct tat cta ttt aaa gga gat cac aaa ttt cct aca aac	646
Arg Thr Arg Pro Tyr Leu Phe Lys Gly Asp His Lys Phe Pro Thr Asn	
162 167 172 177	
aaa gag aac tta cca gtg gtg att ctc tat gcc gaa atg ggt act aga	694
Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr Arg	
178 183 188 193	
aca ttt agt gca ttt cac aaa gta ttg tct gaa aaa gct caa aat gag	742
Thr Phe Ser Ala Phe His Lys Val Leu Ser Glu Lys Ala Gln Asn Glu	
194 199 204 209	
gaa att ctg tat gtt ctt cgc cat tat att cag aaa cca agc tca cgg	790
Glu Ile Leu Tyr Val Leu Arg His Tyr Ile Gln Lys Pro Ser Ser Arg	
210 215 220 225	
aaa atg tac tta tct ggg tat ggt gtg gag cta gca att aag agt aca	838
Lys Met Tyr Leu Ser Gly Tyr Gly Val Glu Leu Ala Ile Lys Ser Thr	
226 231 236 241	
gaa tac aaa gca ctg gat gat acc caa gtt aaa act gtg act aat act	886
Glu Tyr Lys Ala Leu Asp Asp Thr Gln Val Lys Thr Val Thr Asn Thr	
242 247 252 257	
act gta gag gat gag act gaa aca aat gaa gtt caa gga ttt ctc ttt	934
Thr Val Glu Asp Glu Thr Glu Thr Asn Glu Val Gln Gly Phe Leu Phe	
258 263 268 273	
ggg aaa cta aaa gaa ata tat tca gat ctt aga gat aat ctg aca gca	982
Gly Lys Leu Lys Glu Ile Tyr Ser Asp Leu Arg Asp Asn Leu Thr Ala	
274 279 284 289	
ttc caa aaa tac ctg att gag agt aac aaa caa atg atg cct ttg aaa	1030
Phe Gln Lys Tyr Leu Ile Glu Ser Asn Lys Gln Met Met Pro Leu Lys	
290 295 300 305	
gtc tgg gaa cta caa gat ctt agt ttt caa gca gct tct caa ata atg	1078
Val Trp Glu Leu Gln Asp Leu Ser Phe Gln Ala Ala Ser Gln Ile Met	
306 311 316 321	
tcc gct cca gtt tat gat gcc att aaa tta atg aaa gac att tca cag	1126
Ser Ala Pro Val Tyr Asp Ala Ile Lys Leu Met Lys Asp Ile Ser Gln	
322 327 332 337	
aac ttc ccc ata aaa gcc aga tct cta acc aga att gct gta aat caa	1174
Asn Phe Pro Ile Lys Ala Arg Ser Leu Thr Arg Ile Ala Val Asn Gln	
338 343 348 353	

cat atg aga gaa gaa ata aag gaa aat caa aag gat ctt caa gtt aga His Met Arg Glu Glu Ile Lys Glu Asn Gln Lys Asp Leu Gln Val Arg 354 359 364 369	1222
ttt aaa att cag cca ggc gat gct cgt cta ttt ata aat ggc ctt cgt Phe Lys Ile Gln Pro Gly Asp Ala Arg Leu Phe Ile Asn Gly Leu Arg 370 375 380 385	1270
gtt gat atg gat gtt tat gac gct ttt agt att ttg gat atg ctg aaa Val Asp Met Asp Val Tyr Asp Ala Phe Ser Ile Leu Asp Met Leu Lys 386 391 396 401	1318
tta gaa gga aaa atg atg aat ggc ctt cgc aat ctt ggg atc aat ggg Leu Glu Gly Lys Met Met Asn Gly Leu Arg Asn Leu Gly Ile Asn Gly 402 407 412 417	1366
gaa gat atg agc aaa ttt tta aaa tta aat tca cac att tgg gaa tat Glu Asp Met Ser Lys Phe Leu Lys Leu Asn Ser His Ile Trp Glu Tyr 418 423 428 433	1414
act tat gta tta gat att cga cat tct tct ata atg tgg att aat gac Thr Tyr Val Leu Asp Ile Arg His Ser Ser Ile Met Trp Ile Asn Asp 434 439 444 449	1462
tta gaa aat gat gat ttg tat att aca tgg cct aca agt tgc cag aaa Leu Glu Asn Asp Asp Leu Tyr Ile Thr Trp Pro Thr Ser Cys Gln Lys 450 455 460 465	1510
ctt ctg aag cca gta ttt cct gga agt gta cct tcc ata agg cgc aat Leu Leu Lys Pro Val Phe Pro Gly Ser Val Pro Ser Ile Arg Arg Asn 466 471 476 481	1558
ttt cat aat ttg gtt ctg ttt att gat ccg gcc caa gaa tat acc ttg Phe His Asn Leu Val Leu Phe Ile Asp Pro Ala Gln Glu Tyr Thr Leu 482 487 492 497	1606
gat ttt ata aaa ctt gct gat gtt ttc tat tct cac gaa gtt cct ctt Asp Phe Ile Lys Leu Ala Asp Val Phe Tyr Ser His Glu Val Pro Leu 498 503 508 513	1654
aga att ggt ttt gtg ttc att ctt aat aca gat gat gaa gtt gat gga Arg Ile Gly Phe Val Phe Ile Leu Asn Thr Asp Asp Glu Val Asp Gly 514 519 524 529	1702
gca aat gat gct gga gtt gct ctc tgg cga gct ttc aac tat att gca Ala Asn Asp Ala Gly Val Ala Leu Trp Arg Ala Phe Asn Tyr Ile Ala 530 535 540 545	1750
gaa gaa ttt gat ata tca gaa gca ttt att tct ata gta cac atg tac Glu Glu Phe Asp Ile Ser Glu Ala Phe Ile Ser Ile Val His Met Tyr 546 551 556 561	1798
caa aaa gtg aag aag gat caa aat ata ctc act gtg gac aat gtg aag Gln Lys Val Lys Lys Asp Gln Asn Ile Leu Thr Val Asp Asn Val Lys 562 567 572 577	1846
agt gtt ctc caa aat aca ttt cct cat gct aat att tgg gat att ttg	1894

802	807	812	817	
att gct aca gct att	tac tct gga gat aaa	att aaa aca ttc ctt att		2614
Ile Ala Thr Ala Ile	Tyr Ser Gly Asp Lys	Ile Lys Thr Phe Leu Ile		
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gag ggg atg gat aag	aat gct ttt gag aaa	aaa tat aat act gtt gga		2662
Glu Gly Met Asp Lys	Asn Ala Phe Glu Lys	Lys Tyr Asn Thr Val Gly		
834	839	844	849	
gtg aat att ttt cga	act cac cag ttg ttc	tgt caa gat gta ctt aaa		2710
Val Asn Ile Phe Arg	Thr His Gln Leu Phe	Cys Gln Asp Val Leu Lys		
850	855	860	865	
tta cgt cct gga gaa	atg ggt att gtc agc	aat ggg aga ttc tta gga		2758
Leu Arg Pro Gly Glu	Met Gly Ile Val Ser	Asn Gly Arg Phe Leu Gly		
866	871	876	881	
cct tta gat gaa gat	ttt tat gca gaa gat	ttt tac ttg ttg gaa aag		2806
Pro Leu Asp Glu Asp	Phe Tyr Ala Glu Asp	Phe Tyr Leu Leu Glu Lys		
882	887	892	897	
ata aca ttt agt aat	tta gga gag aaa att	aaa ggc att gtt gaa aat		2854
Ile Thr Phe Ser Asn	Leu Gly Glu Lys Ile	Lys Gly Ile Val Glu Asn		
898	903	908	913	
atg gga atc aac gca	aat aac atg agt gac	ttt att atg aaa gtt gat		2902
Met Gly Ile Asn Ala	Asn Asn Met Ser Asp	Phe Ile Met Lys Val Asp		
914	919	924	929	
gcc ctt atg tcc tct	gtg cct aag cgt gca	tct cga tat gat gtc aca		2950
Ala Leu Met Ser Ser	Val Pro Lys Arg Ala	Ser Arg Tyr Asp Val Thr		
930	935	940	945	
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Phe Leu Arg Glu Asn	His Ser Val Ile Lys	Thr Asn Pro Gln Glu Asn		
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gat atg ttc ttc aat	gtc att gct att gtt	gat cca tta aca aga gaa		3046
Asp Met Phe Phe Asn	Val Ile Ala Ile Val	Asp Pro Leu Thr Arg Glu		
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gca cag aaa atg gca	cag ttg ttg gtt gta	ctt ggc aag att atc aac		3094
Ala Gln Lys Met Ala	Gln Leu Leu Val Val	Leu Gly Lys Ile Ile Asn		
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Met Lys Ile Lys Leu	Phe Met Asn Cys Arg	Gly Arg Leu Ser Glu Ala		
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cct tta gaa agc ttt	tac cgt ttt gtt ctg	gaa cca gaa ctg atg tca		3190
Pro Leu Glu Ser Phe	Tyr Arg Phe Val Leu	Glu Pro Glu Leu Met Ser		
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ggg gct aat gac gtt	tct tct ctt gga cca	gtg gca aaa ttt ttg gat		3238
Gly Ala Asn Asp Val	Ser Ser Leu Gly Pro	Val Ala Lys Phe Leu Asp		
1026	1031	1036	1041	

att cct gaa tca ccc ctc cta atc ctc aac atg att act cca gaa ggc Ile Pro Glu Ser Pro Leu Leu Ile Leu Asn Met Ile Thr Pro Glu Gly	3286
1042 1047 1052 1057	
tgg ttg gtt gaa aca gtg cac agc aac tgt gac ctt gat aat att cac Trp Leu Val Glu Thr Val His Ser Asn Cys Asp Leu Asp Asn Ile His	3334
1058 1063 1068 1073	
tta aag gat act gag aaa act gtt aca gca gaa tat gaa cta gaa tac Leu Lys Asp Thr Glu Lys Thr Val Thr Ala Glu Tyr Glu Leu Glu Tyr	3382
1074 1079 1084 1089	
tta cta ctg gaa gga caa tgc ttt gat aaa gtg aca gaa cag cct cct Leu Leu Leu Glu Gly Gln Cys Phe Asp Lys Val Thr Glu Gln Pro Pro	3430
1090 1095 1100 1105	
cgg ggt ctg cag ttc aca cta ggc aca aaa aat aaa cct gct gtg gtt Arg Gly Leu Gln Phe Thr Leu Gly Thr Lys Asn Lys Pro Ala Val Val	3478
1106 1111 1116 1121	
gat aca ata gtg atg gca cat cat ggg tat ttt caa tta aaa gca aac Asp Thr Ile Val Met Ala His His Gly Tyr Phe Gln Leu Lys Ala Asn	3526
1122 1127 1132 1137	
cca ggt gct tgg ata ctg agg tta cac caa gga aaa tct gaa gat att Pro Gly Ala Trp Ile Leu Arg Leu His Gln Gly Lys Ser Glu Asp Ile	3574
1138 1143 1148 1153	
tat caa ata gtt ggg cat gaa gga act gac tct caa gca gac cta gaa Tyr Gln Ile Val Gly His Glu Gly Thr Asp Ser Gln Ala Asp Leu Glu	3622
1154 1159 1164 1169	
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1170 1175 1180 1185	
aaa gtg aaa aaa gaa aca gac aaa att aag gaa gat atc ctt acc gat Lys Val Lys Lys Glu Thr Asp Lys Ile Lys Glu Asp Ile Leu Thr Asp	3718
1186 1191 1196 1201	
gaa gat gaa aaa aca aaa gga ctg tgg gat tcc att aaa agt ttc aca Glu Asp Glu Lys Thr Lys Gly Leu Trp Asp Ser Ile Lys Ser Phe Thr	3766
1202 1207 1212 1217	
gta agc ttg cat aaa gaa aac aaa aag gaa aaa gat gtc cta aac att Val Ser Leu His Lys Glu Asn Lys Lys Glu Lys Asp Val Leu Asn Ile	3814
1218 1223 1228 1233	
ttt tca gtt gct tct ggt cat tta tat gaa cgt ttt tta aga att atg Phe Ser Val Ala Ser Gly His Leu Tyr Glu Arg Phe Leu Arg Ile Met	3862
1234 1239 1244 1249	
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1250 1255 1260 1265	

cta aaa aat tat ctc tca ccg aca ttt aaa gaa gta att cct cac atg	3958
Leu Lys Asn Tyr Leu Ser Pro Thr Phe Lys Glu Val Ile Pro His Met	
1266 1271 1276 1281	
gct aaa gag tat gga ttc cga tat gaa cta gtt caa tat agg tgg ccc	4006
Ala Lys Glu Tyr Gly Phe Arg Tyr Glu Leu Val Gln Tyr Arg Trp Pro	
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Arg Trp Leu Arg Gln Gln Thr Glu Arg Gln Arg Ile Ile Trp Gly Tyr	
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aaa att ctt ttc ctt gat gtt ctt ttc cca cta gca gtg gac aaa atc	4102
Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Leu Ala Val Asp Lys Ile	
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Ile Phe Val Asp Ala Asp Gln Ile Val Arg His Asp Leu Lys Glu Leu	
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Arg Asp Phe Asp Leu Asp Gly Ala Pro Tyr Gly Tyr Thr Pro Phe Cys	
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Asp Ser Arg Arg Glu Met Asp Gly Tyr Arg Phe Trp Lys Thr Gly Tyr	
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Trp Ala Ser His Leu Leu Arg Arg Lys Tyr His Ile Ser Ala Leu Tyr	
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gta gtg gat ctc aag aag ttc agg aga att gga gca ggt gac agg ctc	4342
Val Val Asp Leu Lys Lys Phe Arg Arg Ile Gly Ala Gly Asp Arg Leu	
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Arg Ser Gln Tyr Gln Ala Leu Ser Gln Asp Pro Asn Ser Leu Ser Asn	
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cta gat cag gat ctc ccc aat aat atg att tac caa gtc gcc att aag	4438
Leu Asp Gln Asp Leu Pro Asn Asn Met Ile Tyr Gln Val Ala Ile Lys	
1426 1431 1436 1441	
tct ctt cct caa gac tgg ctg tgg tgt gaa acc tgg tgt gat gat gaa	4486
Ser Leu Pro Gln Asp Trp Leu Trp Cys Glu Thr Trp Cys Asp Asp Glu	
1442 1447 1452 1457	
tcc aaa caa aga gcc aaa aca att gat ctg tgc aat aat ccc aaa aca	4534
Ser Lys Gln Arg Ala Lys Thr Ile Asp Leu Cys Asn Asn Pro Lys Thr	
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aaa gaa tcc aaa cta aaa gct gct gcc aga att gtc cca gaa tgg gtg	4582
Lys Glu Ser Lys Leu Lys Ala Ala Ala Arg Ile Val Pro Glu Trp Val	
1474 1479 1484 1489	
gag tat gat gct gag ata aga caa cta tta gat cat ctt gaa aac aag	4630

Glu Tyr Asp Ala Glu Ile Arg Gln Leu Leu Asp His Leu Glu Asn Lys
 1490 1495 1500 1505

aag caa gat aca att ttg aca cat gat gaa ctc tag cact ggtgtatatg 4680
 Lys Gln Asp Thr Ile Leu Thr His Asp Glu Leu *
 1506 1511 1516

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cccccgatc atg cag ccc cca ctg gac ctc aag cag atc ctg ccc ttc 168
 Met Gln Pro Pro Leu Asp Leu Lys Gln Ile Leu Pro Phe
 1 5 10

cca ctc gag cca gcc cct acc ctt ggc ctc ttc agc aac tac agc acc 216
 Pro Leu Glu Pro Ala Pro Thr Leu Gly Leu Phe Ser Asn Tyr Ser Thr
 14 19 24 29

atg gac cct gtg cag aag gct gtg ctc tcc cac act ttt ggg gga ccc 264
 Met Asp Pro Val Gln Lys Ala Val Leu Ser His Thr Phe Gly Gly Pro
 30 35 40 45

ttg ctc aag acc aaa cgg ccc gtc att tcc tgt aat atc tgt caa atc 312
 Leu Leu Lys Thr Lys Arg Pro Val Ile Ser Cys Asn Ile Cys Gln Ile
 46 51 56 61

cgc ttc aat tct cag agc cag gct gag gcg cac tac aaa ggt aat cgc 360
 Arg Phe Asn Ser Gln Ser Gln Ala Glu Ala His Tyr Lys Gly Asn Arg
 62 67 72 77

cac gcc cga cga gtc aaa ggc att gag gct gcc aag acc aga ggc agg 408
 His Ala Arg Arg Val Lys Gly Ile Glu Ala Ala Lys Thr Arg Gly Arg
 78 83 88 93

gag cct ggc gtc cga gaa cct gga gac cca gct ccc cca ggc agc acc 456

Glu Pro Gly Val Arg	Glu Pro Gly Asp Pro	Ala Pro Pro Gly Ser Thr	
94	99	104	109
cca aca aat ggg gat	ggt gta gca ccc cgt	cca gtt tcc atg gag aat	504
Pro Thr Asn Gly Asp	Gly Val Ala Pro Arg	Pro Val Ser Met Glu Asn	
110	115	120	125
gga ctg ggg cca gcc	cca gga tcc cca gag	aaa cag cct ggc tcc cca	552
Gly Leu Gly Pro Ala	Pro Gly Ser Pro Glu	Lys Gln Pro Gly Ser Pro	
126	131	136	141
tcc cct ccc agc att	ccg gag act ggt cag	ggt gta acc aag ggt gaa	600
Ser Pro Pro Ser Ile	Pro Glu Thr Gly Gln	Gly Val Thr Lys Gly Glu	
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ggg ggg act cca gcc	ccg gct tcc ttg cct	ggg ggt agc aag gaa gag	648
Gly Gly Thr Pro Ala	Pro Ala Ser Leu Pro	Gly Gly Ser Lys Glu Glu	
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gag gag aaa gcc aag	cgg ctg ctc tac tgt	gct ctg tgc aag gtg gct	696
Glu Glu Lys Ala Lys	Arg Leu Leu Tyr Cys	Ala Leu Cys Lys Val Ala	
174	179	184	189
gtg aac tcc ctg tcc	cag ctt gag gca cat	aac aaa ggt act aag cac	744
Val Asn Ser Leu Ser	Gln Leu Glu Ala His	Asn Lys Gly Thr Lys His	
190	195	200	205
aag aca att ctg gag	gcc cga agt ggg ctc	ggg ccc atc aaa gct tac	792
Lys Thr Ile Leu Glu	Ala Arg Ser Gly Leu	Gly Pro Ile Lys Ala Tyr	
206	211	216	221
cct cgg ctg ggg cct	ccc acc ccg ggg gaa	cca gag gct cct gcc cag	840
Pro Arg Leu Gly Pro	Pro Thr Pro Gly Glu	Pro Glu Ala Pro Ala Gln	
222	227	232	237
gac cga act ttc cac	tgt gag atc tgc aat	gtc aag gtc aac tcg gag	888
Asp Arg Thr Phe His	Cys Glu Ile Cys Asn	Val Lys Val Asn Ser Glu	
238	243	248	253
gtc caa ctg aaa cag	cac atc tcc agc cgg	cgg cac cga gac ggc gtg	936
Val Gln Leu Lys Gln	His Ile Ser Ser Arg	Arg His Arg Asp Gly Val	
254	259	264	269
gcc ggg aag ccc aac	cca cta ctg agc cgt	cac aag aag tct agg ggc	984
Ala Gly Lys Pro Asn	Pro Leu Leu Ser Arg	His Lys Lys Ser Arg Gly	
270	275	280	285
gcc ggg gag ctg gcg	ggc acg ctg act ttc	tcc aag gag ctg ccc aag	1032
Ala Gly Glu Leu Ala	Gly Thr Leu Thr Phe	Ser Lys Glu Leu Pro Lys	
286	291	296	301
tcc ctg gcg ggc ggc	ctg ctc ccc agc ccc	ctg gcg gtg gct gca gtg	1080
Ser Leu Ala Gly Gly	Leu Leu Pro Ser Pro	Leu Ala Val Ala Ala Val	
302	307	312	317
atg gca gcg gca gca	ggc tcg ccg ctg tcc	ctg cgc ccg gct cca gcc	1128
Met Ala Ala Ala Ala	Gly Ser Pro Leu Ser	Leu Arg Pro Ala Pro Ala	

318	323	328	333	
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Ala Pro Leu Leu Gln Gly Pro Pro Ile Thr His Pro Leu Leu His Pro				
334	339	344	349	
gcc ccc gga ccc atc cga act gcg cac gga ccc atc ctc ttc tcc ccg				1224
Ala Pro Gly Pro Ile Arg Thr Ala His Gly Pro Ile Leu Phe Ser Pro				
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tac tga cctcaaccct gaacccctcc cattcaactc cccacctcca gccggggaccc				1280
Tyr *				
366				
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ctg ggt ccc ata gcc agc acg gca tgg ttc tcc cct tcc ccc ctt ccc	1094
Leu Gly Pro Ile Ala Ser Thr Ala Trp Phe Ser Pro Ser Pro Leu Pro	
124 129 134 139	
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Arg Ser Gly Glu Leu Asp Lys *	
140 145	
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	Met
	1
gcg cca gcg aaa gcc acg aac gtg gtg cgg ctg cta cta ggc tcc aca	166
Ala Pro Ala Lys Ala Thr Asn Val Val Arg Leu Leu Leu Gly Ser Thr	
2 7 12 17	
gcg ctg tgg ctt tcg cag ctc ggc tcc ggg acg gtc gcc gcg tcc aag	214
Ala Leu Trp Leu Ser Gln Leu Gly Ser Gly Thr Val Ala Ala Ser Lys	
18 23 28 33	
tcg gtg act gcc cac ttg gcc gcg aag tgg ccc gag acc ccg ctg ctg	262
Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu	
34 39 44 49	
ctg gag gca agt gaa ttt atg gca gaa gaa agt aat gaa aaa ttt tgg	310
Leu Glu Ala Ser Glu Phe Met Ala Glu Glu Ser Asn Glu Lys Phe Trp	
50 55 60 65	
cag ttt ttg gaa act gtg caa gaa tta gca att tat aag caa aca gaa	358
Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu	
66 71 76 81	
tca gat tat tct tat tac aac tta atc ctg aag aaa gct gga cag ttt	406
Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln Phe	
82 87 92 97	
cta gac aat tta cac atc aac ctt tta aag ttt gct ttc tct ata agg	454
Leu Asp Asn Leu His Ile Asn Leu Leu Lys Phe Ala Phe Ser Ile Arg	
98 103 108 113	
gca tac tcc cca gct att cag atg ttt cag cag att gca gct gat gag	502
Ala Tyr Ser Pro Ala Ile Gln Met Phe Gln Gln Ile Ala Ala Asp Glu	
114 119 124 129	
cca cca cca gat ggt tgt aat gca ttt gtg gtt att cat aag aag cac	550
Pro Pro Pro Asp Gly Cys Asn Ala Phe Val Val Ile His Lys Lys His	
130 135 140 145	
acc tgt aaa att aat gag att aaa aag ctg ctg aag aaa gct gct tca	598
Thr Cys Lys Ile Asn Glu Ile Lys Lys Leu Leu Lys Lys Ala Ala Ser	
146 151 156 161	
agg act aga cct tat cta ttt aaa gga gat cac aaa ttt cct aca aac	646
Arg Thr Arg Pro Tyr Leu Phe Lys Gly Asp His Lys Phe Pro Thr Asn	
162 167 172 177	
aaa gag aac tta cca gtg gtg att ctc tat gcc gaa atg ggt act aga	694
Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr Arg	
178 183 188 193	
aca ttt agt gca ttt cac aaa gta ttg tct gaa aaa gct caa aat gag	742
Thr Phe Ser Ala Phe His Lys Val Leu Ser Glu Lys Ala Gln Asn Glu	

194	199	204	209	
gaa att ctg tat gtt ctt cgc cat tat att cag aaa cca agc tca cgg				790
Glu Ile Leu Tyr Val Leu Arg His Tyr Ile Gln Lys Pro Ser Ser Arg				
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Lys Met Tyr Leu Ser Gly Tyr Gly Val Glu Leu Ala Ile Lys Ser Thr				
226	231	236	241	
gaa tac aaa gca ctg gat gat acc caa gtt aaa act gtg act aat act				886
Glu Tyr Lys Ala Leu Asp Asp Thr Gln Val Lys Thr Val Thr Asn Thr				
242	247	252	257	
act gta gag gat gag act gaa aca aat gaa gtt caa gga ttt ctc ttt				934
Thr Val Glu Asp Glu Thr Glu Thr Asn Glu Val Gln Gly Phe Leu Phe				
258	263	268	273	
ggg aaa cta aaa gaa ata tat tca gat ctt aga gat aat ctg aca gca				982
Gly Lys Leu Lys Glu Ile Tyr Ser Asp Leu Arg Asp Asn Leu Thr Ala				
274	279	284	289	
ttc caa aaa tac ctg att gag agt aac aaa caa atg atg cct ttg aaa				1030
Phe Gln Lys Tyr Leu Ile Glu Ser Asn Lys Gln Met Met Pro Leu Lys				
290	295	300	305	
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Val Trp Glu Leu Gln Asp Leu Ser Phe Gln Ala Ala Ser Gln Ile Met				
306	311	316	321	
tcc gct cca gtt tat gat gcc att aaa tta atg aaa gac att tca cag				1126
Ser Ala Pro Val Tyr Asp Ala Ile Lys Leu Met Lys Asp Ile Ser Gln				
322	327	332	337	
aac ttc ccc ata aaa gcc aga tct cta acc aga att gct gta aat caa				1174
Asn Phe Pro Ile Lys Ala Arg Ser Leu Thr Arg Ile Ala Val Asn Gln				
338	343	348	353	
cat atg aga gaa gaa ata aag gaa aat caa aag gat ctt caa gtt aga				1222
His Met Arg Glu Glu Ile Lys Glu Asn Gln Lys Asp Leu Gln Val Arg				
354	359	364	369	
ttt aaa att cag cca ggc gat gct cgt cta ttt ata aat ggc ctt cgt				1270
Phe Lys Ile Gln Pro Gly Asp Ala Arg Leu Phe Ile Asn Gly Leu Arg				
370	375	380	385	
gtt gat atg gat gtt tat gac gct ttt agt att ttg gat atg ctg aaa				1318
Val Asp Met Asp Val Tyr Asp Ala Phe Ser Ile Leu Asp Met Leu Lys				
386	391	396	401	
tta gaa gga aaa atg atg aat ggc ctt cgc aat ctt ggg atc aat ggg				1366
Leu Glu Gly Lys Met Met Asn Gly Leu Arg Asn Leu Gly Ile Asn Gly				
402	407	412	417	
gaa gat atg agc aaa ttt tta aaa tta aat tca cac att tgg gaa tat				1414
Glu Asp Met Ser Lys Phe Leu Lys Leu Asn Ser His Ile Trp Glu Tyr				
418	423	428	433	

act tat gta tta gat att cga cat tct tct ata atg tgg att aat gac	1462
Thr Tyr Val Leu Asp Ile Arg His Ser Ser Ile Met Trp Ile Asn Asp	
434 439 444 449	
tta gaa aat gat gat ttg tat att aca tgg cct aca agt tgc cag aaa	1510
Leu Glu Asn Asp Asp Leu Tyr Ile Thr Trp Pro Thr Ser Cys Gln Lys	
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Leu Leu Lys Pro Val Phe Pro Gly Ser Val Pro Ser Ile Arg Arg Asn	
466 471 476 481	
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Phe His Asn Leu Val Leu Phe Ile Asp Pro Ala Gln Glu Tyr Thr Leu	
482 487 492 497	
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Asp Phe Ile Lys Leu Ala Asp Val Phe Tyr Ser His Glu Val Pro Leu	
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Arg Ile Gly Phe Val Phe Ile Leu Asn Thr Asp Asp Glu Val Asp Gly	
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Ala Asn Asp Ala Gly Val Ala Leu Trp Arg Ala Phe Asn Tyr Ile Ala	
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Tyr Lys Met Thr Gly Leu Gly Pro Leu Pro Gln Ala Leu Tyr Asn Gly	
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Glu Pro Phe Lys His Glu Glu Met Asn Ile Lys Glu Leu Lys Met Ala	
626 631 636 641	
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674 679 684 689	
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866 871 876 881	
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Pro Leu Asp Glu Asp Phe Tyr Ala Glu Asp Phe Tyr Leu Leu Glu Lys	
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Ile Thr Phe Ser Asn Leu Gly Glu Lys Ile Lys Gly Ile Val Glu Asn	
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Met Gly Ile Asn Ala Asn Asn Met Ser Asp Phe Ile Met Lys Val Asp	
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Lys Glu Ser Lys Leu Lys Ala Ala Ala Arg Ile Val Pro Glu Trp Val	
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Thr Val Glu	Leu Lys	Ile Pro	Glu Glu	Asn Gln	Pro Pro	Ser Lys	Gln	
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Val Lys Pro	Leu Phe	Arg His	Phe Arg	Arg Ile	Asp Ser	Cys Leu	Gln	
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Arg	Glu	Val	Ile	Ser	Lys	Met	Lys	Pro	Pro	Val	Ile	Pro	Phe	Val	Pro	
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452					457											

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 <211> 1998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (200)..(1879)

<220>
 <221> misc_feature
 <222> (1)...(1998)
 <223> n = a,t,c or g

<400> 34																
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ctgatgagaa	agcggcgcg	ggaggggtgtg	agatggcaga	caggtttgca	ggaaaccctc											120
acaaaggggg	ctggaggatt	tagccactct	gtcctcccct	tccggcagtc	cagggcctcc											180
tcccgagcac	agcggcgct	atg gac tct	cca gga tac	aac tgc ttc	gtg gac											232

Met Asp Ser Pro Gly Tyr Asn Cys Phe Val Asp
1 5

aaa gac aag atg gac gct gcc atc cag gac ctg ggg ccc aag gag ctg	280
Lys Asp Lys Met Asp Ala Ala Ile Gln Asp Leu Gly Pro Lys Glu Leu	
12 17 22 27	
agc tgc act gaa ctg cag gaa ctg aag cag ctg gcg cgc cag ggc tac	328
Ser Cys Thr Glu Leu Gln Glu Leu Lys Gln Leu Ala Arg Gln Gly Tyr	
28 33 38 43	
tgg gcc caa agc cac gcc ctg cgg gga aag gtg tac cag cgc ctg atc	376
Trp Ala Gln Ser His Ala Leu Arg Gly Lys Val Tyr Gln Arg Leu Ile	
44 49 54 59	
cgg gac att ccc tgc cgc acg gtc acg cct gac gcc agc gtg tac agc	424
Arg Asp Ile Pro Cys Arg Thr Val Thr Pro Asp Ala Ser Val Tyr Ser	
60 65 70 75	
gac atc gtg ggc aag atc gtg ggc aag cac agc agc agc tgc ctg ccg	472
Asp Ile Val Gly Lys Ile Val Gly Lys His Ser Ser Ser Cys Leu Pro	
76 81 86 91	
ctg ccc gag ttc gtg gac aac acg cag gtg ccc agc tac tgc ctg aat	520
Leu Pro Glu Phe Val Asp Asn Thr Gln Val Pro Ser Tyr Cys Leu Asn	
92 97 102 107	
gca cgc ggc gag ggg gcc gtg cgc aag atc ctc ctg tgc ctg gcc aac	568
Ala Arg Gly Glu Gly Ala Val Arg Lys Ile Leu Leu Cys Leu Ala Asn	
108 113 118 123	
cag ttc ccc gac atc tcc ttc tgc ccc gcc ctg ccg gcc gtg gtg gcc	616
Gln Phe Pro Asp Ile Ser Phe Cys Pro Ala Leu Pro Ala Val Val Ala	
124 129 134 139	
ctg ctg ctg cac tac agc atc gac gag gcc gag tgc ttc gag aag gcc	664
Leu Leu Leu His Tyr Ser Ile Asp Glu Ala Glu Cys Phe Glu Lys Ala	
140 145 150 155	
tgc cgc atc ctg gcc tgc aat gac ccc ggc agg agg ctg atc gac cag	712
Cys Arg Ile Leu Ala Cys Asn Asp Pro Gly Arg Arg Leu Ile Asp Gln	
156 161 166 171	
agc ttc ctg gcc ttt gag tgc tcc tgc atg acg ttt ggg gac ctg gtg	760
Ser Phe Leu Ala Phe Glu Ser Ser Cys Met Thr Phe Gly Asp Leu Val	
172 177 182 187	
aac aag tac tgc cag gcg gcc cac aag ctg atg gtg gcc gtg tgc gag	808
Asn Lys Tyr Cys Gln Ala Ala His Lys Leu Met Val Ala Val Ser Glu	
188 193 198 203	
gat gtc ctg cag gtc tat gcg gac tgg cag cgc tgg ctg ttt ggg gag	856
Asp Val Leu Gln Val Tyr Ala Asp Trp Gln Arg Trp Leu Phe Gly Glu	
204 209 214 219	
ctg ccc ctc tgc tac ttc gcc cgg gtc ttt gac gtc ttc ctg gtg gag	904
Leu Pro Leu Cys Tyr Phe Ala Arg Val Phe Asp Val Phe Leu Val Glu	

220	225	230	235	
ggc tac aag gtg ctg Gly Tyr Lys Val Leu 236	tac cgc gtg gcg ctg Tyr Arg Val Ala Leu 241	gcc atc ctc aag ttc Ala Ile Leu Lys Phe 246	ttc phe 251	952
cat aag gtg agg gcc His Lys Val Arg Ala 252	ggg cag ccg ctg gag Gly Gln Pro Leu Glu 257	tcg gac agc gtg aag Ser Asp Ser Val Lys 262	cag gln 267	1000
gac atc cgc acg ttc Asp Ile Arg Thr Phe 268	gtc aga gac atc gcg Val Arg Asp Ile Ala 273	aag acg gtg tcc cct Lys Thr Val Ser Pro 278	gag glu 283	1048
aag ctg ctg gag aaa Lys Leu Leu Glu Lys 284	gcg ttc gcc atc cgc Ala Phe Ala Ile Arg 289	ctc ttg tcc cgc aag Leu Leu Ser Arg Lys 294	gag glu 299	1096
atc cag ctc ctg cag Ile Gln Leu Leu Gln 300	atg gcc aat gag aaa Met Ala Asn Glu Lys 305	gcc ctg aag cag aag Ala Leu Lys Gln Lys 310	ggc gly 315	1144
atc acc gtg aag cag Ile Thr Val Lys Gln 316	aag agt gtg tca ctt Lys Ser Val Ser Leu 321	tct aaa agg cag ttt Ser Lys Arg Gln Phe 326	gta val 331	1192
cac ttg gcc gtc cat His Leu Ala Val His 332	gca gag aac ttc cgc Ala Glu Asn Phe Arg 337	tcg gag atc gtc agc Ser Glu Ile Val Ser 342	gtg val 347	1240
agg gag atg aga gac Arg Glu Met Arg Asp 348	atc tgg tcc tgg gtc Ile Trp Ser Trp Val 353	ccc gag cgc ttt gcc Pro Glu Arg Phe Ala 358	ctg leu 363	1288
tgc cag ccc ctt ctg Cys Gln Pro Leu Leu 364	ctg ttc tcc tcc ctg Leu Phe Ser Ser Leu 369	cag cac ggg tac agc Gln His Gly Tyr Ser 374	ctg leu 379	1336
gcc agg ttc tac ttc Ala Arg Phe Tyr Phe 380	cag tgt gaa gga cat Gln Cys Glu Gly His 385	gag cct acc ctc ttg Glu Pro Thr Leu Leu 390	ctc leu 395	1384
atc aag acc acg cag Ile Lys Thr Thr Gln 396	aag gag gtg tgt ggt Lys Glu Val Cys Gly 401	gct tac ctg tcc aca Ala Tyr Leu Ser Thr 406	gac asp 411	1432
tgg agt gag aga aat Trp Ser Glu Arg Asn 412	aag ttt gga ggc aaa Lys Phe Gly Gly Lys 417	ctg ggc ttc ttt ggg Leu Gly Phe Phe Gly 422	acc thr 427	1480
gga gaa tgc ttt gtg Gly Glu Cys Phe Val 428	ttt agg ctg cag cct Phe Arg Leu Gln Pro 433	gag gtg cag cgc tac Glu Val Gln Arg Tyr 438	gag glu 443	1528
tgg gtg gtg atc aag Trp Val Val Ile Lys 444	cac ccc gag ctg acc His Pro Glu Leu Thr 449	aag ccc cca ccc ttg Lys Pro Pro Pro Leu 454	atg met 459	1576

gct gcc gag ccc acc gcc cca ctc agc cac tcc gcc tcc tca gac ccc	1624
Ala Ala Glu Pro Thr Ala Pro Leu Ser His Ser Ala Ser Ser Asp Pro	
460 465 470 475	
gct gac cgc ctc tcg ccc ttc ctg gcc gct cgc cac ttc aac ctg ccc	1672
Ala Asp Arg Leu Ser Pro Phe Leu Ala Ala Arg His Phe Asn Leu Pro	
476 481 486 491	
tcc aag acc gag tcc atg ttc atg gcg ggg ggc agc gac tgc ctc atc	1720
Ser Lys Thr Glu Ser Met Phe Met Ala Gly Gly Ser Asp Cys Leu Ile	
492 497 502 507	
gtc ggg gga gga ggc ggc cag gcg ctc tac atc gat ggg gac ctg aac	1768
Val Gly Gly Gly Gly Gly Gly Gln Ala Leu Tyr Ile Asp Gly Asp Leu Asn	
508 513 518 523	
cgg ggc cgc aca agc cac tgc gac acc ttc aac aac cag ccc ctc tgc	1816
Arg Gly Arg Thr Ser His Cys Asp Thr Phe Asn Asn Gln Pro Leu Cys	
524 529 534 539	
tcc gag aac ttc ctc att gct gcc gtg aag gcc tgg ggc ttc cag gac	1864
Ser Glu Asn Phe Leu Ile Ala Ala Val Lys Ala Trp Gly Phe Gln Asp	
540 545 550 555	
cct gac acc cag tga cggcctgtgc cacggtgact gagccgtggt ggggcggtgg	1919
Pro Asp Thr Gln *	
556	
gccgaaaatg gaaatnccgc ctccgggcagc agagagcaga tgtattgcgt gcgctctaga	1979
cgaaacaagg agtggttcgt	1998

<210> 35
 <211> 1798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (82) .. (1515)

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gttcgcggcc ggagcgcgga g atg ccg ggc agc gac acg gcg ctc acc gtg	111
Met Pro Gly Ser Asp Thr Ala Leu Thr Val	
1 5	
gac cgg acc tac tcg gac ccc ggc cgg cac cac cgc tgc aag agc cgg	159
Asp Arg Thr Tyr Ser Asp Pro Gly Arg His His Arg Cys Lys Ser Arg	
11 16 21 26	
gta gaa cgt cat gac atg aat acc tta agc ctg ccc ctg aac ata cgc	207

Val	Glu	Arg	His	Asp	Met	Asn	Thr	Leu	Ser	Leu	Pro	Leu	Asn	Ile	Arg		
27					32					37					42		
cga	ggg	ggg	tca	gac	acc	aac	ctc	aac	ttt	gat	gtc	ccg	gat	ggc	atc	255	
Arg	Gly	Gly	Ser	Asp	Thr	Asn	Leu	Asn	Phe	Asp	Val	Pro	Asp	Gly	Ile		
43					48					53					58		
ctg	gac	ttc	cac	aag	gtc	aaa	ctc	act	gca	gac	agc	ctg	aag	caa	aaa	303	
Leu	Asp	Phe	His	Lys	Val	Lys	Leu	Thr	Ala	Asp	Ser	Leu	Lys	Gln	Lys		
59					64					69					74		
att	cta	aag	gta	aca	gag	cag	ata	aaa	att	gag	caa	aca	tcg	cgc	gat	351	
Ile	Leu	Lys	Val	Thr	Glu	Gln	Ile	Lys	Ile	Glu	Gln	Thr	Ser	Arg	Asp		
75					80					85					90		
ggg	aat	gtt	gcg	gag	tat	ctg	aaa	cta	gtg	aac	aac	gcg	gac	aag	cag	399	
Gly	Asn	Val	Ala	Glu	Tyr	Leu	Lys	Leu	Val	Asn	Asn	Ala	Asp	Lys	Gln		
91					96					101					106		
cag	gcg	gga	cgt	atc	aag	caa	gtc	ttt	gag	aag	aag	aat	cag	aaa	tca	447	
Gln	Ala	Gly	Arg	Ile	Lys	Gln	Val	Phe	Glu	Lys	Lys	Asn	Gln	Lys	Ser		
107					112					117					122		
gct	cac	tcc	atc	gcc	cag	ctg	cag	aag	aag	tta	gag	cag	tat	cat	cga	495	
Ala	His	Ser	Ile	Ala	Gln	Leu	Gln	Lys	Lys	Leu	Glu	Gln	Tyr	His	Arg		
123					128					133					138		
aag	ctc	aga	gag	atc	gag	cag	aat	gga	gcc	tct	agg	agc	tca	aag	gac	543	
Lys	Leu	Arg	Glu	Ile	Glu	Gln	Asn	Gly	Ala	Ser	Arg	Ser	Ser	Lys	Asp		
139					144					149					154		
att	tcc	aaa	gac	cac	ctg	aag	gat	ata	cat	cgc	tct	ttg	aaa	gat	gcc	591	
Ile	Ser	Lys	Asp	His	Leu	Lys	Asp	Ile	His	Arg	Ser	Leu	Lys	Asp	Ala		
155					160					165					170		
cac	gtg	aaa	tct	cga	act	gcc	ccc	cat	tgc	atg	gag	agc	agc	aaa	tcg	639	
His	Val	Lys	Ser	Arg	Thr	Ala	Pro	His	Cys	Met	Glu	Ser	Ser	Lys	Ser		
171					176					181					186		
ggc	atg	cca	ggg	gtc	tca	ctt	act	cca	cct	gtg	ttc	gtt	ttc	aat	aag	687	
Gly	Met	Pro	Gly	Val	Ser	Leu	Thr	Pro	Pro	Val	Phe	Val	Phe	Asn	Lys		
187					192					197					202		
tcc	aga	gag	ttt	gcc	aac	ctg	atc	cgg	aat	aag	ttt	ggc	agc	gcc	gac	735	
Ser	Arg	Glu	Phe	Ala	Asn	Leu	Ile	Arg	Asn	Lys	Phe	Gly	Ser	Ala	Asp		
203					208					213					218		
aac	att	gct	cac	ttg	aaa	aat	tcc	tta	gag	gag	ttt	agg	cca	gag	gcg	783	
Asn	Ile	Ala	His	Leu	Lys	Asn	Ser	Leu	Glu	Glu	Phe	Arg	Pro	Glu	Ala		
219					224					229					234		
agt	gcc	agg	gcc	tac	ggg	ggc	agc	gct	acc	atc	gtg	aac	aaa	ccc	aag	831	
Ser	Ala	Arg	Ala	Tyr	Gly	Gly	Ser	Ala	Thr	Ile	Val	Asn	Lys	Pro	Lys		
235					240					245					250		
tat	ggc	agt	gat	gat	gaa	tgt	tcg	agt	ggc	acg	tca	ggc	tcg	gcc	gac	879	
Tyr	Gly	Ser	Asp	Asp	Glu	Cys	Ser	Ser	Gly	Thr	Ser	Gly	Ser	Ala	Asp		

251	256	261	266	
agt aac gga aac cag tcg ttt ggg gct ggt gga gcc agc aca ctg gac				927
Ser Asn Gly Asn Gln Ser Phe Gly Ala Gly Gly Ala Ser Thr Leu Asp				
267	272	277	282	
agc cag ggc aag ctc gcc gtg atc ctg gag gaa ctg agg gag atc aag				975
Ser Gln Gly Lys Leu Ala Val Ile Leu Glu Glu Leu Arg Glu Ile Lys				
283	288	293	298	
gat acc caa gct cag ctg gct gag gac atc gag gca ctg aag gtg cag				1023
Asp Thr Gln Ala Gln Leu Ala Glu Asp Ile Glu Ala Leu Lys Val Gln				
299	304	309	314	
ttt aag aga gaa tat ggt ttt att tct cag acc ctg caa gag gaa aga				1071
Phe Lys Arg Glu Tyr Gly Phe Ile Ser Gln Thr Leu Gln Glu Glu Arg				
315	320	325	330	
tac agg tat gag cga ctg gag gac cag ctg cat gac ctg acg gac ctg				1119
Tyr Arg Tyr Glu Arg Leu Glu Asp Gln Leu His Asp Leu Thr Asp Leu				
331	336	341	346	
cat cag cat gag aca gcc aac ctg aag cag gag ctg gcc agc att gag				1167
His Gln His Glu Thr Ala Asn Leu Lys Gln Glu Leu Ala Ser Ile Glu				
347	352	357	362	
gag aag gtg gcc tac cag gcc tac gag cgc tcg cgg gac atc cag gaa				1215
Glu Lys Val Ala Tyr Gln Ala Tyr Glu Arg Ser Arg Asp Ile Gln Glu				
363	368	373	378	
gcc ttg gaa tcc tgc cag act cgc att tct aag ctg gag ctc cac cag				1263
Ala Leu Glu Ser Cys Gln Thr Arg Ile Ser Lys Leu Glu Leu His Gln				
379	384	389	394	
caa gag cag caa gct ctg cag aca gac acc gtg aat gct aaa gtt ctc				1311
Gln Glu Gln Gln Ala Leu Gln Thr Asp Thr Val Asn Ala Lys Val Leu				
395	400	405	410	
ctg ggg agg tgc atc aac gtg atc ctg gcc ttc atg act gtc atc tta				1359
Leu Gly Arg Cys Ile Asn Val Ile Leu Ala Phe Met Thr Val Ile Leu				
411	416	421	426	
gtg tgt gtg tcc acc atc gcg aag ttc gtc tca ccc atg atg aag agt				1407
Val Cys Val Ser Thr Ile Ala Lys Phe Val Ser Pro Met Met Lys Ser				
427	432	437	442	
cgc tgc cac att ctt ggc acc ttc ttt gcc gtg act ctt ctt gct ata				1455
Arg Cys His Ile Leu Gly Thr Phe Phe Ala Val Thr Leu Leu Ala Ile				
443	448	453	458	
ttt tgt aaa aac tgg gac cat atc ctg tgt gcc ata gaa agg atg ata				1503
Phe Cys Lys Asn Trp Asp His Ile Leu Cys Ala Ile Glu Arg Met Ile				
459	464	469	474	
ata cca aga tga agc cactggttcc tgccttcaag ttctttcaag tttttatttt				1558
Ile Pro Arg *				
475				

aaagaaaact ctgtgcatac taccaaattt tacagtgaat gattgtgcgg actcgtgtgt 1618
aagaaaaact aggactgtgt ggtgtaaata actacaattc tcttaactcg gtagcagttg 1678
ccaactcagt ccttgtactt cgtaacacg gatctgtttc agagctctcc taccttgctc 1738
actgccttaa tcagaccgat ttctgcccc cctgaccagc ccaacgtggt aaacctctgt 1798

<210> 36
<211> 1038
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (367) .. (1026)

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ggcagctggt ttgggctgag gtgtccctag ctggctctgc ggctcttccg ggtctgggct 60
cggagattca caggcggccc gcgaggcca gcgaggacg catggccctg aggcggccgc 120
agggcttggc ggggtccgga ggttgacctc gccccgcag cgggccttcg aggtgcctc 180
ctccaggcag cctctggggc ccgcgcccgc gcctgtcag gctcccggtg tcaggctgcc 240
catccctcc ccaccggcgt cccggacgtt gggacctgtg accgtggcct cgggctgggc 300
ttccaaagcc ggccgcagcc cggcgacccc cgaggcctct cgccccgggc ccctagacct 360
ctcact atg acc gcg gcc gcc gcc tcc aac tgg ggg ctg atc acg aac 408
Met Thr Ala Ala Ala Ala Ser Asn Trp Gly Leu Ile Thr Asn
1 5 10
atc gtg aac agc atc gta ggg gtc agt gtc ctc acc atg ccc ttc tgc 456
Ile Val Asn Ser Ile Val Gly Val Ser Val Leu Thr Met Pro Phe Cys
15 20 25 30
ttc aaa cag tgc ggc atc gtc ctg ggg gcg ctg ctc ttg gtc ttc tgc 504
Phe Lys Gln Cys Gly Ile Val Leu Gly Ala Leu Leu Leu Val Phe Cys
31 36 41 46
tca tgg atg acg cac cag tcg tgc atg ttc ttg gtg aag tcg gcc agc 552
Ser Trp Met Thr His Gln Ser Cys Met Phe Leu Val Lys Ser Ala Ser
47 52 57 62
ctg agc aag cgg agg acc tac gcc ggc ctg gca ttc cac gcc tac ggg 600
Leu Ser Lys Arg Arg Thr Tyr Ala Gly Leu Ala Phe His Ala Tyr Gly
63 68 73 78
aag gca ggc aag atg ctg gtg gag acc agc atg atc ggg ctg atg ctg 648
Lys Ala Gly Lys Met Leu Val Glu Thr Ser Met Ile Gly Leu Met Leu
79 84 89 94

ggc acc tgc atc gcc ttc tac gtc gtg atc ggc gac ttg ggg tcc aac	696
Gly Thr Cys Ile Ala Phe Tyr Val Val Ile Gly Asp Leu Gly Ser Asn	
95 100 105 110	
ttc ttt gcc cgg ctg ttc ggg ttt cag gtg ggc ggc acc ttc cgc atg	744
Phe Phe Ala Arg Leu Phe Gly Phe Gln Val Gly Gly Thr Phe Arg Met	
111 116 121 126	
ttc ctg ctg ttc gcc gtg tgc ctg tgc atc gtg ctc ccg ctc agc ctg	792
Phe Leu Leu Phe Ala Val Ser Leu Cys Ile Val Leu Pro Leu Ser Leu	
127 132 137 142	
cag cgg aac atg atg gcc tcc atc cag tcc ttc agc gcc atg gcc ctc	840
Gln Arg Asn Met Met Ala Ser Ile Gln Ser Phe Ser Ala Met Ala Leu	
143 148 153 158	
ctc ttc tac acc gtg ttt atg ttc gtg atc gtg ctc tcc cct ctc aag	888
Leu Phe Tyr Thr Val Phe Met Phe Val Ile Val Leu Ser Pro Leu Lys	
159 164 169 174	
cac ggc ctc ttc agt ggg cag tgg ctg cgg cgg gtc agc tac gtc cgc	936
His Gly Leu Phe Ser Gly Gln Trp Leu Arg Arg Val Ser Tyr Val Arg	
175 180 185 190	
tgg gag ggc gtc ttc cgc tgc atc ccc atc ttc ggg cat gtc ctt cgc	984
Trp Glu Gly Val Phe Arg Cys Ile Pro Ile Phe Gly His Val Leu Arg	
191 196 201 206	
ctg cca gtc cca agt gct gcc cac cta cga cag cct gga tga gccgtca	1033
Leu Pro Val Pro Ser Ala Ala His Leu Arg Gln Pro Gly *	
207 212 217	
gtgat	1038

<210> 37
 <211> 6976
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (226) .. (6417)

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agaattttga tttggctgct gggctgctac cttgaaatcc aagccctaaa aatgccagct	120
tctttggact tagaagatga cctggataaa tgataaaaat taagaaagag attttgaagt	180
tttcttattg tcctcttggc atatgcttct ggaataatat tcacc atg gtt ttg	234
	Met Val Leu
	1

gat gac ctt cca aac tta gaa gac atc tat act tcc ttg tgt tca tca	282
Asp Asp Leu Pro Asn Leu Glu Asp Ile Tyr Thr Ser Leu Cys Ser Ser	
4 9 14 19	
aca atg gaa gac tca gag atg gat ttt gac tct gga cta gaa gat gat	330
Thr Met Glu Asp Ser Glu Met Asp Phe Asp Ser Gly Leu Glu Asp Asp	
20 25 30 35	
gac aca aaa agt gat agt att ttg gag gat tcc aca att ttt gtg gcc	378
Asp Thr Lys Ser Asp Ser Ile Leu Glu Asp Ser Thr Ile Phe Val Ala	
36 41 46 51	
ttc aaa gga aat ata gat gat aaa gac ttc aaa tgg aaa tta gat gca	426
Phe Lys Gly Asn Ile Asp Asp Lys Asp Phe Lys Trp Lys Leu Asp Ala	
52 57 62 67	
ata ttg aaa aac gtg ccc aat ttg tta cac atg gag tcc agc aag cta	474
Ile Leu Lys Asn Val Pro Asn Leu Leu His Met Glu Ser Ser Lys Leu	
68 73 78 83	
aaa gta cag aag gtg gag ccc tgg aac agc gtg cgt gtg aca ttc aac	522
Lys Val Gln Lys Val Glu Pro Trp Asn Ser Val Arg Val Thr Phe Asn	
84 89 94 99	
atc ccc cgg gaa gca gcg gag cgg cta cgg atc ctt gct cag agc aac	570
Ile Pro Arg Glu Ala Ala Glu Arg Leu Arg Ile Leu Ala Gln Ser Asn	
100 105 110 115	
aac cag cag ctt cgg gat tta ggg att ctc tcc gtt cag att gaa ggg	618
Asn Gln Gln Leu Arg Asp Leu Gly Ile Leu Ser Val Gln Ile Glu Gly	
116 121 126 131	
gaa ggt gct att aac ctg gct ttg gct cag aac cga agc caa gat gtg	666
Glu Gly Ala Ile Asn Leu Ala Leu Ala Gln Asn Arg Ser Gln Asp Val	
132 137 142 147	
aga atg aat gga ccc atg gga gct gga aat tca gtt agg atg gag gcg	714
Arg Met Asn Gly Pro Met Gly Ala Gly Asn Ser Val Arg Met Glu Ala	
148 153 158 163	
gga ttt cct atg gca agt ggt cca gga ata ata agg atg aac aac cct	762
Gly Phe Pro Met Ala Ser Gly Pro Gly Ile Ile Arg Met Asn Asn Pro	
164 169 174 179	
gcc act gtt atg ata ccc ccg ggt gga aat gtg tca tct tcc atg atg	810
Ala Thr Val Met Ile Pro Pro Gly Gly Asn Val Ser Ser Ser Met Met	
180 185 190 195	
gca cca ggc ccc aat cca gag ctg cag ccc agg act cct cgc cct gct	858
Ala Pro Gly Pro Asn Pro Glu Leu Gln Pro Arg Thr Pro Arg Pro Ala	
196 201 206 211	
tct cag tca gat gca atg gat cca ctc ctc tct ggg ctc cat ata cag	906
Ser Gln Ser Asp Ala Met Asp Pro Leu Leu Ser Gly Leu His Ile Gln	
212 217 222 227	

cag caa agt cat ccc tca gga tct tta gct ccc cca cat cac cca atg	954
Gln Gln Ser His Pro Ser Gly Ser Leu Ala Pro Pro His His Pro Met	
228 233 238 243	
cag cct gtc tct gtg aac aga caa atg aac cca gct aat ttt ccc cag	1002
Gln Pro Val Ser Val Asn Arg Gln Met Asn Pro Ala Asn Phe Pro Gln	
244 249 254 259	
ctg cag cag cag cag caa caa caa caa cag cag cag cag cag cag cag	1050
Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
260 265 270 275	
cag caa caa cag caa cag cag caa caa cag ttg cag gca aga ccc cca	1098
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Ala Arg Pro Pro	
276 281 286 291	
cag caa cat cag cag caa cag cca cag gga att cga ccc cag ttt act	1146
Gln Gln His Gln Gln Gln Gln Pro Gln Gly Ile Arg Pro Gln Phe Thr	
292 297 302 307	
gcc cca act cag gtg cct gtt cct cca gcc tgg aac cag ctg cct tct	1194
Ala Pro Thr Gln Val Pro Val Pro Pro Gly Trp Asn Gln Leu Pro Ser	
308 313 318 323	
gga gcc ctt caa cct cct cca gcc cag ggt tct ctg gcc aca atg act	1242
Gly Ala Leu Gln Pro Pro Pro Ala Gln Gly Ser Leu Gly Thr Met Thr	
324 329 334 339	
gca aac caa ggg tgg aag aag gct ccc ttg ccc gcc cca atg caa cag	1290
Ala Asn Gln Gly Trp Lys Lys Ala Pro Leu Pro Gly Pro Met Gln Gln	
340 345 350 355	
caa ctc cag gca aga cca tcc tta gcc acg gta cag acg cct tcc cac	1338
Gln Leu Gln Ala Arg Pro Ser Leu Ala Thr Val Gln Thr Pro Ser His	
356 361 366 371	
cct ccc cct cca tat ccc ttt ggc agc cag caa gcc tca caa gcc cac	1386
Pro Pro Pro Pro Tyr Pro Phe Gly Ser Gln Gln Ala Ser Gln Ala His	
372 377 382 387	
aca aac ttt cct cag atg agc aac cca gcc cag ttc aca gct cct cag	1434
Thr Asn Phe Pro Gln Met Ser Asn Pro Gly Gln Phe Thr Ala Pro Gln	
388 393 398 403	
atg aag agt ttg cag gga ggg ccc tct agg gtc cca act ccc ttg cag	1482
Met Lys Ser Leu Gln Gly Gly Pro Ser Arg Val Pro Thr Pro Leu Gln	
404 409 414 419	
cag ccc cac ctc acc aac aag tct cct gcc tcc tca ccc tcc tcc ttc	1530
Gln Pro His Leu Thr Asn Lys Ser Pro Ala Ser Ser Pro Ser Ser Phe	
420 425 430 435	
cag cag gga tcc cct gca tcc tcc cca acg gtt aac caa act cag cag	1578
Gln Gln Gly Ser Pro Ala Ser Ser Pro Thr Val Asn Gln Thr Gln Gln	
436 441 446 451	
cag atg gga cca agg cca cct caa aat aac cca ctt ccc cag gga ttt	1626

Gln Met Gly Pro Arg Pro Pro Gln Asn Asn Pro Leu Pro Gln Gly Phe	
452 457 462 467	
cag cag cct gtc agc tct ccg ggt cgg aat cct atg gtt caa cag gga	1674
Gln Gln Pro Val Ser Ser Pro Gly Arg Asn Pro Met Val Gln Gln Gly	
468 473 478 483	
aat gtg cca cct aac ttc atg gtg atg cag cag caa cca cca aac cag	1722
Asn Val Pro Pro Asn Phe Met Val Met Gln Gln Gln Pro Pro Asn Gln	
484 489 494 499	
ggg cca cag agt tta cat cca ggc cta gga gga atg cct aaa cgc ctc	1770
Gly Pro Gln Ser Leu His Pro Gly Leu Gly Gly Met Pro Lys Arg Leu	
500 505 510 515	
cca cct ggc ttc tca gca gga cag gcc aat ccg aac ttt atg caa ggt	1818
Pro Pro Gly Phe Ser Ala Gly Gln Ala Asn Pro Asn Phe Met Gln Gly	
516 521 526 531	
cag gtg cct tcg acc aca gca acc acc cct ggg aat tca gga gcc cct	1866
Gln Val Pro Ser Thr Thr Ala Thr Thr Pro Gly Asn Ser Gly Ala Pro	
532 537 542 547	
cag ctg caa gca aat caa aat gtc cag cat gca ggt ggt caa gga gct	1914
Gln Leu Gln Ala Asn Gln Asn Val Gln His Ala Gly Gly Gln Gly Ala	
548 553 558 563	
ggg cct cct caa aac cag atg cag gtg tcc cac ggg ccg cca aat atg	1962
Gly Pro Pro Gln Asn Gln Met Gln Val Ser His Gly Pro Pro Asn Met	
564 569 574 579	
atg cag ccc agc ctc atg gga att cat ggc aac atg aac aat cag cag	2010
Met Gln Pro Ser Leu Met Gly Ile His Gly Asn Met Asn Asn Gln Gln	
580 585 590 595	
gct ggt act tct ggg gtt cct caa gtg aac ctc agc aac atg caa ggc	2058
Ala Gly Thr Ser Gly Val Pro Gln Val Asn Leu Ser Asn Met Gln Gly	
596 601 606 611	
cag ccc cag cag ggc cca cca tct cag ctg atg ggc atg cac cag caa	2106
Gln Pro Gln Gln Gly Pro Pro Ser Gln Leu Met Gly Met His Gln Gln	
612 617 622 627	
atc gtg ccc tcc cag ggc cag atg gtc cag caa caa gga acc ttg aac	2154
Ile Val Pro Ser Gln Gly Gln Met Val Gln Gln Gln Gly Thr Leu Asn	
628 633 638 643	
cct cag aac cct atg atc ctt tca agg gcc cag ctt atg cca cag ggc	2202
Pro Gln Asn Pro Met Ile Leu Ser Arg Ala Gln Leu Met Pro Gln Gly	
644 649 654 659	
cag atg atg gtg aac ccc ccg agc caa aat ctt ggg ccc tcg ccc caa	2250
Gln Met Met Val Asn Pro Pro Ser Gln Asn Leu Gly Pro Ser Pro Gln	
660 665 670 675	
agg atg acc cca ccc aag cag atg ctt tcc cag cag ggc cca caa atg	2298
Arg Met Thr Pro Pro Lys Gln Met Leu Ser Gln Gln Gly Pro Gln Met	

676	681	686	691	
atg gcg cca cat aac cag atg atg ggg cct cag ggg cag gtt ttg ctc				2346
Met Ala Pro His Asn Gln Met Met Gly Pro Gln Gly Gln Val Leu Leu				
692	697	702	707	
caa cag aac cca atg ata gag cag att atg acc aat caa atg cag ggg				2394
Gln Gln Asn Pro Met Ile Glu Gln Ile Met Thr Asn Gln Met Gln Gly				
708	713	718	723	
aat aag cag cag ttt aac act cag aac cag tcc aat gtc atg ccg gga				2442
Asn Lys Gln Gln Phe Asn Thr Gln Asn Gln Ser Asn Val Met Pro Gly				
724	729	734	739	
cca gcc cag ata atg agg gga cca act cca aac atg caa gga aat atg				2490
Pro Ala Gln Ile Met Arg Gly Pro Thr Pro Asn Met Gln Gly Asn Met				
740	745	750	755	
gtg cag ttt acg gga cag atg tca gga cag atg ctg ccc cag caa ggg				2538
Val Gln Phe Thr Gly Gln Met Ser Gly Gln Met Leu Pro Gln Gln Gly				
756	761	766	771	
cct gtg aac aac agt cca tct cag gtt atg ggc att cag gga cag gtc				2586
Pro Val Asn Asn Ser Pro Ser Gln Val Met Gly Ile Gln Gly Gln Val				
772	777	782	787	
ctg cgg cca cca ggg ccc agc cca cac atg gcc cag cag cat ggt gat				2634
Leu Arg Pro Pro Gly Pro Ser Pro His Met Ala Gln Gln His Gly Asp				
788	793	798	803	
cct gct act aca gca aat aac gat gtc agt tta tct cag atg atg cct				2682
Pro Ala Thr Thr Ala Asn Asn Asp Val Ser Leu Ser Gln Met Met Pro				
804	809	814	819	
gat gtt agc att caa caa acc aac atg gtc ccc cct cat gtg cag gcc				2730
Asp Val Ser Ile Gln Gln Thr Asn Met Val Pro Pro His Val Gln Ala				
820	825	830	835	
atg cag gga aac agt gcc tcg gga aac cac ttc tca ggc cat ggg atg				2778
Met Gln Gly Asn Ser Ala Ser Gly Asn His Phe Ser Gly His Gly Met				
836	841	846	851	
tct ttc aat gca cct ttc agt gga gct ccc aat gga aat cag atg tcc				2826
Ser Phe Asn Ala Pro Phe Ser Gly Ala Pro Asn Gly Asn Gln Met Ser				
852	857	862	867	
tgt ggt caa aat cca ggc ttc cca gtc aat aag gat gtc acg cta acg				2874
Cys Gly Gln Asn Pro Gly Phe Pro Val Asn Lys Asp Val Thr Leu Thr				
868	873	878	883	
agc cca ttg ttg gtc aac tta ttg cag agt gac ata tct gca ggc cat				2922
Ser Pro Leu Leu Val Asn Leu Leu Gln Ser Asp Ile Ser Ala Gly His				
884	889	894	899	
ttt ggg gta aac aat aag caa aat aat acc aac gca aat aaa ccg aag				2970
Phe Gly Val Asn Asn Lys Gln Asn Asn Thr Asn Ala Asn Lys Pro Lys				
900	905	910	915	

aag aag aaa ccc cct cgg aag aag aaa aat agt cag caa gat cta aac	3018
Lys Lys Lys Pro Pro Arg Lys Lys Lys Asn Ser Gln Gln Asp Leu Asn	
916 921 926 931	
acc cca gat act cgc cca gct ggt ctg gaa gag gct gat cag cca ccg	3066
Thr Pro Asp Thr Arg Pro Ala Gly Leu Glu Glu Ala Asp Gln Pro Pro	
932 937 942 947	
ttg cct gga gaa caa gga att agc ttg gat aac tca ggc cct aaa ctg	3114
Leu Pro Gly Glu Gln Gly Ile Ser Leu Asp Asn Ser Gly Pro Lys Leu	
948 953 958 963	
cca gaa ttt tca aac cgg cca cca ggt tat cct tct caa cca gtt gaa	3162
Pro Glu Phe Ser Asn Arg Pro Pro Gly Tyr Pro Ser Gln Pro Val Glu	
964 969 974 979	
cag agg cca ctt cag cag atg cct cct caa ctc atg cag cat gtg gca	3210
Gln Arg Pro Leu Gln Gln Met Pro Pro Gln Leu Met Gln His Val Ala	
980 985 990 995	
ccc cca cca cag cca cca cag cag cag cca cag cca caa ctg cct cag	3258
Pro Pro Pro Gln Pro Pro Gln Gln Gln Pro Gln Pro Gln Leu Pro Gln	
996 1001 1006 1011	
cag cag cag cca cca cct ccc agt cag cca cag tct cag cag cag cag	3306
Gln Gln Gln Pro Pro Pro Pro Ser Gln Pro Gln Ser Gln Gln Gln Gln	
1012 1017 1022 1027	
cag cag cag caa caa atg atg atg atg ctc atg atg cag cag gat ccc	3354
Gln Gln Gln Gln Gln Met Met Met Met Leu Met Met Gln Gln Asp Pro	
1028 1033 1038 1043	
aaa tca gtt agg ctt cca gtc tct caa aat gtc cat cct cca agg ggc	3402
Lys Ser Val Arg Leu Pro Val Ser Gln Asn Val His Pro Pro Arg Gly	
1044 1049 1054 1059	
ccc ctg aac ccc gac tcc cag aga atg ccc atg caa cag agt ggc agt	3450
Pro Leu Asn Pro Asp Ser Gln Arg Met Pro Met Gln Gln Ser Gly Ser	
1060 1065 1070 1075	
gtg cct gtc atg gtc agt ctg caa gga cct gcc tcc gtg cca cca tca	3498
Val Pro Val Met Val Ser Leu Gln Gly Pro Ala Ser Val Pro Pro Ser	
1076 1081 1086 1091	
cct gat aaa caa aga atg cca atg cct gtg aat act ccc ttg gga agc	3546
Pro Asp Lys Gln Arg Met Pro Met Pro Val Asn Thr Pro Leu Gly Ser	
1092 1097 1102 1107	
aat tca agg aaa atg gtc tat cag gag agc ccg cag aat cct tcc agc	3594
Asn Ser Arg Lys Met Val Tyr Gln Glu Ser Pro Gln Asn Pro Ser Ser	
1108 1113 1118 1123	
tcg cca ctg gcg gag atg gcc tca ctc cct gaa gca agt ggc agt gaa	3642
Ser Pro Leu Ala Glu Met Ala Ser Leu Pro Glu Ala Ser Gly Ser Glu	
1124 1129 1134 1139	

gca cca tct gtc cca gga ggc cca aac aac atg cct tca cat gta gta	3690
Ala Pro Ser Val Pro Gly Gly Pro Asn Asn Met Pro Ser His Val Val	
1140 1145 1150 1155	
ctt ccc cag aat cag tta atg atg aca ggg cca aaa cct gga cca tcg	3738
Leu Pro Gln Asn Gln Leu Met Met Thr Gly Pro Lys Pro Gly Pro Ser	
1156 1161 1166 1171	
ccc ctt tca gca act caa ggt gca act ccc cag caa ccc cct gta aat	3786
Pro Leu Ser Ala Thr Gln Gly Ala Thr Pro Gln Gln Pro Pro Val Asn	
1172 1177 1182 1187	
tcc ctg ccc agc tct cac ggc cac cac ttc cca aat gtg gct gcg cca	3834
Ser Leu Pro Ser Ser His Gly His His Phe Pro Asn Val Ala Ala Pro	
1188 1193 1198 1203	
acc cag aca tct agg ccc aaa aca cca aac aga gcc agc ccc aga ccc	3882
Thr Gln Thr Ser Arg Pro Lys Thr Pro Asn Arg Ala Ser Pro Arg Pro	
1204 1209 1214 1219	
tat tat cct cag aca ccc aac aac cgc cct ccc agc aca gaa cct tca	3930
Tyr Tyr Pro Gln Thr Pro Asn Asn Arg Pro Pro Ser Thr Glu Pro Ser	
1220 1225 1230 1235	
gaa atc agt ctg tca cca gaa aga ctc aat gcc tcc ata gca gga ctc	3978
Glu Ile Ser Leu Ser Pro Glu Arg Leu Asn Ala Ser Ile Ala Gly Leu	
1236 1241 1246 1251	
ttc cct cca cag att aat att cct tta cct cct agg cca aat tta aac	4026
Phe Pro Pro Gln Ile Asn Ile Pro Leu Pro Pro Arg Pro Asn Leu Asn	
1252 1257 1262 1267	
agg ggc ttt gat caa caa ggc cta aat ccg aca att ttg aag gcc atc	4074
Arg Gly Phe Asp Gln Gln Gly Leu Asn Pro Thr Ile Leu Lys Ala Ile	
1268 1273 1278 1283	
ggg caa gca cct tca aat ctt acc atg aat cct tcc aat ttt gct acc	4122
Gly Gln Ala Pro Ser Asn Leu Thr Met Asn Pro Ser Asn Phe Ala Thr	
1284 1289 1294 1299	
cca caa act cac aaa tta gat tct gtg gta gtg aat tct gga aag cag	4170
Pro Gln Thr His Lys Leu Asp Ser Val Val Asn Ser Gly Lys Gln	
1300 1305 1310 1315	
tct aat tct gga gca aca aaa cgg gca agt cca agc aac agt cgc agg	4218
Ser Asn Ser Gly Ala Thr Lys Arg Ala Ser Pro Ser Asn Ser Arg Arg	
1316 1321 1326 1331	
tct agt cct ggg tcc agt agg aaa acc act cca agc cct ggg agg caa	4266
Ser Ser Pro Gly Ser Ser Arg Lys Thr Thr Pro Ser Pro Gly Arg Gln	
1332 1337 1342 1347	
aat tca aaa gcc cct aaa ctt act ctg gcc tct cag aca aat gca gcc	4314
Asn Ser Lys Ala Pro Lys Leu Thr Leu Ala Ser Gln Thr Asn Ala Ala	
1348 1353 1358 1363	
cta ttg cag aat gtg gag ttg ccg aga aat gta ttg gtc agt ccc act	4362

Leu	Leu	Gln	Asn	Val	Glu	Leu	Pro	Arg	Asn	Val	Leu	Val	Ser	Pro	Thr		
1364					1369					1374					1379		
cct	ctg	gcc	aat	ccc	cct	gta	cct	ggg	agc	ttt	cct	aac	aac	agt	ggg	4410	
Pro	Leu	Ala	Asn	Pro	Pro	Val	Pro	Gly	Ser	Phe	Pro	Asn	Asn	Ser	Gly		
1380					1385					1390					1395		
ctg	aat	cct	cag	aat	tct	act	gtg	tct	gtg	gct	gca	gtt	ggg	ggt	gtt	4458	
Leu	Asn	Pro	Gln	Asn	Ser	Thr	Val	Ser	Val	Ala	Ala	Val	Gly	Gly	Val		
1396					1401					1406					1411		
gtt	gag	gat	aac	aag	gag	agc	ttg	aat	gtg	cct	cag	gac	agt	gat	tgc	4506	
Val	Glu	Asp	Asn	Lys	Glu	Ser	Leu	Asn	Val	Pro	Gln	Asp	Ser	Asp	Cys		
1412					1417					1422					1427		
cag	aat	tcc	cag	agt	agg	aag	gaa	cag	gta	aac	att	gaa	cta	aaa	gca	4554	
Gln	Asn	Ser	Gln	Ser	Arg	Lys	Glu	Gln	Val	Asn	Ile	Glu	Leu	Lys	Ala		
1428					1433					1438					1443		
gtc	cct	gcc	caa	gaa	gtt	aaa	atg	gtt	gtc	cct	gaa	gat	cag	tcc	aaa	4602	
Val	Pro	Ala	Gln	Glu	Val	Lys	Met	Val	Val	Pro	Glu	Asp	Gln	Ser	Lys		
1444					1449					1454					1459		
aag	gat	ggg	cag	cct	tcg	gat	cct	aac	aaa	ctt	ccc	agt	gtc	gaa	gag	4650	
Lys	Asp	Gly	Gln	Pro	Ser	Asp	Pro	Asn	Lys	Leu	Pro	Ser	Val	Glu	Glu		
1460					1465					1470					1475		
aac	aaa	aat	ttg	gtg	tct	cct	gct	atg	agg	gaa	gca	cca	aca	tcg	tta	4698	
Asn	Lys	Asn	Leu	Val	Ser	Pro	Ala	Met	Arg	Glu	Ala	Pro	Thr	Ser	Leu		
1476					1481					1486					1491		
agt	caa	ctt	ctt	gac	aac	tct	gga	gct	ccc	aat	gtg	aca	att	aaa	ccc	4746	
Ser	Gln	Leu	Leu	Asp	Asn	Ser	Gly	Ala	Pro	Asn	Val	Thr	Ile	Lys	Pro		
1492					1497					1502					1507		
cct	ggg	ctt	aca	gat	ctg	gaa	gta	aca	cct	cca	gta	gtt	tct	ggg	gag	4794	
Pro	Gly	Leu	Thr	Asp	Leu	Glu	Val	Thr	Pro	Pro	Val	Val	Ser	Gly	Glu		
1508					1513					1518					1523		
gac	ctc	aaa	aaa	gca	tct	gtc	att	ccc	aca	ctg	cag	gat	ctg	tct	tct	4842	
Asp	Leu	Lys	Lys	Ala	Ser	Val	Ile	Pro	Thr	Leu	Gln	Asp	Leu	Ser	Ser		
1524					1529					1534					1539		
tct	aaa	gaa	cct	tct	aat	tcc	cta	aac	tta	cct	cac	agt	aat	gag	ctg	4890	
Ser	Lys	Glu	Pro	Ser	Asn	Ser	Leu	Asn	Leu	Pro	His	Ser	Asn	Glu	Leu		
1540					1545					1550					1555		
tgt	tca	tcc	ctt	gtg	cat	ccc	gaa	ttg	agt	gag	gtc	agt	tct	aac	gtt	4938	
Cys	Ser	Ser	Leu	Val	His	Pro	Glu	Leu	Ser	Glu	Val	Ser	Ser	Asn	Val		
1556					1561					1566					1571		
gca	cca	agc	atc	cct	cca	gta	atg	tca	aga	cct	gtt	agc	tct	tcc	tcc	4986	
Ala	Pro	Ser	Ile	Pro	Pro	Val	Met	Ser	Arg	Pro	Val	Ser	Ser	Ser	Ser		
1572					1577					1582					1587		
att	tcc	act	ccc	ttg	ccc	cca	aat	caa	ata	act	gta	ttt	gtc	act	tcc	5034	
Ile	Ser	Thr	Pro	Leu	Pro	Pro	Asn	Gln	Ile	Thr	Val	Phe	Val	Thr	Ser		

1588	1593	1598	1603	
aat ccc atc aca act tca gct aac aca tca gca gct ttg cca act cac				5082
Asn Pro Ile Thr Thr Ser Ala Asn Thr Ser Ala Ala Leu Pro Thr His				
1604	1609	1614	1619	
ttg cag tct gca ttg atg tca aca gtt gtc aca atg ccc aat gcg ggt				5130
Leu Gln Ser Ala Leu Met Ser Thr Val Val Thr Met Pro Asn Ala Gly				
1620	1625	1630	1635	
agc aag gtt atg gtt tct gag gga cag tca gct gct cag tct aat gcc				5178
Ser Lys Val Met Val Ser Glu Gly Gln Ser Ala Ala Gln Ser Asn Ala				
1636	1641	1646	1651	
cgg cct cag ttc att aca cct gtc ttt atc aat tca tcc tca ata att				5226
Arg Pro Gln Phe Ile Thr Pro Val Phe Ile Asn Ser Ser Ser Ile Ile				
1652	1657	1662	1667	
cag gtt atg aaa gga tca cag cca agc aca att cct gca gcc cca ctg				5274
Gln Val Met Lys Gly Ser Gln Pro Ser Thr Ile Pro Ala Ala Pro Leu				
1668	1673	1678	1683	
aca acc aac tct ggc ctg atg cct ccc tct gtt gca gtt gtt ggc cct				5322
Thr Thr Asn Ser Gly Leu Met Pro Pro Ser Val Ala Val Val Gly Pro				
1684	1689	1694	1699	
tta cac ata cct cag aac ata aaa ttt tct tct gct cct gta ccg cct				5370
Leu His Ile Pro Gln Asn Ile Lys Phe Ser Ser Ala Pro Val Pro Pro				
1700	1705	1710	1715	
aat gcc ctc tcc agt agt cct gct cca aac atc cag aca ggt cga cct				5418
Asn Ala Leu Ser Ser Ser Pro Ala Pro Asn Ile Gln Thr Gly Arg Pro				
1716	1721	1726	1731	
ttg gtc ctt agc tca cga gcc acc cct gtt cag ctt cct tcc cct cct				5466
Leu Val Leu Ser Ser Arg Ala Thr Pro Val Gln Leu Pro Ser Pro Pro				
1732	1737	1742	1747	
tgt acg tct tct cca gtt gtc cct tct cat ccc cct gtg cag caa gtg				5514
Cys Thr Ser Ser Pro Val Val Pro Ser His Pro Pro Val Gln Gln Val				
1748	1753	1758	1763	
aaa gaa ttg aat cca gat gag gct agc cct cag gtg aac acc tca gca				5562
Lys Glu Leu Asn Pro Asp Glu Ala Ser Pro Gln Val Asn Thr Ser Ala				
1764	1769	1774	1779	
gat cag aac act ctt ccc tct tca cag tca acc aca atg gtt tct ccc				5610
Asp Gln Asn Thr Leu Pro Ser Ser Gln Ser Thr Thr Met Val Ser Pro				
1780	1785	1790	1795	
ctt ttg acc aat agt cca ggg tcc tct ggc aac cgg cga agc cca gtc				5658
Leu Leu Thr Asn Ser Pro Gly Ser Ser Gly Asn Arg Arg Ser Pro Val				
1796	1801	1806	1811	
tcg tct agt aag ggc aaa gga aaa gtg gac aaa att ggc caa att ttg				5706
Ser Ser Ser Lys Gly Lys Gly Lys Val Asp Lys Ile Gly Gln Ile Leu				
1812	1817	1822	1827	

ttg acc aag gca tgt aag aaa gtt aca ggc tct ctt gag aaa ggg gaa	5754
Leu Thr Lys Ala Cys Lys Lys Val Thr Gly Ser Leu Glu Lys Gly Glu	
1828 1833 1838 1843	
gaa caa tat ggt gca gat gga gag act gaa ggc caa ggg cta gac acc	5802
Glu Gln Tyr Gly Ala Asp Gly Glu Thr Glu Gly Gln Gly Leu Asp Thr	
1844 1849 1854 1859	
aca gct ccg ggg ctc atg gga aca gag cag tta tcc aca gag ctg gac	5850
Thr Ala Pro Gly Leu Met Gly Thr Glu Gln Leu Ser Thr Glu Leu Asp	
1860 1865 1870 1875	
agt aaa acc cca acg ccc cca gca ccc act ctg cta aaa atg acc tct	5898
Ser Lys Thr Pro Thr Pro Pro Ala Pro Thr Leu Leu Lys Met Thr Ser	
1876 1881 1886 1891	
agc cct gtg ggc ccg ggc act gcc tca gca gga ccc agc tta cct ggc	5946
Ser Pro Val Gly Pro Gly Thr Ala Ser Ala Gly Pro Ser Leu Pro Gly	
1892 1897 1902 1907	
ggt gct ctc ccc acc agt gta cgc tcg ata gta acc act ctg gta ccc	5994
Gly Ala Leu Pro Thr Ser Val Arg Ser Ile Val Thr Thr Leu Val Pro	
1908 1913 1918 1923	
tcc gag ctc atc tcc gcc gta ccg acc aca aaa agc aat cat ggt ggc	6042
Ser Glu Leu Ile Ser Ala Val Pro Thr Thr Lys Ser Asn His Gly Gly	
1924 1929 1934 1939	
ata gca tct gag tca ctt gcg ggt ggc cta gtg gag gag aag gtg gga	6090
Ile Ala Ser Glu Ser Leu Ala Gly Gly Leu Val Glu Glu Lys Val Gly	
1940 1945 1950 1955	
tcc cat cca gaa ctt cta ccc agc ata gcc ccg tcg cag aat tta gtc	6138
Ser His Pro Glu Leu Leu Pro Ser Ile Ala Pro Ser Gln Asn Leu Val	
1956 1961 1966 1971	
tca aag gaa act tca acc aca gca ctg cag gcc tct gtt gcc aga cca	6186
Ser Lys Glu Thr Ser Thr Thr Ala Leu Gln Ala Ser Val Ala Arg Pro	
1972 1977 1982 1987	
gag ctg gag gta aat gct gcc ata gtc tct gga caa agc agt gag ccc	6234
Glu Leu Glu Val Asn Ala Ala Ile Val Ser Gly Gln Ser Ser Glu Pro	
1988 1993 1998 2003	
aaa gag ata gtt gaa aag tcc aaa atc cca ggc cga aga aac tcc cga	6282
Lys Glu Ile Val Glu Lys Ser Lys Ile Pro Gly Arg Arg Asn Ser Arg	
2004 2009 2014 2019	
act gaa gag cca act gtg gcc tct gaa agt gtg gaa aat gga cat cgt	6330
Thr Glu Glu Pro Thr Val Ala Ser Glu Ser Val Glu Asn Gly His Arg	
2020 2025 2030 2035	
aaa cga tct tct cga cct gct tca gcc tcc agc tct act aaa gac ata	6378
Lys Arg Ser Ser Arg Pro Ala Ser Ala Ser Ser Ser Thr Lys Asp Ile	
2036 2041 2046 2051	

acc agt gcg gtg caa tcc aag cga aga aaa tcc aag taa acaagcagga 6427
 Thr Ser Ala Val Gln Ser Lys Arg Arg Lys Ser Lys *
 2052 2057 2062

ctgcgacttg atacttgga atgtgtgtga cttttacaaa gagcaatttt gagctgtgac 6487
 ttttttaaat caatttctgt acagttagta attttaataa tgtggccctt ttcctagtcc 6547
 ctgcaacctg tttcataaag tgcaatgggg aaagcaggac tgttgagccc ttttggtgtt 6607
 gcgagttgaa gttcaagggt tctaaaatgt tgtcttgtat tgaaaggagc taatgccatt 6667
 ataaatgtta ctagttttca catttcctaa gcagcctaga gtacagggtg agcattttta 6727
 gatctcctaa tgatattgtg ccgtggaagt actgtgtgtg aatagcagta gtgggggcaa 6787
 aagcaatctt ctcatttgga aatgttgtaa ataattttat tatatagtgt tttggatgta 6847
 tttgtttag aaatggacca gtgaataaag agaatctaag gatttgtaca atgtgaaata 6907
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 aaaaaaaaaa 6976

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 tgtgagtctc tcgccgccgg aggaag atg agg ctg aag att gga ttc atc tta 113
 Met Arg Leu Lys Ile Gly Phe Ile Leu
 1 5

cgc agt ttg ctg gtg gtg gga agc ttc ctg ggg cta gtg gtc ctc tgg 161
 Arg Ser Leu Leu Val Val Gly Ser Phe Leu Gly Leu Val Val Leu Trp
 10 15 20 25

tct tcc ctg acc ccg cgg ccg gac gac cca agc ccg ctg agc agg atg 209
 Ser Ser Leu Thr Pro Arg Pro Asp Asp Pro Ser Pro Leu Ser Arg Met
 26 31 36 41

agg gaa gac aga gat gtc aat gac ccc atg ccc aac cga ggc ggc aat 257
 Arg Glu Asp Arg Asp Val Asn Asp Pro Met Pro Asn Arg Gly Gly Asn
 42 47 52 57

gga cta gct cct ggg gag gac aga ttc aaa cct gtg gta cca tgg cct 305
 Gly Leu Ala Pro Gly Glu Asp Arg Phe Lys Pro Val Val Pro Trp Pro

58	63	68	73	
cat gtt gaa gga gta gaa gtg gac tta gag tct att aga aga ata aac				353
His Val Glu Gly Val Glu Val Asp Leu Glu Ser Ile Arg Arg Ile Asn				
74	79	84	89	
aag gcc aaa aat gaa caa gag cac cat gct gga gga gat tcc cag aaa				401
Lys Ala Lys Asn Glu Gln Glu His His Ala Gly Gly Asp Ser Gln Lys				
90	95	100	105	
gat atc atg cag agg cag tat ctc aca ttt aag cct cag aca ttc acc				449
Asp Ile Met Gln Arg Gln Tyr Leu Thr Phe Lys Pro Gln Thr Phe Thr				
106	111	116	121	
tac cat gat cct gtg ctt cgc cca ggg atc ctc ggt aac ttt gaa ccc				497
Tyr His Asp Pro Val Leu Arg Pro Gly Ile Leu Gly Asn Phe Glu Pro				
122	127	132	137	
aaa gaa cct gag cct cct gga gtg gtt ggt ggc cct ggg aga gaa agc				545
Lys Glu Pro Glu Pro Pro Gly Val Val Gly Gly Pro Gly Arg Glu Ser				
138	143	148	153	
caa gcc att ggt ttt ggg gcc cag aat tta aac aag caa ttc aag cca				593
Gln Ala Ile Gly Phe Gly Ala Gln Asn Leu Asn Lys Gln Phe Lys Pro				
154	159	164	169	
gca ttt aaa gag ttt ggg ttt aac atg gtg gca agt gac atg ttc tca				641
Ala Phe Lys Glu Phe Gly Phe Asn Met Val Ala Ser Asp Met Phe Ser				
170	175	180	185	
ctg gac cgc aac gtc aat gac tta cgc caa gaa gaa tgc aag tat tgg				689
Leu Asp Arg Asn Val Asn Asp Leu Arg Gln Glu Glu Cys Lys Tyr Trp				
186	191	196	201	
cat tat gat gaa aac ttg ctc act tcg agc gtt gtc att gtc ttc cat				737
His Tyr Asp Glu Asn Leu Leu Thr Ser Ser Val Val Ile Val Phe His				
202	207	212	217	
aat gaa gga tgg tca acc ctc atg aga aca gtc cac agt gta att aaa				785
Asn Glu Gly Trp Ser Thr Leu Met Arg Thr Val His Ser Val Ile Lys				
218	223	228	233	
agg act cca agg aaa tat tta gca gaa att gtg tta att gac gat ttc				833
Arg Thr Pro Arg Lys Tyr Leu Ala Glu Ile Val Leu Ile Asp Asp Phe				
234	239	244	249	
agt aat aaa gaa cac tta aaa gaa aaa ctg gat gaa tat att aag ctg				881
Ser Asn Lys Glu His Leu Lys Glu Lys Leu Asp Glu Tyr Ile Lys Leu				
250	255	260	265	
tgg aat ggc cta gtg aag gta ttt cga aat gaa aga agg gaa ggt tta				929
Trp Asn Gly Leu Val Lys Val Phe Arg Asn Glu Arg Arg Glu Gly Leu				
266	271	276	281	
att caa gca cga agt att ggt gct cag aag gct aaa ctt gga cag gtt				977
Ile Gln Ala Arg Ser Ile Gly Ala Gln Lys Ala Lys Leu Gly Gln Val				
282	287	292	297	

ttg ata tac ctt gat gcc cac tgt gag gtg gca gtt aac tgg tat gca	1025
Leu Ile Tyr Leu Asp Ala His Cys Glu Val Ala Val Asn Trp Tyr Ala	
298 303 308 313	
cca ctt gta gct ccc ata tct aag gac aga acc att tgc act gtg ccg	1073
Pro Leu Val Ala Pro Ile Ser Lys Asp Arg Thr Ile Cys Thr Val Pro	
314 319 324 329	
ctt ata gat gtc ata aat ggc aac aca tat gaa att ata ccc caa ggg	1121
Leu Ile Asp Val Ile Asn Gly Asn Thr Tyr Glu Ile Ile Pro Gln Gly	
330 335 340 345	
ggg ggt gat gaa gat ggg tat gcc cga gga gca tgg gat tgg agt atg	1169
Gly Gly Asp Glu Asp Gly Tyr Ala Arg Gly Ala Trp Asp Trp Ser Met	
346 351 356 361	
ctc tgg aaa cgg gtg cct ctg acc cct caa gag aag aga ctg aga aag	1217
Leu Trp Lys Arg Val Pro Leu Thr Pro Gln Glu Lys Arg Leu Arg Lys	
362 367 372 377	
aca aaa act gaa ccg tat cgg tcc cca gcc atg gct ggg gga tta tgt	1265
Thr Lys Thr Glu Pro Tyr Arg Ser Pro Ala Met Ala Gly Gly Leu Cys	
378 383 388 393	
gcc att gaa cga gag ttc ttc ttt gaa ttg ggt ctc tat gat cca ggt	1313
Ala Ile Glu Arg Glu Phe Phe Phe Glu Leu Gly Leu Tyr Asp Pro Gly	
394 399 404 409	
ctc cag att tgg ggt ggt gaa aac ttt gag atc tca tac aag ata tgg	1361
Leu Gln Ile Trp Gly Gly Glu Asn Phe Glu Ile Ser Tyr Lys Ile Trp	
410 415 420 425	
cag tgt ggt ggc aaa tta tta ttt gtt cct tgt tct cgt gtt gga cat	1409
Gln Cys Gly Gly Lys Leu Leu Phe Val Pro Cys Ser Arg Val Gly His	
426 431 436 441	
atc tac cgt ctt gag ggc tgg caa gga aat cct ccg ccc att tat gtt	1457
Ile Tyr Arg Leu Glu Gly Trp Gln Gly Asn Pro Pro Pro Ile Tyr Val	
442 447 452 457	
ggg tct tct cca act ctg aag aat tat gtt aga gtt gtg gag gtt tgg	1505
Gly Ser Ser Pro Thr Leu Lys Asn Tyr Val Arg Val Val Glu Val Trp	
458 463 468 473	
tgg gat gaa tat aaa gac tac ttc tat gct agt cgt cct gaa tcg cag	1553
Trp Asp Glu Tyr Lys Asp Tyr Phe Tyr Ala Ser Arg Pro Glu Ser Gln	
474 479 484 489	
gca tta cca tat ggg gat ata tcg gag ctg aaa aaa ttt cga gaa gat	1601
Ala Leu Pro Tyr Gly Asp Ile Ser Glu Leu Lys Lys Phe Arg Glu Asp	
490 495 500 505	
cac aac tgc aaa agt ttt aag tgg ttc atg gaa gaa ata gct tat gat	1649
His Asn Cys Lys Ser Phe Lys Trp Phe Met Glu Glu Ile Ala Tyr Asp	
506 511 516 521	

atc acc tca cac tac cct ttg cca ccc aaa aat gtt gac tgg gga gaa	1697
Ile Thr Ser His Tyr Pro Leu Pro Pro Lys Asn Val Asp Trp Gly Glu	
522 527 532 537	
atc aga ggc ttc gaa act gct tac tgc att gat agc atg gga aaa aca	1745
Ile Arg Gly Phe Glu Thr Ala Tyr Cys Ile Asp Ser Met Gly Lys Thr	
538 543 548 553	
aat gga ggc ttt gtt gaa cta gga ccc tgc cac agg atg gga ggg aat	1793
Asn Gly Gly Phe Val Glu Leu Gly Pro Cys His Arg Met Gly Gly Asn	
554 559 564 569	
cag ctt ttc aga atc aat gaa gca aat caa ctc atg cag tat gac cag	1841
Gln Leu Phe Arg Ile Asn Glu Ala Asn Gln Leu Met Gln Tyr Asp Gln	
570 575 580 585	
tgt ttg aca aag gga gct gat gga tca aaa gtt atg att aca cac tgt	1889
Cys Leu Thr Lys Gly Ala Asp Gly Ser Lys Val Met Ile Thr His Cys	
586 591 596 601	
aat cta aat gaa ttt aag gaa tgg cag tac ttc aag aac ctg cac aga	1937
Asn Leu Asn Glu Phe Lys Glu Trp Gln Tyr Phe Lys Asn Leu His Arg	
602 607 612 617	
ttt act cat att cct tca gga aag tgt tta gat cgc tca gag gtc ctg	1985
Phe Thr His Ile Pro Ser Gly Lys Cys Leu Asp Arg Ser Glu Val Leu	
618 623 628 633	
cat caa gta ttc atc tcc aat tgt gac tcc agt aaa acg act caa aaa	2033
His Gln Val Phe Ile Ser Asn Cys Asp Ser Ser Lys Thr Thr Gln Lys	
634 639 644 649	
tgga gaa atg aat aac atc cat agt gtt tag a gagaaaaaaaa taaaccaata	2084
Trp Glu Met Asn Asn Ile His Ser Val *	
650 655	
acctacctac tgacaagtaa atttatacag gactgaaaac cgctgaaac ctgctgcaac	2144
tattgttatt aactctgtat agctccaaac ctggaacctc ctgatcagtt tgaaggacat	2204
tgataaactg tgattttaca ataacattat catctgcagg tactgggttac aagactgctt	2264
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gaa atc tta aac ctg aca tgg tgg ccg ctc ttt cga gat gtg tct ttc 987
 Glu Ile Leu Asn Leu Thr Trp Trp Pro Leu Phe Arg Asp Val Ser Phe
 186 191 196 201

tac att gtt gac ttg atc atg ctg atc ata ttt ttc ctg gat aat gtc 1035
 Tyr Ile Val Asp Leu Ile Met Leu Ile Ile Phe Phe Leu Asp Asn Val
 202 207 212 217

atc atg tgg tgg gaa agc ttg ctt ctc tta aca gct tat ttt tgc tat 1083
 Ile Met Trp Trp Glu Ser Leu Leu Leu Leu Thr Ala Tyr Phe Cys Tyr
 218 223 228 233

gtg gtt ttc atg aaa ttc aac gtc caa gta gaa aaa tgg gtg aag caa 1131
 Val Val Phe Met Lys Phe Asn Val Gln Val Glu Lys Trp Val Lys Gln
 234 239 244 249

atg ata aac cgc aat aag gtc gtc aag gtg aca gca cca gaa gcc caa 1179
 Met Ile Asn Arg Asn Lys Val Val Lys Val Thr Ala Pro Glu Ala Gln
 250 255 260 265

gca aag cca tct gca gcc agg gac aag gat gaa cca act cta ccg gct 1227
 Ala Lys Pro Ser Ala Ala Arg Asp Lys Asp Glu Pro Thr Leu Pro Ala
 266 271 276 281

aag ccg cgt ctc cag cga ggt gga agc tct gcc tcc ctc cac aac agt 1275
 Lys Pro Arg Leu Gln Arg Gly Gly Ser Ser Ala Ser Leu His Asn Ser
 282 287 292 297

ctc atg agg aat agc atc ttc caa ctc atg ata cac acc ctt gac cca 1323
 Leu Met Arg Asn Ser Ile Phe Gln Leu Met Ile His Thr Leu Asp Pro
 298 303 308 313

ctc gcc gaa gaa ctt gga tca tat gga aaa cta aaa tat tat gac aca 1371
 Leu Ala Glu Glu Leu Gly Ser Tyr Gly Lys Leu Lys Tyr Tyr Asp Thr
 314 319 324 329

atg act gaa gaa ggg agg ttc aga gaa aag gct tca att ctc cac aag 1419
 Met Thr Glu Glu Gly Arg Phe Arg Glu Lys Ala Ser Ile Leu His Lys
 330 335 340 345

atc gcc aag aag aaa tgt cat gtg gat gag aac gag cgg cag aat ggg 1467
 Ile Ala Lys Lys Lys Cys His Val Asp Glu Asn Glu Arg Gln Asn Gly
 346 351 356 361

gct gcc aac cac gtg gaa aaa att gag ctt cca aac agc acc agc aca 1515
 Ala Ala Asn His Val Glu Lys Ile Glu Leu Pro Asn Ser Thr Ser Thr
 362 367 372 377

gat gtt gaa atg aca cca tcc agt gat gct tca gaa cct gta caa aat 1563
 Asp Val Glu Met Thr Pro Ser Ser Asp Ala Ser Glu Pro Val Gln Asn
 378 383 388 393

gga aat ctc tcc cac aac att gaa ggt gca gaa gcc cag acc gct gat 1611
 Gly Asn Leu Ser His Asn Ile Glu Gly Ala Glu Ala Gln Thr Ala Asp

394	399	404	409	
gag gag gag gac cag cct ctc agc ctt gcc tgg cct tct gaa acc cgc				1659
Glu Glu Glu Asp Gln Pro Leu Ser Leu Ala Trp Pro Ser Glu Thr Arg				
410	415	420	425	
aag caa gtc acg ttt ctg att gtt ttc ccc ata gtg ttt cct ctc tgg				1707
Lys Gln Val Thr Phe Leu Ile Val Phe Pro Ile Val Phe Pro Leu Trp				
426	431	436	441	
att acg tta cct gac gtt cgc aaa cct tca tgc agg aag ttt ttt ccc				1755
Ile Thr Leu Pro Asp Val Arg Lys Pro Ser Ser Arg Lys Phe Phe Pro				
442	447	452	457	
atc acg ttc ttt ggc tcc att acc tgg att gca gta ttc tct tac ttg				1803
Ile Thr Phe Phe Gly Ser Ile Thr Trp Ile Ala Val Phe Ser Tyr Leu				
458	463	468	473	
atg gtc tgg tgg gcg cac cag gtt gga gag aca att ggc atc agt gaa				1851
Met Val Trp Trp Ala His Gln Val Gly Glu Thr Ile Gly Ile Ser Glu				
474	479	484	489	
gag att atg ggc ctg acc atc ttg gct gct ggg acc tcc atc cct gat				1899
Glu Ile Met Gly Leu Thr Ile Leu Ala Ala Gly Thr Ser Ile Pro Asp				
490	495	500	505	
ctt atc acc agt gtc ata gtg gcc cgg aag ggg cta ggg gac atg gct				1947
Leu Ile Thr Ser Val Ile Val Ala Arg Lys Gly Leu Gly Asp Met Ala				
506	511	516	521	
gtg tcc agc tct gtt gga agc aac att ttt gac atc act gta ggg ctc				1995
Val Ser Ser Ser Val Gly Ser Asn Ile Phe Asp Ile Thr Val Gly Leu				
522	527	532	537	
cca ctg ccc tgg ctc ctg tac acc gtc att cac aga ttc cag cca gtg				2043
Pro Leu Pro Trp Leu Leu Tyr Thr Val Ile His Arg Phe Gln Pro Val				
538	543	548	553	
gct gtc agc agc aat ggc ctt ttc tgt gcc atc gtc ctt ctc ttc atc				2091
Ala Val Ser Ser Asn Gly Leu Phe Cys Ala Ile Val Leu Leu Phe Ile				
554	559	564	569	
atg ctg ctc ttc gtc atc ctc tct atc gcc ctc tgc aag tgg cga atg				2139
Met Leu Leu Phe Val Ile Leu Ser Ile Ala Leu Cys Lys Trp Arg Met				
570	575	580	585	
aac aaa atc ctg ggc ttc atc atg ttt ggc ctc tac ttt gtg ttc ctg				2187
Asn Lys Ile Leu Gly Phe Ile Met Phe Gly Leu Tyr Phe Val Phe Leu				
586	591	596	601	
gtg gtg agc gtt ctc cta gaa gac aga att ctt aca tgc ccc gtc tcc				2235
Val Val Ser Val Leu Leu Glu Asp Arg Ile Leu Thr Cys Pro Val Ser				
602	607	612	617	
atc tag caggaaaagc catatcttgc accagcagca tgaatggtcc ctccacactc				2291
Ile *				
618				

tgggctctgg gctccttgac ctcttgagaa gaggcagctg gcacacagcc ctgggtgcca 2351
 agtgtccctc cttggtgaat ttgaggagag atggattcac actgggcca ttcacttcac 2411
 aggctgcttc caccctgcct actgaaatga cttcatgtaa aagacaaaga gaaccgtcaa 2471
 tacagggctt ctccctattc accactgaca agtacacctc gc 2513

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 tctgtttcct catctatcaa tgaagatgat actatgaacc caataaggct gttaaaacag 180
 gtttttttatt acctaccacg gggggtgta catctctgac gtacagaagg aggacgcct 240
 ctccacctat cgctgcatca ccaagcacia gtatagcggg gagaccggc agagcaatgg 300
 ggcacgcctc tctgtgacag accctgctga gtgatcccc accatcctgg atggcttcca 360
 ctcccaggaa gtgtgggccc gccacaccgt ggagctgccc tgcaccgcct cgggctaccc 420
 tatccccgcc atccgctggc tcaaggatgg ccggcccctc ccggctgaca gccgctggac 480
 caagcgcctc acagggtgta ccatcagcga cttgctggacc gaggacagcg gcacctacat 540
 ttgtgaggtc accaacacct tcggttcggc agaggccaca ggcacccctc atg gtc 595
 Met Val
 1

att gat ccc ctt cat gtg acc ctg aca cca aag aag ctg aag acc ggc 643
 Ile Asp Pro Leu His Val Thr Leu Thr Pro Lys Lys Leu Lys Thr Gly
 3 8 13 18

att ggc agc acg gtc atc ctc tcc tgt gcc ctg acg ggc tcc cca gag 691
 Ile Gly Ser Thr Val Ile Leu Ser Cys Ala Leu Thr Gly Ser Pro Glu
 19 24 29 34

ttc acc atc cgc tgg tat cgc aac acg gag ctg gtg ctg cct gac gag 739
 Phe Thr Ile Arg Trp Tyr Arg Asn Thr Glu Leu Val Leu Pro Asp Glu
 35 40 45 50

gcc atc tcc atc cgc ggg ctc agc aac gag acg ctg ctc atc acc tcg 787

Ala	Ile	Ser	Ile	Arg	Gly	Leu	Ser	Asn	Glu	Thr	Leu	Leu	Ile	Thr	Ser		
51					56					61					66		
gcc	cag	aag	agc	cat	tcc	ggg	gcc	tac	cag	tgc	ttc	gct	acc	cgc	aag	835	
Ala	Gln	Lys	Ser	His	Ser	Gly	Ala	Tyr	Gln	Cys	Phe	Ala	Thr	Arg	Lys		
67					72					77					82		
gcc	cag	acc	gcc	cag	gac	ttt	gcc	atc	att	gca	ctt	gag	gat	ggc	acg	883	
Ala	Gln	Thr	Ala	Gln	Asp	Phe	Ala	Ile	Ile	Ala	Leu	Glu	Asp	Gly	Thr		
83					88					93					98		
ccc	cgc	atc	gtc	tgc	tcc	ttc	agc	gag	aag	gtg	gtc	aac	ccc	ggg	gag	931	
Pro	Arg	Ile	Val	Ser	Ser	Phe	Ser	Glu	Lys	Val	Val	Asn	Pro	Gly	Glu		
99					104					109					114		
cag	ttc	tca	ctg	atg	tgt	gcg	gcc	aag	ggc	gcc	ccg	ccc	ccc	acg	gtc	979	
Gln	Phe	Ser	Leu	Met	Cys	Ala	Ala	Lys	Gly	Ala	Pro	Pro	Pro	Thr	Val		
115					120					125					130		
acc	tgg	gcc	ctc	gac	gat	gag	ccc	atc	gtg	cgg	gat	ggc	agc	cac	cgc	1027	
Thr	Trp	Ala	Leu	Asp	Asp	Glu	Pro	Ile	Val	Arg	Asp	Gly	Ser	His	Arg		
131					136					141					146		
acc	aac	cag	tac	acc	atg	tgc	gac	ggc	acc	acc	atc	agc	cac	atg	aac	1075	
Thr	Asn	Gln	Tyr	Thr	Met	Ser	Asp	Gly	Thr	Thr	Ile	Ser	His	Met	Asn		
147					152					157					162		
gtc	aca	ggc	ccc	cag	atc	cgc	gac	ggg	ggc	gtg	tac	cgg	tgc	aca	gcg	1123	
Val	Thr	Gly	Pro	Gln	Ile	Arg	Asp	Gly	Gly	Val	Tyr	Arg	Cys	Thr	Ala		
163					168					173					178		
cgg	aac	ttg	gtg	ggc	agt	gct	gaa	tat	cag	gcg	cga	ata	aac	gta	aga	1171	
Arg	Asn	Leu	Val	Gly	Ser	Ala	Glu	Tyr	Gln	Ala	Arg	Ile	Asn	Val	Arg		
179					184					189					194		
ggc	cca	ccc	agc	atc	cgg	gct	atg	cgg	aac	atc	aca	gca	gtc	gcc	ggg	1219	
Gly	Pro	Pro	Ser	Ile	Arg	Ala	Met	Arg	Asn	Ile	Thr	Ala	Val	Ala	Gly		
195					200					205					210		
cgg	gac	acc	ctt	atc	aac	tgc	agg	gtc	atc	ggc	tat	ccc	tac	tac	tcc	1267	
Arg	Asp	Thr	Leu	Ile	Asn	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser		
211					216					221					226		
atc	aag	tgg	tac	aag	gat	gcc	ctg	ctg	ctg	cca	gac	aac	cac	cgc	cag	1315	
Ile	Lys	Trp	Tyr	Lys	Asp	Ala	Leu	Leu	Leu	Pro	Asp	Asn	His	Arg	Gln		
227					232					237					242		
gtg	gtg	ttt	gag	aat	ggg	acc	ctc	aag	ctg	act	gac	gtg	cag	aag	ggc	1363	
Val	Val	Phe	Glu	Asn	Gly	Thr	Leu	Lys	Leu	Thr	Asp	Val	Gln	Lys	Gly		
243					248					253					258		
atg	gat	gag	ggg	gag	tac	ctg	tgc	agt	gtc	ctc	atc	cag	ccc	cag	ctc	1411	
Met	Asp	Glu	Gly	Glu	Tyr	Leu	Cys	Ser	Val	Leu	Ile	Gln	Pro	Gln	Leu		
259					264					269					274		
tcc	atc	agc	cag	agc	gtt	cac	gta	gcc	gtc	aaa	gtg	ccc	cct	ctg	atc	1459	
Ser	Ile	Ser	Gln	Ser	Val	His	Val	Ala	Val	Lys	Val	Pro	Pro	Leu	Ile		

275	280	285	290	
cag ccc ttc gaa ttc cca ccc gcc tcc atc ggc cag ctg ctc tac att				1507
Gln Pro Phe Glu Phe Pro Pro Ala Ser Ile Gly Gln Leu Leu Tyr Ile				
291	296	301	306	
ccc tgt gtg gtg tcc tcg ggg gac atg ccc atc cgt atc acc tgg agg				1555
Pro Cys Val Val Ser Ser Gly Asp Met Pro Ile Arg Ile Thr Trp Arg				
307	312	317	322	
aag gac gga cag gtg atc atc tca ggc tcg ggc gtg acc atc gag agc				1603
Lys Asp Gly Gln Val Ile Ile Ser Gly Ser Gly Val Thr Ile Glu Ser				
323	328	333	338	
aag gaa ttc atg agc tcc ctg cag atc tct agc gtc tcc ctc aag cac				1651
Lys Glu Phe Met Ser Ser Leu Gln Ile Ser Ser Val Ser Leu Lys His				
339	344	349	354	
aac ggc aac tat aca tgc atc gcc agc aac gca gcc gcc acc gtg agc				1699
Asn Gly Asn Tyr Thr Cys Ile Ala Ser Asn Ala Ala Ala Thr Val Ser				
355	360	365	370	
cgg gag cgc cag ctc atc gtg cgt gtg ccc cct cga ttt gtg gtg caa				1747
Arg Glu Arg Gln Leu Ile Val Arg Val Pro Pro Arg Phe Val Val Gln				
371	376	381	386	
ccc aac aac cag gat ggc atc tac ggc aaa gct ggt gtg ctc aac tgc				1795
Pro Asn Asn Gln Asp Gly Ile Tyr Gly Lys Ala Gly Val Leu Asn Cys				
387	392	397	402	
tcg gtg gac ggc tac ccc cca ccc aag gtc atg tgg aag cat gcc aag				1843
Ser Val Asp Gly Tyr Pro Pro Pro Lys Val Met Trp Lys His Ala Lys				
403	408	413	418	
ggg agc ggg aac ccc cag cag tac cac cct gtg ccc ctc act ggc cgc				1891
Gly Ser Gly Asn Pro Gln Gln Tyr His Pro Val Pro Leu Thr Gly Arg				
419	424	429	434	
atc cag atc ctg ccc aac agc tcg ctg ctg atc cgc cac gtc cta gaa				1939
Ile Gln Ile Leu Pro Asn Ser Ser Leu Leu Ile Arg His Val Leu Glu				
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gag gac atc ggc tac tac ctc tgc cag gcc agc aac ggc gta ggc acc				1987
Glu Asp Ile Gly Tyr Tyr Leu Cys Gln Ala Ser Asn Gly Val Gly Thr				
451	456	461	466	
gac atc agc aag tcc atg ttc ctc aca gtc aag atc ccg gcc atg atc				2035
Asp Ile Ser Lys Ser Met Phe Leu Thr Val Lys Ile Pro Ala Met Ile				
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Thr Ser His Pro Asn Thr Thr Ile Ala Ile Lys Gly His Ala Lys Glu				
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cta aac tgc acg gca cgg ggt gag cgg ccc atc atc atc cgc tgg gag				2131
Leu Asn Cys Thr Ala Arg Gly Glu Arg Pro Ile Ile Ile Arg Trp Glu				
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Lys Gly Asp Thr Val Ile Asp Pro Asp Arg Val Met Arg Tyr Ala Ile	
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Ala Thr Lys Asp Asn Gly Asp Glu Val Val Ser Thr Leu Lys Leu Lys	
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ccc gct gac cgt ggg gac tct gtg ttc ttc agc tgc cat gcc atc aac	2275
Pro Ala Asp Arg Gly Asp Ser Val Phe Phe Ser Cys His Ala Ile Asn	
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Ser Tyr Gly Glu Asp Arg Gly Leu Ile Gln Leu Thr Val Gln Glu Pro	
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Pro Asp Pro Pro Glu Leu Glu Ile Arg Glu Val Lys Ala Arg Ser Met	
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Asn Leu Arg Trp Thr Gln Arg Phe Asp Gly Asn Ser Ile Ile Thr Gly	
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Phe Asp Ile Glu Tyr Lys Asn Lys Ser Asp Ser Trp Asp Phe Lys Gln	
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Leu His Pro Ala Ser Val Tyr Ser Ile Arg Met Tyr Ser Phe Asn Lys	
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Ala Ala Pro Asp Gly Pro Pro Met Asp Val Thr Leu Gln Pro Val Thr	
675 680 685 690	
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Ser Gln Ser Ile Gln Val Thr Trp Lys Ala Pro Lys Lys Glu Leu Gln	
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Asn Gly Val Ile Arg Gly Tyr Gln Ile Gly Tyr Arg Glu Asn Ser Pro	
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Gly Ser Asn Gly Gln Tyr Ser Ile Val Glu Met Lys Ala Thr Gly Asp	
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                      . Met Arg Arg
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Arg Ser Gly Thr Leu Val Ile Asp Phe Arg Ser Gly Gly Arg Pro Glu
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 ccgcctctaa agagagcaat cactacactt atg gct ggg att ttg cgc tta 171
 Met Ala Gly Ile Leu Arg Leu
 1 5
 gta gtt caa tgg ccc cca ggc aga cta cag acc gtg aca aaa ggt gtg 219
 Val Val Gln Trp Pro Pro Gly Arg Leu Gln Thr Val Thr Lys Gly Val
 8 13 18 23
 gag tct ctt att tgt aca gat tgg att cgt cac aaa ttc acc aga tca 267
 Glu Ser Leu Ile Cys Thr Asp Trp Ile Arg His Lys Phe Thr Arg Ser
 24 29 34 39
 aga att cca gaa aaa gtg ttt cag gcc tca cct gaa gat cat gaa aaa 315
 Arg Ile Pro Glu Lys Val Phe Gln Ala Ser Pro Glu Asp His Glu Lys
 40 45 50 55
 tac ggt ggg gat cca cag aac cct cat aaa ctg cat att gtt acc aga 363
 Tyr Gly Gly Asp Pro Gln Asn Pro His Lys Leu His Ile Val Thr Arg

56	61	66	71	
ata aaa agt aca aga aga cgt cca tat tgg gaa aaa gat ata ata aag				411
Ile Lys Ser Thr Arg Arg Arg Pro Tyr Trp Glu Lys Asp Ile Ile Lys				
72	77	82	87	
atg ctt gga tta gaa aaa gca cat acc cct caa gtt cac aag aat atc				459
Met Leu Gly Leu Glu Lys Ala His Thr Pro Gln Val His Lys Asn Ile				
88	93	98	103	
cct tca gtg aat gca aaa ttg aaa gta gtt aag cat ttg ata aga atc				507
Pro Ser Val Asn Ala Lys Leu Lys Val Val Lys His Leu Ile Arg Ile				
104	109	114	119	
aag ccc ttg aag ttg cca caa gga ctt cca aca gag gag aac atg tct				555
Lys Pro Leu Lys Leu Pro Gln Gly Leu Pro Thr Glu Glu Asn Met Ser				
120	125	130	135	
aac acg tgc ctc aaa agc act ggg gag tta gta gtg cag tgg cat ctg				603
Asn Thr Cys Leu Lys Ser Thr Gly Glu Leu Val Val Gln Trp His Leu				
136	141	146	151	
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Lys Pro Val Glu Gln Lys Ala His Glu Ser *				
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aattgtaagg gaggttcagt agtggggaat tctgtgacag ctgattgaag atgatgatga				774
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caacaatgac attgtcatgc ttattgtccc aatatccatc ctgtcgtaga tcttaatggt				894
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Met Pro Glu Glu Lys Asp Cys Gly Gly Gly Asp Ala		
1 5 10		

ctc tcc aat ggc atc aag aaa cac aga aca agt ttg cct tct cct atg	157
Leu Ser Asn Gly Ile Lys Lys His Arg Thr Ser Leu Pro Ser Pro Met	
13 18 23 28	
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Phe Ser Arg Asn Asp Phe Ser Ile Trp Ser Ile Leu Arg Lys Cys Ile	
29 34 39 44	
gga atg gaa cta tcc aag atc acg atg cca gtt ata ttt aat gag cct	253
Gly Met Glu Leu Ser Lys Ile Thr Met Pro Val Ile Phe Asn Glu Pro	
45 50 55 60	
ctg agc ttc cta cag cgc cta act gaa tac atg gag cat act tac ctc	301
Leu Ser Phe Leu Gln Arg Leu Thr Glu Tyr Met Glu His Thr Tyr Leu	
61 66 71 76	
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Ile His Lys Ala Ser Ser Leu Ser Asp Pro Val Glu Arg Met Gln Cys	
77 82 87 92	
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Val Ala Ala Phe Ala Val Ser Ala Val Ala Ser Gln Trp Glu Arg Thr	
93 98 103 108	
gga aaa cct ttc aac cca ctg ctg gga gag act tat gaa tta gtg cga	445
Gly Lys Pro Phe Asn Pro Leu Leu Gly Glu Thr Tyr Glu Leu Val Arg	
109 114 119 124	
gat gac ctt gga ttt aga ctc atc tcc gaa cag gtc agc cat cac cca	493
Asp Asp Leu Gly Phe Arg Leu Ile Ser Glu Gln Val Ser His His Pro	
125 130 135 140	
cca atc agt gca ttt cat gct gaa gga tta aac aat gac ttc atc ttt	541
Pro Ile Ser Ala Phe His Ala Glu Gly Leu Asn Asn Asp Phe Ile Phe	
141 146 151 156	
cat ggc tct atc tat ccc aaa ctg aaa ttc tgg ggg aag agt gta gaa	589
His Gly Ser Ile Tyr Pro Lys Leu Lys Phe Trp Gly Lys Ser Val Glu	
157 162 167 172	
gca gaa ccc aaa gga acc atc acc ttg gag ctc ctt gaa cac aat gag	637
Ala Glu Pro Lys Gly Thr Ile Thr Leu Glu Leu Leu Glu His Asn Glu	
173 178 183 188	
gca tat aca tgg aca aat ccc acc tgc tgt gtg cat aat atc att gtg	685
Ala Tyr Thr Trp Thr Asn Pro Thr Cys Cys Val His Asn Ile Ile Val	
189 194 199 204	
ggt aaa ctg tgg atc gaa cag tat ggc aat gtg gaa att ata aac cac	733
Gly Lys Leu Trp Ile Glu Gln Tyr Gly Asn Val Glu Ile Ile Asn His	
205 210 215 220	
aag act ggg gac aaa tgt gtg ttg aat ttt aag cca tgt ggc ctt ttt	781
Lys Thr Gly Asp Lys Cys Val Leu Asn Phe Lys Pro Cys Gly Leu Phe	
221 226 231 236	
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Gly Lys Glu Leu His Lys Val Glu Gly Tyr Ile Gln Asp Lys Ser Lys	
237 242 247 252	
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Lys Lys Leu Cys Ala Leu Tyr Gly Lys Trp Thr Glu Cys Leu Tyr Ser	
253 258 263 268	
gtt gac cct gcc acg ttt gac gct tac aaa aaa aat gat aag aaa aat	925
Val Asp Pro Ala Thr Phe Asp Ala Tyr Lys Lys Asn Asp Lys Lys Asn	
269 274 279 284	
aca gaa gag aag aag aac agc aaa cag atg agc acc tct gag gag ttg	973
Thr Glu Glu Lys Lys Asn Ser Lys Gln Met Ser Thr Ser Glu Glu Leu	
285 290 295 300	
gat gaa atg cca gtg ccg gat tct gaa agt gta ttc att atc cct gga	1021
Asp Glu Met Pro Val Pro Asp Ser Glu Ser Val Phe Ile Ile Pro Gly	
301 306 311 316	
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Ser Val Leu Leu Trp Arg Ile Ala Pro Arg Pro Pro Asn Ser Ala Gln	
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Met Tyr Asn Phe Thr Ser Phe Ala Met Val Leu Asn Glu Val Asp Lys	
333 338 343 348	
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Asp Met Glu Ser Val Ile Pro Lys Thr Asp Cys Arg Leu Arg Pro Asp	
349 354 359 364	
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Ile Arg Ala Met Glu Asn Gly Glu Ile Asp Gln Ala Ser Glu Glu Lys	
365 370 375 380	
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Lys Arg Leu Glu Glu Lys Gln Arg Ala Ala Arg Lys Asn Arg Ser Lys	
381 386 391 396	
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Ser Glu Glu Asp Trp Lys Thr Arg Trp Phe His Gln Gly Pro Asn Pro	
397 402 407 412	
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Tyr Asn Gly Ala Gln Asp Trp Ile Tyr Ser Gly Ser Tyr Trp Asp Arg	
413 418 423 428	
aat tac ttc aat ttg cct gac att tat taa a atgcatacaa gtcagggtgt	1408
Asn Tyr Phe Asn Leu Pro Asp Ile Tyr *	
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tcc ctt agt cga atc aag agc aac gtg gat ggg cgg tac ctg gtg gac 96
 Ser Leu Ser Arg Ile Lys Ser Asn Val Asp Gly Arg Tyr Leu Val Asp
 17 22 27 32

ggc gtc cct ttc agc tgc tgc aat cct agc tcg cca cgg ccc tgc atc 144
 Gly Val Pro Phe Ser Cys Cys Asn Pro Ser Ser Pro Arg Pro Cys Ile
 33 38 43 48

cag tat cag atc acc aac aac tca gca cac tac agt tac gac cac cag 192
 Gln Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr Ser Tyr Asp His Gln
 49 54 59 64

acg gag gag ctc aac ctg tgg gtg cgt ggc tgc agg gct gcc ctg ctg 240
 Thr Glu Glu Leu Asn Leu Trp Val Arg Gly Cys Arg Ala Ala Leu Leu
 65 70 75 80

agc tac tac agc agc ctc atg aac tcc atg ggt gtc gtc acg ctc ctc 288
 Ser Tyr Tyr Ser Ser Leu Met Asn Ser Met Gly Val Val Thr Leu Leu
 81 86 91 96

att tgg ctc ttc gag gtg acc att aca att ggg ctg cgc tac cta cag 336
 Ile Trp Leu Phe Glu Val Thr Ile Thr Ile Gly Leu Arg Tyr Leu Gln
 97 102 107 112

acg tcg ctg gat ggt gtg tcc aac ccc gag gaa tct gag agc gag agc 384
 Thr Ser Leu Asp Gly Val Ser Asn Pro Glu Glu Ser Glu Ser Glu Ser
 113 118 123 128

gag ggc tgg ctg ctg gag aag agc gtg ccg gag acc tgg aag gcc ttt 432
 Glu Gly Trp Leu Leu Glu Lys Ser Val Pro Glu Thr Trp Lys Ala Phe
 129 134 139 144

ctg gag agt gtg aag aag ctg ggc aag ggc aac cag gtg act gtg gct 480
 Leu Glu Ser Val Lys Lys Leu Gly Lys Gly Asn Gln Val Thr Val Ala
 145 150 155 160

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Ile Asn Lys Asn Ile Ser Ser Asp Pro Leu Pro Arg Ala Val Asp Asn	
161 166 171 176	
gaa ttt gag aca gtt gcc act cag ctc cta aaa agg acc caa gct atg	576
Glu Phe Glu Thr Val Ala Thr Gln Leu Leu Lys Arg Thr Gln Ala Met	
177 182 187 192	
ctt aac aaa tac aga tgc ctg ctc cta gaa gat gcc atg cga atc aat	624
Leu Asn Lys Tyr Arg Cys Leu Leu Leu Glu Asp Ala Met Arg Ile Asn	
193 198 203 208	
ccc tct gct gag atg gtg atg atc gat agg atg ttc aac cag gag gaa	672
Pro Ser Ala Glu Met Val Met Ile Asp Arg Met Phe Asn Gln Glu Glu	
209 214 219 224	
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Arg Ala Ser Leu Ser Arg Asp Lys Arg Leu Ala Leu Val Asp Pro Glu	
225 230 235 240	
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Gly Phe Gln Ala Asp Phe Cys Cys Ser Phe Lys Leu Asp Lys Ala Ala	
241 246 251 256	
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His Glu Thr Gln Phe Gly Arg Ser Asp Gln His Gly Ser Lys Ala Ser	
257 262 267 272	
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Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln Gly Arg Asp Arg Ala Lys	
273 278 283 288	
acc ggt gtg acg gaa ccc atg aat cat gac cag ttt cat cta gtg cct	912
Thr Gly Val Thr Glu Pro Met Asn His Asp Gln Phe His Leu Val Pro	
289 294 299 304	
aat cac atc gtg gtc tct gca gaa gga aac att tct aaa aaa aca gaa	960
Asn His Ile Val Val Ser Ala Glu Gly Asn Ile Ser Lys Lys Thr Glu	
305 310 315 320	
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Cys Leu Gly Arg Ala Leu Lys Phe Asp Lys Val Gly Leu Val Gln Tyr	
321 326 331 336	
cag agc acg tct gaa gag aag gcc agc cgg aga gag cct ctg aag gcc	1056
Gln Ser Thr Ser Glu Glu Lys Ala Ser Arg Arg Glu Pro Leu Lys Ala	
337 342 347 352	
agt cag tgc tct ccc ggc cct gag ggg cac cgg aaa acc tca tcc aga	1104
Ser Gln Cys Ser Pro Gly Pro Glu Gly His Arg Lys Thr Ser Ser Arg	
353 358 363 368	
tcg gat cat ggt act gag agc aaa ctg tca agc atc cta gca gat tcg	1152
Ser Asp His Gly Thr Glu Ser Lys Leu Ser Ser Ile Leu Ala Asp Ser	
369 374 379 384	
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385					390					395					400	
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Asn	Ser	Pro	Lys	Asn	Glu	Val	Leu	His	Thr	Asp	Ile	Met	Lys	Gly	Ser	
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Phe	Lys	Asn	Ile	Leu	Glu	Leu	Lys	Lys	Ala	Gly	Arg	Gln	Pro	Gln	Ser	
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Asp	Pro	Thr	Val	Ser	Gly	Ser	Val	Glu	Leu	Asp	Phe	Pro	Asn	Phe	Ser	
449					454					459					464	
cct	atg	gct	tca	cag	gaa	aac	tgc	ctg	gaa	aag	ttc	atc	ccg	gac	cac	1440
Pro	Met	Ala	Ser	Gln	Glu	Asn	Cys	Leu	Glu	Lys	Phe	Ile	Pro	Asp	His	
465					470					475					480	
agt	gac	gtt	gtc	atg	gat	gat	gat	gat	gac	tcg	tgt	ctc	ctt	gat	ctt	1488
Ser	Asp	Val	Val	Met	Asp	Asp	Asp	Asp	Asp	Ser	Cys	Leu	Leu	Asp	Leu	
481					486					491					496	
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Ile	Gly	Asp	Pro	Gln	Ala	Leu	Asn	Tyr	Phe	Leu	His	Gly	Pro	Ser	Asn	
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Lys	Ser	Ser	Asn	Asp	Asp	Leu	Thr	Asn	Ala	Gly	Tyr	Ser	Ala	Ala	Asn	
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Ser	Asn	Ser	Ile	Phe	Ala	Asn	Ser	Ser	Asn	Ala	Asp	Pro	Lys	Ser	Ser	
529					534					539					544	
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Leu	Lys	Gly	Val	Ser	Asn	Gln	Leu	Gly	Glu	Gly	Pro	Ser	Asp	Gly	Leu	
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Pro	Leu	Ser	Ser	Ser	Leu	Gln	Phe	Leu	Glu	Asp	Glu	Leu	Glu	Ser	Ser	
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gtcggccgct ctagaggatc caagcttacg tacgcgtgca tgcgacgtca tagctcttct 2498
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<222> (15) .. (1172)

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Arg Gly Ala Arg Asn Ala Arg Val Leu Arg Gly Ile Leu Ala Gly Ala
13 18 23 28

aca gct aac aag gct tct cat aac agg acc cgg gcc ctg caa agc cac 146
Thr Ala Asn Lys Ala Ser His Asn Arg Thr Arg Ala Leu Gln Ser His
29 34 39 44

agc tcc cca gag ggc aag gag gaa cct gaa ccc cta tcc ccg gag ctg 194
Ser Ser Pro Glu Gly Lys Glu Glu Pro Glu Pro Leu Ser Pro Glu Leu
45 50 55 60

gaa tac att ccc aga aag agg ggc aag aac ccc atg aaa gct gtg gga 242
Glu Tyr Ile Pro Arg Lys Arg Gly Lys Asn Pro Met Lys Ala Val Gly
61 66 71 76

ctg gcc tgg tac agc ctg tac acc cgc acc tgg ctc ggg tac ctc ttc 290
Leu Ala Trp Tyr Ser Leu Tyr Thr Arg Thr Trp Leu Gly Tyr Leu Phe
77 82 87 92

tac cga cag cag ctg cgc agg gct cgg aat cgc tac cct aaa ggc cac 338
Tyr Arg Gln Gln Leu Arg Arg Ala Arg Asn Arg Tyr Pro Lys Gly His
93 98 103 108

tcg aaa acc cag ccc cgc ctc ttc aat gga gtg aag gtg ctt ccc atc 386

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Gln	Leu	Ala	Val	Ala	Val	Asp	Pro	Ser	Asp	Pro	Arg	Ala	Val	Gln	Ala		
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Lys	His	Trp	Asp	His	Ser	Gly	Gly	Asn	Arg	Asp	Leu	Ser	Arg	Arg	His		
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Arg	Asp	Cys	Arg	Val	Tyr	Gly	Ser	Pro	Gln	Asp	Gly	Ile	Pro	Tyr	Leu		
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Thr	His	Pro	Leu	Cys	His	Gln	Asp	Val	Val	Ser	Val	Gly	Arg	Leu	Gln		
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atc	cgg	gcc	ctg	gct	aca	cct	ggc	cac	aca	caa	ggc	cat	ctg	gtc	tac	722	
Ile	Arg	Ala	Leu	Ala	Thr	Pro	Gly	His	Thr	Gln	Gly	His	Leu	Val	Tyr		
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cta	ctg	gat	ggg	gag	ccc	tac	aag	ggt	ccc	tcc	tgc	ctc	ttc	tca	ggg	770	
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Ala Leu Gln Glu Ala Leu Gly Pro Gly Pro Gly Pro Thr Gly Asp Asp				
349	354	359	364	
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Asp Tyr Ser Arg Ala Gln Leu Leu Glu Glu Leu Arg Arg Leu Lys Asp				
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Met His Lys Ser Lys *				
381	386			
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ttgggctgag cagaggacga c atg ttg ctt ttc gtg gag cag gta gca tct 171

Met Leu Leu Phe Val Glu Gln Val Ala Ser
1 5

aaa gga act ggt tta aat cct aat gcc aaa gta tgg caa gaa att gct 219

Lys Gly Thr Gly Leu Asn Pro Asn Ala Lys Val Trp Gln Glu Ile Ala
11 16 21 26

cct gga aat act gat gcc acc cca gta act cat gga act gaa agc tct 267

Pro Gly Asn Thr Asp Ala Thr Pro Val Thr His Gly Thr Glu Ser Ser
27 32 37 42

tgg cat gaa ata gca gct aca tca ggt gct cat cct gag ggt aat gca 315

Trp His Glu Ile Ala Ala Thr Ser Gly Ala His Pro Glu Gly Asn Ala
43 48 53 58

gag ctc tca gaa gat ata tgt aaa gaa tat gaa gta atg tat tct tca 363

Glu Leu Ser Glu Asp Ile Cys Lys Glu Tyr Glu Val Met Tyr Ser Ser
59 64 69 74

tct tgt gaa acc aca aga aat act aca ggc att gaa gaa tca act gat 411

Ser Cys Glu Thr Thr Arg Asn Thr Thr Gly Ile Glu Glu Ser Thr Asp
75 80 85 90

ggg atg att tta gga cca gaa gat ctg agt tac caa ata tat gat gtt 459

Gly Met Ile Leu Gly Pro Glu Asp Leu Ser Tyr Gln Ile Tyr Asp Val
91 96 101 106

tcc gga gaa agc aat tca gca gtt tct aca gaa gac cta aaa gaa tgt 507

Ser Gly Glu Ser Asn Ser Ala Val Ser Thr Glu Asp Leu Lys Glu Cys
107 112 117 122

ctg aag aaa caa tta gaa ttc tgt ttt tca cga gaa aat ttt tca aag 555

Leu Lys Lys Gln Leu Glu Phe Cys Phe Ser Arg Glu Asn Phe Ser Lys
123 128 133 138

gat ctt tac ttg ata tct caa atg gat agt gat cag ttc atc cca att	603
Asp Leu Tyr Leu Ile Ser Gln Met Asp Ser Asp Gln Phe Ile Pro Ile	
139 144 149 154	
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Trp Thr Val Ala Asn Met Glu Glu Ile Lys Lys Leu Thr Thr Asp Pro	
155 160 165 170	
gat cta att ctt gaa gtg tta aga tct tct ccc atg gta caa gtt gat	699
Asp Leu Ile Leu Glu Val Leu Arg Ser Ser Pro Met Val Gln Val Asp	
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gag aag ggt gag aaa gtg aga cca agt cat aag cgt tgt att gta att	747
Glu Lys Gly Glu Lys Val Arg Pro Ser His Lys Arg Cys Ile Val Ile	
187 192 197 202	
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203 208 213 218	
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Phe Lys Ser Glu Asn Cys Pro Lys Val Ile Ser Cys Glu Phe Ala His	
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Asn Ser Asn Trp Tyr Ile Thr Phe Gln Ser Asp Thr Asp Ala Gln Gln	
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Ala Phe Lys Tyr Leu Arg Glu Glu Val Lys Thr Phe Gln Gly Lys Pro	
251 256 261 266	
att atg gca agg ata aaa gcc atc aat aca ttt ttt gct aag aat ggt	987
Ile Met Ala Arg Ile Lys Ala Ile Asn Thr Phe Phe Ala Lys Asn Gly	
267 272 277 282	
tat cga tta atg gat tct agt atc tat agt cac ccc att caa act caa	1035
Tyr Arg Leu Met Asp Ser Ser Ile Tyr Ser His Pro Ile Gln Thr Gln	
283 288 293 298	
gca cag tat gcc tcc cca gtc ttt atg cag cct gta tat aat cct cac	1083
Ala Gln Tyr Ala Ser Pro Val Phe Met Gln Pro Val Tyr Asn Pro His	
299 304 309 314	
caa cag tac tcg gtc tat agt att gtg cct cag tct tgg tct cca aat	1131
Gln Gln Tyr Ser Val Tyr Ser Ile Val Pro Gln Ser Trp Ser Pro Asn	
315 320 325 330	
cct aca cct tac ttt gaa aca cca ctg gct ccc ttt ccc aat ggt agt	1179
Pro Thr Pro Tyr Phe Glu Thr Pro Leu Ala Pro Phe Pro Asn Gly Ser	
331 336 341 346	
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Phe Val Asn Gly Phe Asn Ser Pro Gly Ser Tyr Lys Thr Asn Ala Ala	
347 352 357 362	

gct atg aat atg ggt cga cca ttc caa aaa aat cgt gtg aag cct cag	1275
Ala Met Asn Met Gly Arg Pro Phe Gln Lys Asn Arg Val Lys Pro Gln	
363 368 373 378	
ttt agg tca tct ggt ggt tca gaa cac tca aca gag ggc tct gta tcc	1323
Phe Arg Ser Ser Gly Gly Ser Glu His Ser Thr Glu Gly Ser Val Ser	
379 384 389 394	
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Leu Gly Asp Gly Gln Leu Asn Arg Tyr Ser Ser Arg Asn Phe Pro Ala	
395 400 405 410	
gaa cgg cat aac ccc aca gta act ggg cat cag gag caa act tac ctt	1419
Glu Arg His Asn Pro Thr Val Thr Gly His Gln Glu Gln Thr Tyr Leu	
411 416 421 426	
cag aag gag act tcc act ttg cag gtg gaa cag aat ggg gac tat ggt	1467
Gln Lys Glu Thr Ser Thr Leu Gln Val Glu Gln Asn Gly Asp Tyr Gly	
427 432 437 442	
agg ggc agg taa gaa aataaagtac ctgaaaacct ttgataataa tgtgatcatc	1522
Arg Gly Arg *	
443	
ctgaataatt gaagaacgtg atcttcataa taattaaatg agcatttaatt tattggtata	1582
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ctgaccgcaa cccctacccc cgcccaccag c atg gcc cgg cac gtg ttc cta	172
Met Ala Arg His Val Phe Leu	
1 5	
acg ggg ccc cca gga gtt gga aaa aca aca ttg atc cat aaa gcc agt	220
Thr Gly Pro Pro Gly Val Gly Lys Thr Thr Leu Ile His Lys Ala Ser	
8 13 18 23	
gag gtt tta aaa tcc tct ggt gtg cct gtt gat gga ttt tat acc gaa	268
Glu Val Leu Lys Ser Ser Gly Val Pro Val Asp Gly Phe Tyr Thr Glu	
24 29 34 39	

gaa gtc aga cag gga ggg aga aga ata gga ttc gat gtc gtc acg ttg	316
Glu Val Arg Gln Gly Gly Arg Arg Ile Gly Phe Asp Val Val Thr Leu	
40 45 50 55	
tcc ggc acc cgg ggg cct tta tcg aga gtt ggg tta gag cct cca cct	364
Ser Gly Thr Arg Gly Pro Leu Ser Arg Val Gly Leu Glu Pro Pro Pro	
56 61 66 71	
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Gly Lys Arg Glu Cys Arg Val Gly Gln Tyr Val Val Asp Leu Thr Ser	
72 77 82 87	
ttt gag cag ttg gca cta ccc gtc ttg agg aat gcc gac tgc agc agt	460
Phe Glu Gln Leu Ala Leu Pro Val Leu Arg Asn Ala Asp Cys Ser Ser	
88 93 98 103	
ggc cca ggg caa aga gtg tgc gtc atc gat gag att ggg aag atg gag	508
Gly Pro Gly Gln Arg Val Cys Val Ile Asp Glu Ile Gly Lys Met Glu	
104 109 114 119	
ctc ttc agt cag ctt ttc att caa gct gtt cgt cag acg ctg tct acc	556
Leu Phe Ser Gln Leu Phe Ile Gln Ala Val Arg Gln Thr Leu Ser Thr	
120 125 130 135	
cca ggg act ata atc ctt ggc aca atc cca gtt cct aaa gga aag cca	604
Pro Gly Thr Ile Ile Leu Gly Thr Ile Pro Val Pro Lys Gly Lys Pro	
136 141 146 151	
ctg gct ctt gta gaa gaa atc aga aac aga aag gat gtg aag gtg ttt	652
Leu Ala Leu Val Glu Glu Ile Arg Asn Arg Lys Asp Val Lys Val Phe	
152 157 162 167	
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Asn Val Thr Lys Glu Asn Arg Asn His Leu Leu Pro Asp Ile Val Thr	
168 173 178 183	
tgc gtg cag agc agc agg aag tga agacacgtgc attcctgcct tccgtgaagg	754
Cys Val Gln Ser Ser Arg Lys *	
184 189	
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Glu Pro Val Gly Cys Cys Gly Glu Cys Arg Gly Ser Ser Val Asp Pro
2 7 12 17

cgg agc acc ttc gtg ttg agt aac ctg gcg gag gtg gtg gag cgt gtg 154
Arg Ser Thr Phe Val Leu Ser Asn Leu Ala Glu Val Val Glu Arg Val
18 23 28 33

ctc acc ttc ctg ccc gcc aag gcg ttg ctg cgg gtg gcc tgc gtg tgc 202
Leu Thr Phe Leu Pro Ala Lys Ala Leu Leu Arg Val Ala Cys Val Cys
34 39 44 49

cgc tta tgg agg gag tgt gtg cgc aga gta ttg cgg acc cat cgg agc 250
Arg Leu Trp Arg Glu Cys Val Arg Arg Val Leu Arg Thr His Arg Ser
50 55 60 65

gta acc tgg atc tcc gca ggc ctg gcg gag gcc ggc cac ctg gag ggg 298
Val Thr Trp Ile Ser Ala Gly Leu Ala Glu Ala Gly His Leu Glu Gly
66 71 76 81

cat tgc ttg gtt cgc gtg gta gca gag gag ctt gag aat gtt cgc atc 346
His Cys Leu Val Arg Val Val Ala Glu Glu Leu Glu Asn Val Arg Ile
82 87 92 97

tta cca cat aca gtt ctt tac atg gct gat tca gaa act ttc att agt 394
Leu Pro His Thr Val Leu Tyr Met Ala Asp Ser Glu Thr Phe Ile Ser
98 103 108 113

ctg gaa gag tgt cgt gcc cat aag aga gca agg aaa aga act agt atg 442
Leu Glu Glu Cys Arg Gly His Lys Arg Ala Arg Lys Arg Thr Ser Met
114 119 124 129

gaa aca gca ctt gcc ctt gag aag cta ttc ccc aaa caa tgc caa gtc 490
Glu Thr Ala Leu Ala Leu Glu Lys Leu Phe Pro Lys Gln Cys Gln Val
130 135 140 145

ctt ggg att gtg acc cca gga att gta gtg act cca atg gga tca ggt 538
Leu Gly Ile Val Thr Pro Gly Ile Val Val Thr Pro Met Gly Ser Gly
146 151 156 161

agc aat cga cct cag gaa ata gaa att gga gaa tct ggt ttt gct tta 586
Ser Asn Arg Pro Gln Glu Ile Glu Ile Gly Glu Ser Gly Phe Ala Leu
162 167 172 177

tta ttc cct caa att gaa gga ata aaa ata caa ccc ttt cat ttt att 634
Leu Phe Pro Gln Ile Glu Gly Ile Lys Ile Gln Pro Phe His Phe Ile
178 183 188 193

aag gat cca aag aat tta aca tta gaa aga cat caa ctc act gaa gta 682
Lys Asp Pro Lys Asn Leu Thr Leu Glu Arg His Gln Leu Thr Glu Val
194 199 204 209

ggt ctt tta gat aac cct gaa ctt cgt gtg gtc ctt gtc ttt ggt tat	730
Gly Leu Leu Asp Asn Pro Glu Leu Arg Val Val Leu Val Phe Gly Tyr	
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aat tgc tgt aag gtg gga gcc agt aat tat ctg cag caa gta gtc agc	778
Asn Cys Cys Lys Val Gly Ala Ser Asn Tyr Leu Gln Gln Val Val Ser	
226 231 236 241	
act ttc agt gat atg aat atc atc ttg gct gga gcc cag gtg gac aac	826
Thr Phe Ser Asp Met Asn Ile Ile Leu Ala Gly Gly Gln Val Asp Asn	
242 247 252 257	
ctg tca tca ctg act tct gaa aag aac cct ctg gat att gat gcc tcg	874
Leu Ser Ser Leu Thr Ser Glu Lys Asn Pro Leu Asp Ile Asp Ala Ser	
258 263 268 273	
ggt gtg gtt gga ctg tca ttt agt gga cac cga atc cag agt gcc act	922
Gly Val Val Gly Leu Ser Phe Ser Gly His Arg Ile Gln Ser Ala Thr	
274 279 284 289	
gtg ctc ctc aac gag gac gtc agt gat gag aag act gct gag gct gcg	970
Val Leu Leu Asn Glu Asp Val Ser Asp Glu Lys Thr Ala Glu Ala Ala	
290 295 300 305	
atg cag cgc ctc aaa gcg gcc aac att cca gag cat aac acc att ggc	1018
Met Gln Arg Leu Lys Ala Ala Asn Ile Pro Glu His Asn Thr Ile Gly	
306 311 316 321	
ttc atg ttt gca tgc gtt gcc agg gcc ttt cag tat tac aga gcc aag	1066
Phe Met Phe Ala Cys Val Gly Arg Gly Phe Gln Tyr Tyr Arg Ala Lys	
322 327 332 337	
ggg aat gtt gag gct gat gca ttt aga aag ttt ttt cct agt gtt ccc	1114
Gly Asn Val Glu Ala Asp Ala Phe Arg Lys Phe Phe Pro Ser Val Pro	
338 343 348 353	
tta ttc ggc ttc ttt gga aat gga gaa att gga tgt gat cgg ata gtc	1162
Leu Phe Gly Phe Phe Gly Asn Gly Glu Ile Gly Cys Asp Arg Ile Val	
354 359 364 369	
act ggg aac ttt ata ttg agg aaa tgt aat gag gta aaa gat gat gat	1210
Thr Gly Asn Phe Ile Leu Arg Lys Cys Asn Glu Val Lys Asp Asp Asp	
370 375 380 385	
ctg ttt cat agc tat aca aca ata atg gca ctc ata cat ctg ggg tca	1258
Leu Phe His Ser Tyr Thr Thr Ile Met Ala Leu Ile His Leu Gly Ser	
386 391 396 401	
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Ser Lys *	
402	

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Gly Ile Leu Ala Gly Gly Ala Arg Glu Ala Ser Cys Arg Tyr Pro Ala
  4                               9                               14                               19

ctg ggg cct cgc ctc gcc gct cac ttt cca gcg cag cgg ccg ccg cag      152
Leu Gly Pro Arg Leu Ala Ala His Phe Pro Ala Gln Arg Pro Pro Gln
  20                               25                               30                               35

cgg aca ctc cag aac ggc ctg gcc ctg cag cgg tgc ctg cac gcg acg      200
Arg Thr Leu Gln Asn Gly Leu Ala Leu Gln Arg Cys Leu His Ala Thr
  36                               41                               46                               51

gcg acc cgg gct ctc ccg ctc att ccc atc gtg gtg gag cag acg ggt      248
Ala Thr Arg Ala Leu Pro Leu Ile Pro Ile Val Val Glu Gln Thr Gly
  52                               57                               62                               67

cgc ggc gag cgc gcc tat gac atc tac tcg cgg ctg ctg cgg gag cgc      296
Arg Gly Glu Arg Ala Tyr Asp Ile Tyr Ser Arg Leu Leu Arg Glu Arg
  68                               73                               78                               83

atc gtg tgc gtc atg ggc ccg atc gat gac agc gtt gcc agc ctt gtt      344
Ile Val Cys Val Met Gly Pro Ile Asp Asp Ser Val Ala Ser Leu Val
  84                               89                               94                               99

atc gca cag ctc ctc ttc ctg ctt ctc gcc gcc ggc acc cca ggc atg      392
Ile Ala Gln Leu Leu Phe Leu Leu Leu Ala Ala Gly Thr Pro Gly Met
  100                               105                               110                               115

cgc cac tcg ctc ccc aac tcc cgt atc atg atc cac cag ccc tca gga      440
Arg His Ser Leu Pro Asn Ser Arg Ile Met Ile His Gln Pro Ser Gly
  116                               121                               126                               131

ggc gcc cgg ggc caa gcc aca gac att gcc atc cag gca gag gag atc      488
Gly Ala Arg Gly Gln Ala Thr Asp Ile Ala Ile Gln Ala Glu Glu Ile
  132                               137                               142                               147

atg aag ctc aag aag cag ctc tat aac atc tac gcc aag cac acc aaa      536
Met Lys Leu Lys Lys Gln Leu Tyr Asn Ile Tyr Ala Lys His Thr Lys
  148                               153                               158                               163

cag agc ctg cag gtg atc gag tcc gcc atg gag agg gac cgc tac atg      584
Gln Ser Leu Gln Val Ile Glu Ser Ala Met Glu Arg Asp Arg Tyr Met
  164                               169                               174                               179

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Ser Pro Met Glu Ala Gln Glu Phe Gly Ile Leu Asp Lys Val Leu Val	
180 185 190 195	
cac cct ccc cag gac ggt gag gat gag ccc acg ctg gtg cag aag gag	680
His Pro Pro Gln Asp Gly Glu Asp Glu Pro Thr Leu Val Gln Lys Glu	
196 201 206 211	
cct gta gaa gca gcg ccg gca gca gaa cct gtc cca gct agc acc tga	728
Pro Val Glu Ala Ala Pro Ala Ala Glu Pro Val Pro Ala Ser Thr *	
212 217 222 227	
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Met Leu Thr Ser Leu Ser Arg Pro	
1 5	
ata act acc atg gct ctc agt gcc ttg gtg tac cct ggg atg tgt ggc	159
Ile Thr Thr Met Ala Leu Ser Ala Leu Val Tyr Pro Gly Met Cys Gly	
9 14 19 24	
ctt ctg gcc aag cat ctg tca ttt cat att gtt gga gca ttc ctt ata	207
Leu Leu Ala Lys His Leu Ser Phe His Ile Val Gly Ala Phe Leu Ile	
25 30 35 40	
acc ctg ggg ttg cag ctc tct gta agt ttg ctg tgg cct gac caa gaa	255
Thr Leu Gly Leu Gln Leu Ser Val Ser Leu Leu Trp Pro Asp Gln Glu	
41 46 51 56	
aga agg cat atg cag att tct aca gaa att ata att gaa tta aag aat	303
Arg Arg His Met Gln Ile Ser Thr Glu Ile Ile Ile Glu Leu Lys Asn	
57 62 67 72	
ttg agg tga ggaaggc taatatctct cagagtacaa agtgattttg gaacataaag	359

Leu Arg *

73

tattttctttg ggttgaatta cataaaagtt tgtcactgta cctgtgttcc tgaactatct	419
gtgaaacatg aatatgtggg ctaagaaatt gtttatctta ataaataatt aacaaaccct	479
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tactaccggtt aagcaaattc cagacttcat aatttggggg aagtaactat cagatttcat	599
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Met Ser Gly Arg Leu Trp Ser Lys Ala Ile Phe Ala Gly Tyr Lys Arg	
1 5 10 15	
ggt ctc cgg aac caa agg gag cac aca gct ctt ctt aaa att gaa ggt	153
Gly Leu Arg Asn Gln Arg Glu His Thr Ala Leu Leu Lys Ile Glu Gly	
17 22 27 32	
gtt tac gcc cga gat gaa aca gaa ttc tat ttg ggc aag aga tgc gct	201
Val Tyr Ala Arg Asp Glu Thr Glu Phe Tyr Leu Gly Lys Arg Cys Ala	
33 38 43 48	
tat gta tat aaa gca aag aac aac aca gtc act cct ggc ggc aaa cca	249
Tyr Val Tyr Lys Ala Lys Asn Asn Thr Val Thr Pro Gly Gly Lys Pro	
49 54 59 64	
aac aaa acc aga gtc atc tgg gga aaa gta act cgg gcc cat gga aac	297
Asn Lys Thr Arg Val Ile Trp Gly Lys Val Thr Arg Ala His Gly Asn	
65 70 75 80	
agt ggc atg gtt cgt gcc aaa ttc cga agc aat ctt cct gct aag gcc	345
Ser Gly Met Val Arg Ala Lys Phe Arg Ser Asn Leu Pro Ala Lys Ala	
81 86 91 96	
att gga cac aga atc cga gtg atg ctg tac ccc tca agg att taa act	393
Ile Gly His Arg Ile Arg Val Met Leu Tyr Pro Ser Arg Ile *	
97 102 107	

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401

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gagcaaaaagt tgcacagcta aaccaggggc tcattcccag gacagac atg cag tta 176
Met Gln Leutgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta 224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu
4 9 14 19aac gca gta tcc gag aca gtg gct aca tcg act gct ggg att ccg agc 272
Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser
20 25 30 35gca gcg act ccc tct ctc ctc ctc gcc acg gca gag atg att cct tcg 320
Ala Ala Thr Pro Ser Leu Leu Leu Ala Thr Ala Glu Met Ile Pro Ser
36 41 46 51aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca 368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro
52 57 62 67gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa 416
Asp Val Val Leu Arg Gly Ser Ser Asp Gly Arg Gly Ser Asp Ser Glu
68 73 78 83tcc gac ttg cct cat cgg aag ctg cca gat gtg aag aag gat gac atg 464
Ser Asp Leu Pro His Arg Lys Leu Pro Asp Val Lys Lys Asp Asp Met
84 89 94 99tct gca cgg cgg act tcc cat ggt gag ccg aaa tca gca gtg cct ttt 512
Ser Ala Arg Arg Thr Ser His Gly Glu Pro Lys Ser Ala Val Pro Phe
100 105 110 115aac cag tac ctc ccg aac aaa agc aat cag acg gcc tac gtc ccc gcg 560
Asn Gln Tyr Leu Pro Asn Lys Ser Asn Gln Thr Ala Tyr Val Pro Ala
116 121 126 131cct ctg aga aag aag aaa gca gag aga gag gaa tac cgc aag agc tgg 608
Pro Leu Arg Lys Lys Lys Ala Glu Arg Glu Glu Tyr Arg Lys Ser Trp

132	137	142	147	
agt acc gcc acc tcc ccg ctg ggt ggg gag agg ccc ttc aga tac ggt				656
Ser Thr Ala Thr Ser Pro Leu Gly Gly Glu Arg Pro Phe Arg Tyr Gly				
148	153	158	163	
ccg aga act cct gtg tct gat gac gca gag agc acc agc atg ttt gac				704
Pro Arg Thr Pro Val Ser Asp Asp Ala Glu Ser Thr Ser Met Phe Asp				
164	169	174	179	
atg cgg tgt gag gag gag gcc gcg gtg cag ccg cac agc agg gcc cgc				752
Met Arg Cys Glu Glu Glu Ala Ala Val Gln Pro His Ser Arg Ala Arg				
180	185	190	195	
cag gag cag ctg cag ctg ata aat aac cag ctg agg gaa gag gac gac				800
Gln Glu Gln Leu Gln Leu Ile Asn Asn Gln Leu Arg Glu Glu Asp Asp				
196	201	206	211	
aaa tgg caa gat gac ctg gct cgt tgg aag agt cgt aga aga agt gtt				848
Lys Trp Gln Asp Asp Leu Ala Arg Trp Lys Ser Arg Arg Arg Ser Val				
212	217	222	227	
tct cag gac tta atc aag aaa gag gaa gaa agg aaa aaa atg gag aag				896
Ser Gln Asp Leu Ile Lys Lys Glu Glu Glu Arg Lys Lys Met Glu Lys				
228	233	238	243	
tta ctg gct gga gaa gat ggg aca agt gaa cga agg aaa agc atc aaa				944
Leu Leu Ala Gly Glu Asp Gly Thr Ser Glu Arg Arg Lys Ser Ile Lys				
244	249	254	259	
acc tac aga gaa att gtt caa gaa aaa gag ccg aga gag aga gag ctg				992
Thr Tyr Arg Glu Ile Val Gln Glu Lys Glu Arg Arg Glu Arg Glu Leu				
260	265	270	275	
cat gaa gca tat aag aac gct cgg tcc cag gag gag gca gag ggg atc				1040
His Glu Ala Tyr Lys Asn Ala Arg Ser Gln Glu Glu Ala Glu Gly Ile				
276	281	286	291	
ctt caa cag tac att gag agg ttc acc atc agt gag gct gtt ctc gaa				1088
Leu Gln Gln Tyr Ile Glu Arg Phe Thr Ile Ser Glu Ala Val Leu Glu				
292	297	302	307	
cgc ttg gag atg cca aaa att ctg gaa aga agc cat tca aca gag cca				1136
Arg Leu Glu Met Pro Lys Ile Leu Glu Arg Ser His Ser Thr Glu Pro				
308	313	318	323	
aat tta tcc tcc ttc ctg aat gac ccc aat ccc atg aaa tac ctg ccg				1184
Asn Leu Ser Ser Phe Leu Asn Asp Pro Asn Pro Met Lys Tyr Leu Arg				
324	329	334	339	
caa cag tca ctg cct cca ccc aaa ttc act gcc act gtt gaa acc acc				1232
Gln Gln Ser Leu Pro Pro Pro Lys Phe Thr Ala Thr Val Glu Thr Thr				
340	345	350	355	
att gct cgt gcc agt gtt ctg gat acc agc atg tca gca ggc agt ggg				1280
Ile Ala Arg Ala Ser Val Leu Asp Thr Ser Met Ser Ala Gly Ser Gly				
356	361	366	371	

tct cca agc aaa act gtc act ccc aaa gca gtg cct atg ctg aca ccc	1328
Ser Pro Ser Lys Thr Val Thr Pro Lys Ala Val Pro Met Leu Thr Pro	
372 377 382 387	
aag cct tac tcc cag ccc aaa aat tct caa gat gtt ctg aag acc ttt	1376
Lys Pro Tyr Ser Gln Pro Lys Asn Ser Gln Asp Val Leu Lys Thr Phe	
388 393 398 403	
aag gta gac ggg aaa gtc agt gtg aat gga gag acg gtt cat aga gag	1424
Lys Val Asp Gly Lys Val Ser Val Asn Gly Glu Thr Val His Arg Glu	
404 409 414 419	
gag gag aag gaa aga gag tgt ccc acg gtg gca cct gcc cac tcc tta	1472
Glu Glu Lys Glu Arg Glu Cys Pro Thr Val Ala Pro Ala His Ser Leu	
420 425 430 435	
acc aaa tcc cag atg ttt gaa ggt gtg gcc aga gtg cac ggg tct cca	1520
Thr Lys Ser Gln Met Phe Glu Gly Val Ala Arg Val His Gly Ser Pro	
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Leu Glu Leu Lys Gln Asp Asn Gly Ser Ile Glu Ile Asn Ile Lys Lys	
452 457 462 467	
cca aac tct gtt ccc caa gag ctc gca gca acc act gag aaa acg gaa	1616
Pro Asn Ser Val Pro Gln Glu Leu Ala Ala Thr Thr Glu Lys Thr Glu	
468 473 478 483	
ccg aat agt caa gag gac aag aat gat ggt gga aaa tca aga aaa ggg	1664
Pro Asn Ser Gln Glu Asp Lys Asn Asp Gly Gly Lys Ser Arg Lys Gly	
484 489 494 499	
aat ata gaa ctt gcc tca tca gaa cca cag cat ttt aca aca act gtg	1712
Asn Ile Glu Leu Ala Ser Ser Glu Pro Gln His Phe Thr Thr Thr Val	
500 505 510 515	
act cga tgc agc ccg acc gtg gcc ttt gtg gaa ttt ccc tcc agc ccc	1760
Thr Arg Cys Ser Pro Thr Val Ala Phe Val Glu Phe Pro Ser Ser Pro	
516 521 526 531	
cag ctg aag aat gat gtg tcg gaa gaa aaa gac cag aag aaa cca gaa	1808
Gln Leu Lys Asn Asp Val Ser Glu Glu Lys Asp Gln Lys Lys Pro Glu	
532 537 542 547	
aat gaa atg agt gga aag gtg gag ttg gtg ctg tca caa aag gtg gta	1856
Asn Glu Met Ser Gly Lys Val Glu Leu Val Leu Ser Gln Lys Val Val	
548 553 558 563	
aag cca aaa tct cca gaa ccc gaa gca acg ctg aca ttt cca ttt ctg	1904
Lys Pro Lys Ser Pro Glu Pro Glu Ala Thr Leu Thr Phe Pro Phe Leu	
564 569 574 579	
gac aaa atg cct gaa gcc aac caa cta cat ttg cca aat ctc aat tct	1952
Asp Lys Met Pro Glu Ala Asn Gln Leu His Leu Pro Asn Leu Asn Ser	
580 585 590 595	

caa gtg gat tct cca agc agt gag aag tca cct gtt acg aca cct ttt	2000
Gln Val Asp Ser Pro Ser Ser Glu Lys Ser Pro Val Thr Thr Pro Phe	
596 601 606 611	
aag ttc tgg gca tgg gac cca gaa gag gag cgc agg cga cag gaa aaa	2048
Lys Phe Trp Ala Trp Asp Pro Glu Glu Glu Arg Arg Arg Gln Glu Lys	
612 617 622 627	
tgg caa cag gaa cag gaa cgt ttg ctc cag gag aga tac cag aag gag	2096
Trp Gln Gln Glu Gln Glu Arg Leu Leu Gln Glu Arg Tyr Gln Lys Glu	
628 633 638 643	
cag gac aag ctg aaa gaa gag tgg gaa aag gcc caa aag gag gtg gaa	2144
Gln Asp Lys Leu Lys Glu Glu Trp Glu Lys Ala Gln Lys Glu Val Glu	
644 649 654 659	
gag gaa gaa cgc aga tac tat gag gag gag cgt aag ata att gaa gac	2192
Glu Glu Glu Arg Arg Tyr Tyr Glu Glu Glu Arg Lys Ile Ile Glu Asp	
660 665 670 675	
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Thr Val Val Pro Phe Thr Val Ser Ser Ser Ser Ala Asp Gln Leu Ser	
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708 713 718 723	
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Phe Gln Gly Asp Asp Ser Asp Leu Leu Leu Lys Thr Arg Glu Ser Asp	
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cga ctg gag gag aag ggc agc cta act gaa ggg gcc ttg gct cat tct	2432
Arg Leu Glu Glu Lys Gly Ser Leu Thr Glu Gly Ala Leu Ala His Ser	
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Val Lys Pro Lys Thr Leu Pro Leu Asp Lys Ser Ile Asn His Gln Ile	
804 809 814 819	
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 Ala Trp Glu Cys Gly Ser Ser Arg Gly Pro Trp Gly Leu Leu Arg Tyr
 38 43 48 53
 acc ttt gcc cct gta agg gcc tct agg ccc tgg gcc tgc ctc ccc aag 485
 Thr Phe Ala Pro Val Arg Ala Ser Arg Pro Trp Ala Cys Leu Pro Lys
 54 59 64 69
 ggc tca cta agc cag agg cca aag gtg ccc cct ccc gtt cac cta cca 533
 Gly Ser Leu Ser Gln Arg Pro Lys Val Pro Pro Pro Val His Leu Pro
 70 75 80 85
 ccc aag tcc tca tgc cct ccg agg gct ggg gga gga ggg gct caa gga 581
 Pro Lys Ser Ser Cys Pro Pro Arg Ala Gly Gly Gly Gly Ala Gln Gly
 86 91 96 101
 agg cgg gtt cca tgt aca tat tta tca ccc ctt tca cat agc ccc aag 629
 Arg Arg Val Pro Cys Thr Tyr Leu Ser Pro Leu Ser His Ser Pro Lys
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 Thr Phe Cys Thr Phe Leu Gln Gly Cys Pro *
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671

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 cattcttttc ctctcathtt ttgtagcact tctggggccc agtagccaac tgggggtcttc 240
 ccattgctgc catcaatgat atg aaa aag tct cca gag att atc agt ggg 290
 Met Lys Lys Ser Pro Glu Ile Ile Ser Gly
 1 5
 cgg atg aca ttt ggt aca gcc tcg gaa ctg gct tct gtt tgc atg cca 338
 Arg Met Thr Phe Gly Thr Ala Ser Glu Leu Ala Ser Val Cys Met Pro
 11 16 21 26
 cgc aac aaa tga agt agcccagctc atccagggag ggcggcttat caaacacgag 393
 Arg Asn Lys *
 27
 atgactaaaa cggcatctgc ataacaatgg aaaaggaaga acacggtctt gaagggacag 453
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cgccgcgggc ggggaccgg catccgggca ggctgcgcgc ggggtgcgggg cgagggcgcc 540
gcggggactg ggacgcacgg cccgcgcgcg ggacacggcc atg gag gac gcg gga 595
Met Glu Asp Ala Gly
1
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Ala Ala Gly Pro Gly Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
6 11 16 21
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Glu Pro Ala Pro Glu Pro Glu Pro Glu Pro Lys Pro Gly Ala Gly Thr
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Ser Glu Ala Phe Ser Arg Leu Trp Thr Asp Val Met Gly Ile Leu Asp
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54 59 64 69
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Tyr Asn Thr Cys Phe Ser Asp Val Cys Glu Arg Met Glu Glu Leu Arg
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Lys Arg Arg Val Ser Gln Asp Leu Glu Val Glu Lys Pro Asp Ala Ser
86 91 96 101
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Pro Thr Ser Leu Gln Leu Arg Ser Gln Ile Glu Glu Ser Leu Gly Phe
102 107 112 117
tgt agc gcc gtg tca acc cca gaa gtg gaa aga aag aac cct ctt cat 979
Cys Ser Ala Val Ser Thr Pro Glu Val Glu Arg Lys Asn Pro Leu His
118 123 128 133
aaa tca aac tca gaa gac agc tct gta gga aaa gga gac tgg aag aag 1027
Lys Ser Asn Ser Glu Asp Ser Ser Val Gly Lys Gly Asp Trp Lys Lys

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Lys Asn Lys Tyr Phe Trp Gln Asn Phe Arg Lys Asn Gln Lys Gly Ile				
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atg aga cag act tca aaa gga gaa gac gtt ggt tat gtt gcc agt gaa				1123
Met Arg Gln Thr Ser Lys Gly Glu Asp Val Gly Tyr Val Ala Ser Glu				
166	171	176	181	
ata acg atg agc gat gag gag cgg att cag cta atg atg atg gtc aaa				1171
Ile Thr Met Ser Asp Glu Glu Arg Ile Gln Leu Met Met Met Val Lys				
182	187	192	197	
gaa aag atg atc aca att gag gaa gca ctt gct agg ctc aag gaa tac				1219
Glu Lys Met Ile Thr Ile Glu Glu Ala Leu Ala Arg Leu Lys Glu Tyr				
198	203	208	213	
gag gcc cag cac cgg cag tcg gct gcc ctg gac cct gct gac tgg cca				1267
Glu Ala Gln His Arg Gln Ser Ala Ala Leu Asp Pro Ala Asp Trp Pro				
214	219	224	229	
gat ggt tct tac cca acg ttt gat ggc tca tca aac tgc aat tca aga				1315
Asp Gly Ser Tyr Pro Thr Phe Asp Gly Ser Ser Asn Cys Asn Ser Arg				
230	235	240	245	
gaa caa tcg gat gat gag act gag gag tcg gtg aag ttt aag agg tta				1363
Glu Gln Ser Asp Asp Glu Thr Glu Glu Ser Val Lys Phe Lys Arg Leu				
246	251	256	261	
cac aag ctg gta aac tcc act cgc aga gtc aga aag aaa cta att agg				1411
His Lys Leu Val Asn Ser Thr Arg Arg Val Arg Lys Lys Leu Ile Arg				
262	267	272	277	
gtg gaa gaa atg aaa aaa ccc agc act gaa ggt ggg gag gag cac gtg				1459
Val Glu Glu Met Lys Lys Pro Ser Thr Glu Gly Gly Glu Glu His Val				
278	283	288	293	
ttt gag aat tcg ccg gtc ctg gat gaa cgg tcc gcc ctc tac tct ggc				1507
Phe Glu Asn Ser Pro Val Leu Asp Glu Arg Ser Ala Leu Tyr Ser Gly				
294	299	304	309	
gtg cac aag aag ccc ctt ttc ttt gat ggc tct cct gag aaa cct ccc				1555
Val His Lys Lys Pro Leu Phe Phe Asp Gly Ser Pro Glu Lys Pro Pro				
310	315	320	325	
gaa gat gac tca gac tct ctc acc acg tct cca tcc tcc agc agc ctg				1603
Glu Asp Asp Ser Asp Ser Leu Thr Thr Ser Pro Ser Ser Ser Ser Leu				
326	331	336	341	
gac acc tgg ggg gct ggc cgg aag ttg gtc aaa acc ttc agc aaa gga				1651
Asp Thr Trp Gly Ala Gly Arg Lys Leu Val Lys Thr Phe Ser Lys Gly				
342	347	352	357	
gag agc cgg ggc ctg att aag ccc ccc aag aag atg ggg aca ttc ttc				1699
Glu Ser Arg Gly Leu Ile Lys Pro Pro Lys Lys Met Gly Thr Phe Phe				
358	363	368	373	

<p> tcc tac cca gaa gaa gaa aag gcc cag aaa gtg tcc cgc tcc ctc acc Ser Tyr Pro Glu Glu Glu Lys Ala Gln Lys Val Ser Arg Ser Leu Thr 374 379 384 389 </p>	1747
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<p> tgc agt ttt gga gga ttt gac ttg acg aat cgc tct ctg cac gtt ggc Cys Ser Phe Gly Gly Phe Asp Leu Thr Asn Arg Ser Leu His Val Gly 406 411 416 421 </p>	1843
<p> agt aat aat tct gac cca atg ggt aaa gaa gga gac ttt gtg tac aaa Ser Asn Asn Ser Asp Pro Met Gly Lys Glu Gly Asp Phe Val Tyr Lys 422 427 432 437 </p>	1891
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<p> gtg aaa tca gtg aaa gag acg atg aga aag aga atg tct aaa aaa tac Val Lys Ser Val Lys Glu Thr Met Arg Lys Arg Met Ser Lys Lys Tyr 454 459 464 469 </p>	1987
<p> agc agc tct gtc tct gag cag gac tcg ggc ctt gat gga atg cct ggc Ser Ser Ser Val Ser Glu Gln Asp Ser Gly Leu Asp Gly Met Pro Gly 470 475 480 485 </p>	2035
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<p> ctc aag gcc ggg ggt tct gta gaa agt ctt cgc agt tct ctc agt ggg Leu Lys Ala Gly Gly Ser Val Glu Ser Leu Arg Ser Ser Leu Ser Gly 502 507 512 517 </p>	2131
<p> cag agc tcc atg agc ggt caa aca gtg agc acc act gat tcc tca acc Gln Ser Ser Met Ser Gly Gln Thr Val Ser Thr Thr Asp Ser Ser Thr 518 523 528 533 </p>	2179
<p> agc aac cgg gaa agc gtc aag tcg gaa gat ggg gat gac gaa gag ccg Ser Asn Arg Glu Ser Val Lys Ser Glu Asp Gly Asp Asp Glu Glu Pro 534 539 544 549 </p>	2227
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<p> acc ccc agt ccc tat gac aca gac tca ctc aag ctc aag aaa gga gat Thr Pro Ser Pro Tyr Asp Thr Asp Ser Leu Lys Leu Lys Lys Gly Asp 566 571 576 581 </p>	2323
<p> atc atc gat ata atc agc aag cca ccc atg ggg acc tgg atg ggc ctg Ile Ile Asp Ile Ile Ser Lys Pro Pro Met Gly Thr Trp Met Gly Leu 582 587 592 597 </p>	2371

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Leu Asn Asn Lys Val Gly Thr Phe Lys Phe Ile Tyr Val Asp Val Leu	
598 603 608 613	
agt gaa gac gag gag aaa ccc aaa cgc ccc acc agg agg cgt cgg aaa	2467
Ser Glu Asp Glu Glu Lys Pro Lys Arg Pro Thr Arg Arg Arg Arg Lys	
614 619 624 629	
gga cga cca ccc cag ccc aag tct gtg gag gat ctc ctg gat cgg att	2515
Gly Arg Pro Pro Gln Pro Lys Ser Val Glu Asp Leu Leu Asp Arg Ile	
630 635 640 645	
aac cta aaa gag cac atg ccc act ttc ctg ttc aat gga tat gaa gat	2563
Asn Leu Lys Glu His Met Pro Thr Phe Leu Phe Asn Gly Tyr Glu Asp	
646 651 656 661	
ttg gac acc ttt aag ctg ctg gag gag gaa gac ttg gat gag tta aat	2611
Leu Asp Thr Phe Lys Leu Leu Glu Glu Glu Asp Leu Asp Glu Leu Asn	
662 667 672 677	
atc agg gac ccg gaa cac aga gct gtt ctc ttg aca gca gtg gag ctg	2659
Ile Arg Asp Pro Glu His Arg Ala Val Leu Leu Thr Ala Val Glu Leu	
678 683 688 693	
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Leu Gln Glu Tyr Asp Ser Asn Ser Asp Gln Ser Gly Ser Gln Glu Lys	
694 699 704 709	
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Leu Leu Val Asp Ser Gln Gly Leu Ser Gly Cys Ser Pro Arg Asp Ser	
710 715 720 725	
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Gly Cys Tyr Glu Ser Ser Glu Asn Leu Glu Asn Gly Lys Thr Arg Lys	
726 731 736 741	
gct agc ctc cta tct gcc aag tca tcc acc gag ccc agc ttg aag tct	2851
Ala Ser Leu Leu Ser Ala Lys Ser Ser Thr Glu Pro Ser Leu Lys Ser	
742 747 752 757	
ttt agc aga aac cag ttg ggc aat tac cca aca ttg cct tta atg aaa	2899
Phe Ser Arg Asn Gln Leu Gly Asn Tyr Pro Thr Leu Pro Leu Met Lys	
758 763 768 773	
tca ggg gat gca ctg aag cag gga cag gag gag ggc agg ctg ggt ggt	2947
Ser Gly Asp Ala Leu Lys Gln Gly Gln Glu Glu Gly Arg Leu Gly Gly	
774 779 784 789	
ggc ctt gcc cca gac acg tcc aag agc tgt gac cca cct ggt gtg act	2995
Gly Leu Ala Pro Asp Thr Ser Lys Ser Cys Asp Pro Pro Gly Val Thr	
790 795 800 805	
ggt ttg aat aaa aac cga aga agc ctc cca gtt tcc atc tgc cgg agc	3043
Gly Leu Asn Lys Asn Arg Arg Ser Leu Pro Val Ser Ile Cys Arg Ser	
806 811 816 821	
tgt gag acc ctg gag ggc ccc cag act gtg gac act tgg ccc cga tcc	3091

Cys	Glu	Thr	Leu	Glu	Gly	Pro	Gln	Thr	Val	Asp	Thr	Trp	Pro	Arg	Ser	
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cat	tcc	ctg	gat	gac	ctt	caa	gtg	gag	cct	ggc	gct	gag	caa	gac	gtg	3139
His	Ser	Leu	Asp	Asp	Leu	Gln	Val	Glu	Pro	Gly	Ala	Glu	Gln	Asp	Val	
838					843					848					853	
cct	acc	gag	gtg	aca	gaa	ccg	ccc	cct	cag	att	gta	cct	gaa	gtg	cca	3187
Pro	Thr	Glu	Val	Thr	Glu	Pro	Pro	Pro	Gln	Ile	Val	Pro	Glu	Val	Pro	
854					859					864					869	
cag	aag	acg	acc	gcc	tct	tcc	acg	aag	gcc	cag	ccc	ctg	gag	cga	gac	3235
Gln	Lys	Thr	Thr	Ala	Ser	Ser	Thr	Lys	Ala	Gln	Pro	Leu	Glu	Arg	Asp	
870					875					880					885	
tct	gct	gtc	gac	aat	gca	ttg	cta	ctg	acc	caa	agc	aag	aga	ttt	tct	3283
Ser	Ala	Val	Asp	Asn	Ala	Leu	Leu	Leu	Thr	Gln	Ser	Lys	Arg	Phe	Ser	
886					891					896					901	
gaa	cct	cag	aaa	ttg	aca	act	aag	aaa	ctg	gag	ggc	tca	atc	gca	gcc	3331
Glu	Pro	Gln	Lys	Leu	Thr	Thr	Lys	Lys	Leu	Glu	Gly	Ser	Ile	Ala	Ala	
902					907					912					917	
tct	ggc	cgc	ggc	ctg	tca	ccc	cct	cag	tgt	ttg	ccc	aga	aac	tat	gat	3379
Ser	Gly	Arg	Gly	Leu	Ser	Pro	Pro	Gln	Cys	Leu	Pro	Arg	Asn	Tyr	Asp	
918					923					928					933	
gct	cag	cct	cct	gga	gct	aaa	cac	ggc	tta	gca	agg	acg	cct	ctg	gag	3427
Ala	Gln	Pro	Pro	Gly	Ala	Lys	His	Gly	Leu	Ala	Arg	Thr	Pro	Leu	Glu	
934					939					944					949	
ggc	cac	aga	aaa	gga	cac	gag	ttt	gaa	gga	aca	cac	cat	ccc	ctg	ggc	3475
Gly	His	Arg	Lys	Gly	His	Glu	Phe	Glu	Gly	Thr	His	His	Pro	Leu	Gly	
950					955					960					965	
acc	aaa	gaa	ggg	gta	gat	gct	gag	cag	aga	atg	cag	ccc	aaa	att	cca	3523
Thr	Lys	Glu	Gly	Val	Asp	Ala	Glu	Gln	Arg	Met	Gln	Pro	Lys	Ile	Pro	
966					971					976					981	
tca	cag	cct	cca	cct	gtt	cct	gcc	aaa	aag	agc	aga	gaa	cgc	ctt	gct	3571
Ser	Gln	Pro	Pro	Pro	Val	Pro	Ala	Lys	Lys	Ser	Arg	Glu	Arg	Leu	Ala	
982					987					992					997	
aac	gga	ctc	cac	cct	gtt	ccc	atg	ggc	ccc	agt	ggg	gcc	ctc	ccc	agt	3619
Asn	Gly	Leu	His	Pro	Val	Pro	Met	Gly	Pro	Ser	Gly	Ala	Leu	Pro	Ser	
998					1003					1008					1013	
ccc	gat	gcg	cca	tgc	ctg	cca	gtg	aaa	agg	ggc	agc	ccc	gcc	agc	ccc	3667
Pro	Asp	Ala	Pro	Cys	Leu	Pro	Val	Lys	Arg	Gly	Ser	Pro	Ala	Ser	Pro	
1014					1019					1024					1029	
acc	agc	cct	agc	gac	tgt	ccc	cca	gca	ctg	gct	ccc	agg	cct	ctc	tca	3715
Thr	Ser	Pro	Ser	Asp	Cys	Pro	Pro	Ala	Leu	Ala	Pro	Arg	Pro	Leu	Ser	
1030					1035					1040					1045	
ggg	cag	gcg	cct	ggc	agc	cca	cca	agc	aca	agg	ccg	ccc	ccc	tgg	ctc	3763
Gly	Gln	Ala	Pro	Gly	Ser	Pro	Pro	Ser	Thr	Arg	Pro	Pro	Pro	Trp	Leu	

1046	1051	1056	1061	
tca gag ctc ccc gag aac aca agc ctc cag gag cac ggt gtg aag ctg				3811
Ser Glu Leu Pro Glu Asn Thr Ser Leu Gln Glu His Gly Val Lys Leu				
1062	1067	1072	1077	
ggc ccg gct ttg acc agg aag gtc tcc tgt gcc cgg gga gtg gat cta				3859
Gly Pro Ala Leu Thr Arg Lys Val Ser Cys Ala Arg Gly Val Asp Leu				
1078	1083	1088	1093	
gaa acg ctc act gaa aac aag ctg cac gct gaa ggc atc gat ctc acg				3907
Glu Thr Leu Thr Glu Asn Lys Leu His Ala Glu Gly Ile Asp Leu Thr				
1094	1099	1104	1109	
gag gag ccg tat tct gat aag cat ggc cgc tgt ggg att cct gaa gcc				3955
Glu Glu Pro Tyr Ser Asp Lys His Gly Arg Cys Gly Ile Pro Glu Ala				
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ctg gtg cag aga tac gca gag gac ttg gat cag ccc gag cgg gac gtc				4003
Leu Val Gln Arg Tyr Ala Glu Asp Leu Asp Gln Pro Glu Arg Asp Val				
1126	1131	1136	1141	
gcc gcc aac atg gac cag atc cgg gtg aag cag ctt cgg aag cag cac				4051
Ala Ala Asn Met Asp Gln Ile Arg Val Lys Gln Leu Arg Lys Gln His				
1142	1147	1152	1157	
cgc atg gcg att cca agt ggt gga ctc acg gaa atc tgc cga aag ccc				4099
Arg Met Ala Ile Pro Ser Gly Gly Leu Thr Glu Ile Cys Arg Lys Pro				
1158	1163	1168	1173	
gtc tct cct ggg tgc att tcg tct gtg tca gat tgg ctc att tcc atc				4147
Val Ser Pro Gly Cys Ile Ser Ser Val Ser Asp Trp Leu Ile Ser Ile				
1174	1179	1184	1189	
ggc ctg ccc atg tac gcc ggc acc ctc tcc acc gcg ggc ttc agc aca				4195
Gly Leu Pro Met Tyr Ala Gly Thr Leu Ser Thr Ala Gly Phe Ser Thr				
1190	1195	1200	1205	
ctg agc caa gtg cct tct ctg tct cac act tgc ctt cag gag gcc ggc				4243
Leu Ser Gln Val Pro Ser Leu Ser His Thr Cys Leu Gln Glu Ala Gly				
1206	1211	1216	1221	
atc aca gag gag aga cac ata aga aag ctc cta tct gca gcc aga ctc				4291
Ile Thr Glu Glu Arg His Ile Arg Lys Leu Leu Ser Ala Ala Arg Leu				
1222	1227	1232	1237	
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Phe Lys Leu Pro Pro Gly Pro Glu Ala Met *				
1238	1243	1248		
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ccttggcaca ggactgagga tcctctcctc cagaaaagcc ccctcgagga aataaattag				4522
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gcacgagcca ggcgtactga cagggtggacc agcggactgg tggag atg gcg acg 174
Met Ala Thr
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ctc tct ctg acc gtg aat tca gga gac cct ccg cta gga gct ttg ctg 222
Leu Ser Leu Thr Val Asn Ser Gly Asp Pro Pro Leu Gly Ala Leu Leu
4 9 14 19
gca gta gaa cac gtg aaa gac gat gtc agc att tcc gtt gaa gaa ggg 270
Ala Val Glu His Val Lys Asp Asp Val Ser Ile Ser Val Glu Glu Gly
20 25 30 35
aaa gag aat att ctt cat gtt tct gaa aat gtg ata ttc aca gat gtg 318
Lys Glu Asn Ile Leu His Val Ser Glu Asn Val Ile Phe Thr Asp Val
36 41 46 51
aat tct ata ctt cgc tac ttg gct aga gtt gca act aca gct ggg tta 366
Asn Ser Ile Leu Arg Tyr Leu Ala Arg Val Ala Thr Thr Ala Gly Leu
52 57 62 67
tat ggc tct aat ctg atg gaa cat act gag att gat cac tgg ttg gag 414
Tyr Gly Ser Asn Leu Met Glu His Thr Glu Ile Asp His Trp Leu Glu
68 73 78 83
ttc agt gct aca aaa tta tct tca tgt gat tcc ttt act tct aca att 462
Phe Ser Ala Thr Lys Leu Ser Ser Cys Asp Ser Phe Thr Ser Thr Ile
84 89 94 99
aat gaa ctc aat cat tgc ctg tct ctg aga aca tac tta gtt gga aac 510

Asn Glu Leu Asn His Cys Leu Ser Leu Arg Thr Tyr Leu Val Gly Asn	
100 105 110 115	
tcc ttg agt tta gca gat tta tgt gtt tgg gcc acc cta aaa gga aat	558
Ser Leu Ser Leu Ala Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn	
116 121 126 131	
gct gcc tgg caa gaa cag ttg aaa cag aag aaa gct cca gtt cat gta	606
Ala Ala Trp Gln Glu Gln Leu Lys Gln Lys Lys Ala Pro Val His Val	
132 137 142 147	
aaa cgt tgg ttt ggc ttt ctt gaa gcc cag cag gcc ttc cag tca gta	654
Lys Arg Trp Phe Gly Phe Leu Glu Ala Gln Gln Ala Phe Gln Ser Val	
148 153 158 163	
ggg acc aag tgg gat gtt tca aca acc aaa gct cga gtg gca cct gag	702
Gly Thr Lys Trp Asp Val Ser Thr Thr Lys Ala Arg Val Ala Pro Glu	
164 169 174 179	
aaa aag caa gat gtt ggg aaa ttt gtt gag ctt cca ggt gcg gag atg	750
Lys Lys Gln Asp Val Gly Lys Phe Val Glu Leu Pro Gly Ala Glu Met	
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Gly Lys Val Thr Val Arg Phe Pro Pro Glu Ala Ser Gly Tyr Leu His	
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Ile Gly His Ala Lys Ala Ala Leu Leu Asn Gln His Tyr Gln Val Asn	
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Phe Lys Gly Lys Leu Ile Met Arg Phe Asp Asp Thr Asn Pro Glu Lys	
228 233 238 243	
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Lys Lys Glu Asp Phe Glu Lys Val Ile Leu Glu Asp Val Ala Met Leu	
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His Ile Lys Pro Asp Gln Phe Thr Tyr Thr Ser Asp His Phe Glu Thr	
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ata atg aag tat gca gag aag cta att caa gaa ggg aag gct tat gtg	1038
Ile Met Lys Tyr Ala Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val	
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gat gat act cct gct gaa cag atg aaa gca gaa cgt gag cag agg ata	1086
Asp Asp Thr Pro Ala Glu Gln Met Lys Ala Glu Arg Glu Gln Arg Ile	
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Glu Ser Lys His Arg Lys Asn Pro Ile Glu Lys Asn Leu Gln Met Trp	
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Glu Glu Met Lys Lys Gly Ser Gln Phe Gly Gln Ser Cys Cys Leu Arg	

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Ala Lys Ile Asp Met	Ser Ser Asn Asn Gly	Cys Met Arg Asp Pro	Thr	
340	345	350	355	
ctt tat cgc tgc aaa	att caa cca cat cca	aga act gga aat aaa	tac	1278
Leu Tyr Arg Cys Lys	Ile Gln Pro His Pro	Arg Thr Gly Asn Lys	Tyr	
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aat gtt tat cca aca	tat gat ttt gcc tgc	ccc ata gtt gac agc	atc	1326
Asn Val Tyr Pro Thr	Tyr Asp Phe Ala Cys	Pro Ile Val Asp Ser	Ile	
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Glu Gly Val Thr His	Ala Leu Arg Thr Thr	Glu Tyr His Asp Arg	Asp	
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Glu Gln Phe Tyr Trp	Ile Ile Glu Ala Leu	Gly Ile Arg Lys Pro	Tyr	
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Ile Trp Glu Tyr Ser	Arg Leu Asn Leu Asn	Asn Thr Val Leu Ser	Lys	
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Arg Lys Leu Thr Trp	Phe Val Asn Glu Gly	Leu Val Asp Gly Trp	Asp	
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Asp Pro Arg Phe Pro	Thr Val Arg Gly Val	Leu Arg Arg Gly Met	Thr	
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Val Glu Gly Leu Lys	Gln Phe Ile Ala Ala	Gln Gly Ser Ser Arg	Ser	
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Val Val Asn Met Glu	Trp Asp Lys Ile Trp	Ala Phe Asn Lys Lys	Val	
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Lys His Pro Lys Asn	Pro Glu Val Gly Leu	Lys Pro Val Trp Tyr	Ser	
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Pro Lys Val Phe Ile	Glu Gly Ala Asp Ala	Glu Thr Phe Ser Glu	Gly	
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Cys Lys Glu Ala Pro Cys Val Leu Ile Tyr Ile Pro Asp Gly His Thr	
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Pro Pro Ala Glu Ile Gly Gln Asn Ile Ser Ser Asn Ser Ser Ala Ser	
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Asp Tyr Thr Thr Thr Ile Glu Ala Phe Ile Ser Ala Ser Gly Arg Ala	
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Leu Phe Thr Arg Ala Ser Glu Asp Leu Lys Thr His Met Val Val Ala				
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Gln Ile Pro Phe Cys Gly Glu Ile Asp Cys Glu Asp Trp Ile Lys Lys				
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Met Pro Phe Pro Val Thr	
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Gln Ser Val Ile Glu Asn Val Gly Gly Lys Ile Phe Thr Phe Gly Ser	
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Tyr Arg Leu Gly Val His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys	
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Gln Lys Lys Lys Lys His Ser Thr Glu Gly Val Lys Leu Thr Ala Leu	
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Val Pro Ser Pro Thr Ser Ala Thr Lys Thr Ser Pro Leu Asn Ser Ser	
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Gly Ser Ser Gln Gly Arg Asn Ser Pro Ala Pro Ala Val Thr Ala Ala	
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Val Val Ser Ser Thr Arg Leu Val Asn Pro Pro Pro Arg Ser Ser Gly	
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Leu Ala Ser Gln Lys Thr Ser Ser Thr Asp Leu Ser Asp Ile Pro Ala	
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732

737

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His Gln Asn Trp Gly Arg Asp Gly Gly Pro Arg Ser Ser Gly Gly Gly
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Tyr Gly Gly Gly Pro Ala Gly Gly His Gly Gly Asn Arg Gly Ser Gly
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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Arg Gly Gly Arg Gly Arg His
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Pro Gly His Leu Lys Gly Arg Glu Ile Gly Met Trp Tyr Ala Lys Lys
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Ala Pro Glu Asp His Gly Tyr Gly Thr Glu Val Ser Thr Lys Asn Thr
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Gln Lys Leu Leu Glu Asp Leu Gln Lys Lys Lys Asn Asp Leu Arg Tyr	
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Phe Ser Glu Tyr Phe Gly Asn Cys Pro Met Ile His Ile Pro Gly Phe	
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Thr Phe Pro Val Val Glu Tyr Leu Leu Glu Asp Val Ile Glu Lys Ile	
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Val Ile Asp Gly Gly Lys Ile Lys Glu Thr His Phe Asp Thr Gln Asn	
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Lys Thr Ile Ala Phe	Val Lys Ala Val Glu	Ser Gly Gln Leu Val Ser	
153	158	163	168
gtg cat gag aaa gaa agt	atc aaa cat ctc aaa	gag gaa cag ggt tta	640
Val His Glu Lys Glu Ser	Ile Lys His Leu Lys	Glu Glu Gln Gly Leu	
169	174	179	184
gtg aaa aac act gaa cag	agt aga aga aaa aag	cgc aag aaa ata agt	688
Val Lys Asn Thr Glu Gln	Ser Arg Arg Lys Lys	Arg Lys Lys Ile Ser	
185	190	195	200
ggc ccc aat cct ctt agt	tgt ttg aag aaa aag	aaa aag gca ccg gac	736
Gly Pro Asn Pro Leu Ser	Cys Leu Lys Lys Lys	Lys Lys Lys Ala Pro Asp	
201	206	211	216
aca caa tca tct gct tct	gaa aag aaa aga aaa	aga aaa aga att cgg	784
Thr Gln Ser Ser Ala Ser	Glu Lys Lys Arg Lys	Arg Lys Arg Ile Arg	
217	222	227	232
aac aga tct aac cca aaa	gta ctt tct gag aag	cag aat gca gaa gga	832
Asn Arg Ser Asn Pro Lys	Val Leu Ser Glu Lys	Gln Asn Ala Glu Gly	
233	238	243	248
gaa tga atcctttgga tactttcaag	gacattcaaa tgtgaaaatg	aatttttttac	888
Glu *			
249			
aactagaagt atttataata aaagaccaaa	cttattttttg taaatgaacc	catatgcttt	948
actaaaatta attataaaat aaaaacagtg	accagtctag ccagcatgga	aaaccccatc	1008
tctactaaaa tacaaaaatt agctgggcat	gatgggtgcac agttgtaatt	ccagctactc	1068
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ggttgtttct ccaggtaaaa ttgtcgctc	tctgggtccca ttcccacctt	caaacattat	1308
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agcg atg cgg gaa tgc ata tca gtc cac gtg ggc caa gcg gga gtt cag	169
Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln	
1 5 10	
att ggc aat gcc tgc tgg gag ctc ttc tgc ctg gaa cac ggc atc cag	217
Ile Gly Asn Ala Cys Trp Glu Leu Phe Cys Leu Glu His Gly Ile Gln	
16 21 26 31	
gca gac ggc act ttt gat gct caa gct agc aag atc aac gat gat gac	265
Ala Asp Gly Thr Phe Asp Ala Gln Ala Ser Lys Ile Asn Asp Asp Asp	
32 37 42 47	
tcc ttc acc acc ttt ttc agc gag act ggc aat ggg aag cat gtg ccc	313
Ser Phe Thr Thr Phe Phe Ser Glu Thr Gly Asn Gly Lys His Val Pro	
48 53 58 63	
cgg gcc gtc atg ata gat ctg gag cct act gta gtg gat gag gtt cgg	361
Arg Ala Val Met Ile Asp Leu Glu Pro Thr Val Val Asp Glu Val Arg	
64 69 74 79	
gca gga acc tac cgc cag ctc ttc cat cca gag cag ctg atc aca gga	409
Ala Gly Thr Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly	
80 85 90 95	
aag gag gat gca gcc aac aac tat gcc cgg ggc cac tac acg gtg ggc	457
Lys Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Val Gly	
96 101 106 111	
aag gag agc att gac ctg gtg ctg gac cgc ata cgg aag ctg aca gat	505
Lys Glu Ser Ile Asp Leu Val Leu Asp Arg Ile Arg Lys Leu Thr Asp	
112 117 122 127	
gct tgc tct ggc ctg cag ggc ttc ctg att ttc cac agt ttt ggt ggg	553
Ala Cys Ser Gly Leu Gln Gly Phe Leu Ile Phe His Ser Phe Gly Gly	
128 133 138 143	
ggc act ggc tcc ggc ttc act tct ctg ctg atg gaa cgc ctc tcc ctg	601
Gly Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Leu	
144 149 154 159	
gat tat ggc aag aaa tcc aag ctg gag ttt gcc atc tac cca gcc ccc	649
Asp Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ala Ile Tyr Pro Ala Pro	
160 165 170 175	
cag gtc tct act gca gtg gtg gag ccc tac aac tcc atc ctg acc acc	697
Gln Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr	
176 181 186 191	

cac acc aca ctg gaa cat tca gat tgt gct ttc atg gtg gac aac gaa His Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu 192 197 202 207	745
gcc atc tat gac atc tgc cgc agg aac ctt gac att gag cgc cct acc Ala Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr 208 213 218 223	793
tat acc aac ctc aac cgc ctc atc agt cag att gtg tcc tca atc act Tyr Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr 224 229 234 239	841
gct tct ctc cgc ttt gac ggg gcc ctc aat gtg gac ctc act gag ttc Ala Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe 240 245 250 255	889
cag acc aac ctg gtg ccc tac ccc cgc atc cac ttc ccg ctg gtc acc Gln Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Val Thr 256 261 266 271	937
tac gcg ccc atc atc tct gcc gag aaa gcc tat cac gaa cag ctc tct Tyr Ala Pro Ile Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser 272 277 282 287	985
gtg gcc gag ata acc agc tcc tgc ttt gag ccc aac agc cag atg gtg Val Ala Glu Ile Thr Ser Ser Cys Phe Glu Pro Asn Ser Gln Met Val 288 293 298 303	1033
aag tgc gac ccg aga cat ggc aag tac atg gcc tgc tgc atg ctc tac Lys Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Met Leu Tyr 304 309 314 319	1081
cgg ggc gac gtg gtg ccc aag gat gtg aat gtc gct att gct gcc atc Arg Gly Asp Val Val Pro Lys Asp Val Asn Val Ala Ile Ala Ala Ile 320 325 330 335	1129
aag acc aag agg acc atc cag ttt gta gac tgg tgt ccc aca ggc ttc Lys Thr Lys Arg Thr Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe 336 341 346 351	1177
aag gtg ggc atc aac tac cag ccc ccg acc gtg gtc ccc ggg gga gac Lys Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp 352 357 362 367	1225
ctg gcc aag gtg cag cgg gcc gtc tgc atg ctc agc aac acc acg gcc Leu Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala 368 373 378 383	1273
att gcg gag gcc tgg gcc cgc ctc gac cac aag ttc gac ctc atg tac Ile Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr 384 389 394 399	1321
gcc aag cgg gcc ttt gtg cat tgg tat gtg gga gag ggg atg gaa gaa Ala Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu 400 405 410 415	1369
gga gaa ttt tct gag gcc agg gaa gac tta gct gcc ctg gag aag gat	1417

Gly Glu Phe Ser Glu Ala Arg Glu Asp Leu Ala Ala Leu Glu Lys Asp
 416 421 426 431

tat gaa gaa gtg ggg act gat tcg ttt gaa gaa gaa aat gaa ggg gag 1465
 Tyr Glu Glu Val Gly Thr Asp Ser Phe Glu Glu Asn Glu Gly Glu
 432 437 442 447

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 Glu Phe *
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 Met Asp Glu
 1

gat tct tcg ttg aga gat tat act gta agc ttg gac tct gac atg gat 165
 Asp Ser Ser Leu Arg Asp Tyr Thr Val Ser Leu Asp Ser Asp Met Asp
 4 9 14 19

gat gca tct aaa ttt ctt cag gat tat gat att cga act ggc aac acc 213
 Asp Ala Ser Lys Phe Leu Gln Asp Tyr Asp Ile Arg Thr Gly Asn Thr
 20 25 30 35

agg gaa gct ttg agt cct tgt cca agt act gta agt acc aag tct cag 261
 Arg Glu Ala Leu Ser Pro Cys Pro Ser Thr Val Ser Thr Lys Ser Gln
 36 41 46 51

cca ggc agc agt gct tct tct agt tct gga gtt aaa atg acc agc ttt 309
 Pro Gly Ser Ser Ala Ser Ser Ser Ser Gly Val Lys Met Thr Ser Phe
 52 57 62 67

gct gaa caa aaa ttc agg aaa ctg aat cat acc gat gga aaa agt agt 357
 Ala Glu Gln Lys Phe Arg Lys Leu Asn His Thr Asp Gly Lys Ser Ser
 68 73 78 83

gga agc agt tct caa aaa act aca cca gaa ggc tct gaa ctt aat att 405
 Gly Ser Ser Ser Gln Lys Thr Thr Pro Glu Gly Ser Glu Leu Asn Ile
 84 89 94 99

cct cat gtg gtt gct tgg gca caa att cca gaa gaa aca ggg ctt cca 453
 Pro His Val Val Ala Trp Ala Gln Ile Pro Glu Glu Thr Gly Leu Pro

100	105	110	115	
cag gga cgg gac act	acc cag ctg ttg gcc	tct gaa atg gtg cat	ctt	501
Gln Gly Arg Asp Thr	Thr Gln Leu Leu Ala	Ser Glu Met Val His	Leu	
116	121	126	131	
agg atg aaa cta gaa	gaa aag agg cgt gct	ata gaa gcc cag aaa	aag	549
Arg Met Lys Leu Glu	Glu Lys Arg Arg Ala	Ile Glu Ala Gln Lys	Lys	
132	137	142	147	
aaa atg gaa gct gct	ttt acc aaa cag aga	cag aaa atg gga agg	aca	597
Lys Met Glu Ala Ala	Phe Thr Lys Gln Arg	Gln Lys Met Gly Arg	Thr	
148	153	158	163	
gca ttc ctt act gta	gtg aaa aag aaa ggg	gat ggg ata tct cct	cta	645
Ala Phe Leu Thr Val	Val Lys Lys Lys Gly	Asp Gly Ile Ser Pro	Leu	
164	169	174	179	
cga gag gaa gcg gcg	ggt gca gaa gat gag	aaa gta tat act gat	cga	693
Arg Glu Glu Ala Ala	Gly Ala Glu Asp Glu	Lys Val Tyr Thr Asp	Arg	
180	185	190	195	
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Ala Lys Glu Lys Glu	Ser Gln Lys Thr Asp	Gly Gln Arg Ser Lys	Ser	
196	201	206	211	
ctg gca gat ata aaa	gag agc atg gag aat	cct caa gcc aaa tgg	cta	789
Leu Ala Asp Ile Lys	Glu Ser Met Glu Asn	Pro Gln Ala Lys Trp	Leu	
212	217	222	227	
aag tct cca act aca	cct att gat cct gag	aag cag tgg aac ctg	gca	837
Lys Ser Pro Thr Thr	Pro Ile Asp Pro Glu	Lys Gln Trp Asn Leu	Ala	
228	233	238	243	
agc ccc tca gaa gaa	act tta aat gaa gga	gag att tta gaa tat	acc	885
Ser Pro Ser Glu Glu	Thr Leu Asn Glu Gly	Glu Ile Leu Glu Tyr	Thr	
244	249	254	259	
aaa tcc att gaa aag	tta aat tca tcc ctg	cat ttt cta caa caa	gaa	933
Lys Ser Ile Glu Lys	Leu Asn Ser Ser Leu	His Phe Leu Gln Gln	Glu	
260	265	270	275	
atg caa cgc ttg tca	ctt cag cag gag atg	tta atg cag atg aga	gag	981
Met Gln Arg Leu Ser	Leu Gln Gln Glu Met	Leu Met Gln Met Arg	Glu	
276	281	286	291	
caa caa tct tgg gtg	att tca cct cca caa	ccc tct cca cag aaa	cag	1029
Gln Gln Ser Trp Val	Ile Ser Pro Pro Gln	Pro Ser Pro Gln Lys	Gln	
292	297	302	307	
att cga gat ttt aag	cct tct aag cag gca	ggc ctg tca tca gcc	att	1077
Ile Arg Asp Phe Lys	Pro Ser Lys Gln Ala	Gly Leu Ser Ser Ala	Ile	
308	313	318	323	
gca cca ttc tcc tca	gac tcc cct cgt cct	act cac cca tct cca	cag	1125
Ala Pro Phe Ser Ser	Asp Ser Pro Arg Pro	Thr His Pro Ser Pro	Gln	
324	329	334	339	

tct tct aac agg aaa agt gca tct ttt tct gtt aaa agt caa agg act	1173
Ser Ser Asn Arg Lys Ser Ala Ser Phe Ser Val Lys Ser Gln Arg Thr	
340 345 350 355	
cct agg cca aat gag tta aaa ata aca cct ttg aat cga acc ttg aca	1221
Pro Arg Pro Asn Glu Leu Lys Ile Thr Pro Leu Asn Arg Thr Leu Thr	
356 361 366 371	
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Pro Pro Arg Ser Val Asp Ser Leu Pro Arg Leu Arg Arg Phe Ser Pro	
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Ser Gln Val Pro Ile Gln Thr Arg Ser Phe Val Cys Phe Gly Asp Asp	
388 393 398 403	
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404 409 414 419	
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Glu Glu Leu Glu Ser Lys Gly Thr Leu Glu Gln Arg Gly His Asn Pro	
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Glu Glu Lys Glu Ile Lys Pro Phe Glu Ser Thr Val Ser Glu Val Leu	
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Ser Leu Pro Val Thr Glu Thr Val Cys Leu Thr Pro Asn Glu Asp Gln	
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ttg aat caa ccc aca gaa ccc cct cct aaa ccc gtt ttc cca ccc act	1557
Leu Asn Gln Pro Thr Glu Pro Pro Pro Lys Pro Val Phe Pro Pro Thr	
468 473 478 483	
gct cca aaa aat gtt aat ctg att gaa gtt tcc ctc tca gat ttg aaa	1605
Ala Pro Lys Asn Val Asn Leu Ile Glu Val Ser Leu Ser Asp Leu Lys	
484 489 494 499	
ccc cct gaa aag gct gat gta cct gtt gaa aaa tat gat gga gaa agt	1653
Pro Pro Glu Lys Ala Asp Val Pro Val Glu Lys Tyr Asp Gly Glu Ser	
500 505 510 515	
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Asp Lys Glu Gln Phe Asp Asp Asp Gln Lys Val Cys Cys Gly Phe Phe	
516 521 526 531	
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Phe Lys Asp Asp Gln Lys Ala Glu Asn Asp Met Ala Met Lys Arg Ala	
532 537 542 547	
gct ttg ttg gag aaa aga tta aga agg gaa aag gaa act cag ctc cgg	1797
Ala Leu Leu Glu Lys Arg Leu Arg Arg Glu Lys Glu Thr Gln Leu Arg	
548 553 558 563	

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cgt aaa act gag gaa gaa cgt cag aag aaa gaa gat gag aga gca cgc Arg Lys Thr Glu Glu Glu Arg Gln Lys Lys Glu Asp Glu Arg Ala Arg 580 585 590 595	1893
aga gaa ttt att agg caa gaa tat atg agg cgg aaa caa ctg aaa cta Arg Glu Phe Ile Arg Gln Glu Tyr Met Arg Arg Lys Gln Leu Lys Leu 596 601 606 611	1941
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gaa atg gag aaa tca gat gcc aac aac ttc tta atc ttg ttc cgg gat Glu Met Glu Lys Ser Asp Ala Asn Asn Phe Leu Ile Leu Phe Arg Asp 756 761 766 771	2421
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Met Gly Phe Pro Ala Ala Ala Leu Leu Cys Ala Leu	
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Cys Cys Gly Leu Leu Ala Pro Ala Ala Arg Ala Gly Tyr Ser Glu Glu	
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Arg Cys Ser Trp Arg Gly Ser Gly Leu Thr Gln Glu Pro Gly Ser Val	
29 34 39 44	
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Gly Gln Leu Ala Leu Ala Cys Ala Glu Gly Ala Val Glu Trp Leu Tyr	
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Pro Ala Gly Ala Leu Arg Leu Thr Leu Gly Gly Pro Asp Pro Arg Ala	
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cgg ccc ggc atc gcc tgt ctg cgg ccg gtg cgg ccc ttc gcg ggc gcc	471
Arg Pro Gly Ile Ala Cys Leu Arg Pro Val Arg Pro Phe Ala Gly Ala	
77 82 87 92	
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Gln Val Phe Ala Glu Arg Ala Gly Gly Ala Leu Glu Leu Leu Leu Ala	
93 98 103 108	
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Glu Gly Pro Gly Pro Ala Gly Gly Arg Cys Val Arg Trp Gly Pro Arg	
109 114 119 124	
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Glu Arg Arg Ala Leu Phe Leu Gln Ala Thr Pro His Gln Asp Ile Ser	
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Glu Leu Pro Pro Gln Ala His Gly Leu Gly Val Asp Gly Ala Cys Arg	
157 162 167 172	

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Pro Cys Ser Asp Ala Glu Leu Leu Leu Ala Ala Cys Thr Ser Asp Phe	
173 178 183 188	
gta att cac ggg atc atc cat ggg gtc acc cat gac gtg gag ctg cag	807
Val Ile His Gly Ile Ile His Gly Val Thr His Asp Val Glu Leu Gln	
189 194 199 204	
gag tct gtc atc act gtg gtg gcc gcc cgt gtc ctc cgc cag aca ccg	855
Glu Ser Val Ile Thr Val Val Ala Ala Arg Val Leu Arg Gln Thr Pro	
205 210 215 220	
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Pro Leu Phe Gln Ala Gly Arg Ser Gly Asp Gln Gly Leu Thr Ser Ile	
221 226 231 236	
cgt acc cca ctg cgc tgt ggc gtc cac ccg ggc cca ggc acc ttc ctc	951
Arg Thr Pro Leu Arg Cys Gly Val His Pro Gly Pro Gly Thr Phe Leu	
237 242 247 252	
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Phe Met Gly Trp Ser Arg Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro	
253 258 263 268	
cga ttc cag gag ttc cgc cgt gcc tac gag gct gcc cgt gct gcc cac	1047
Arg Phe Gln Glu Phe Arg Arg Ala Tyr Glu Ala Ala Arg Ala Ala His	
269 274 279 284	
ctc cac ccc tgc gag gtg gcg ctg cac tga g gggctgggtg ctggggaggg	1098
Leu His Pro Cys Glu Val Ala Leu His *	
285 290	
gctggtagga gggaggggtg gccactgct ttggaggtga tgggactatc aataagaact	1158
ctgttcacgc aaaaaaaaaa aa	1180

<210> 67
 <211> 1540
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (210)..(1322)

<220>
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 <222> (1)...(1540)
 <223> n = a,t,c or g

<400> 67
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Asn Asp Arg Arg Leu Ala Asp His Phe Gly Gly Lys Leu His Leu Gly	
201 206 211 216	
ttc att cag atc cga gag aag ctt gat cag ttg agg aaa act gtc gct	905
Phe Ile Gln Ile Arg Glu Lys Leu Asp Gln Leu Arg Lys Thr Val Ala	
217 222 227 232	
gaa aag cag gag aag aga aat cag gat cgc ttg agg agg aga gag gag	953
Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu Arg Arg Arg Glu Glu	
233 238 243 248	
agg gaa cgg gag gag cgt ctg agc agg agg tcg gga tca aga acc aga	1001
Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser Gly Ser Arg Thr Arg	
249 254 259 264	
gat cgc agg agg tca cgc tcc cgg gat cgg cgt cgg agg cgg tca aga	1049
Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Arg Arg Ser Arg	
265 270 275 280	
tct acc tcc cga gag cga cgg aaa ttg tcc cgg tcc cgg tcc cga gat	1097
Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg Ser Arg Ser Arg Asp	
281 286 291 296	
aga cat cgg cgc cac cgc agc cgt tcc cgg agc cac agc cgg gga cat	1145
Arg His Arg Arg His Arg Ser Arg Ser Arg Ser His Ser Arg Gly His	
297 302 307 312	
cgt cgg gct tcc cgg gac cga agt gcg aaa tac aag ttc tcc aga gag	1193
Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr Lys Phe Ser Arg Glu	
313 318 323 328	
cgg gca tcc aga gag gag tcc tgg gag agc ggg cgg agc gag cga ggg	1241
Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly Arg Ser Glu Arg Gly	
329 334 339 344	
ccc ccg gac tgg agg ctt gag agc tcc aac ggg aag atg gct tca cgg	1289
Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly Lys Met Ala Ser Arg	
345 350 355 360	
agg tca gaa gag aag gag gcc ggc gag atc tga acccgtct cccgggtgct	1340
Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
361 366 371	
gtaaatagtc tgataaacgt tcacacagtc taaaattacc ctttatattt gctgaataca	1400
actcatcttt tgtagtttaa aattttctatt gttttggagc tagctgtgag tttctagaag	1460
tgtagacagagt tgctcctgtg ttccccgggtc atgttgagta ggaataaata aatctgatgc	1520
tgccctcctga aaaaaaaaaa	1540

<210> 68
 <211> 1363
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)..(1145)

<220>

<221> misc_feature

<222> (1)...(1363)

<223> n = a,t,c or g

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gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg 120

accgacacga ccattcatttg tcgacgccgc tgccaccgcc tgccctgagag aagtcgtcgc 180

ggccgacccc gtcgcctccg ccggctacc atg tcc gcc cag gcg cag atg cgg 233
Met Ser Ala Gln Ala Gln Met Arg
1 5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga 281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
9 14 19 24

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg 329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
25 30 35 40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga 377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
41 46 51 56

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att 425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
57 62 67 72

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac 473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His
73 78 83 88

ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag 521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys
89 94 99 104

aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca 569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala
105 110 115 120

aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt 617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu
121 126 131 136

gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag 665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln
137 142 147 152

aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
153 158 163 168	
gag aaa act gtc gct gaa aag cag gag aag aga aat cag gat cgc ttg	761
Glu Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu	
169 174 179 184	
agg agg aga gag gag agg gaa cgg gag gag cgt ctg agc agg agg tcg	809
Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser	
185 190 195 200	
gga tca aga acc aga gat cgc agg agg tca cgc tcc cgg gat cgg cgt	857
Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg	
201 206 211 216	
cgg agg cgg tca aga tct acc tcc cga gag cga cgg aaa ttg tcc cgg	905
Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg	
217 222 227 232	
tcc cgg tcc cga gat aga cat cgg cgc cac cgc agc cgt tcc cgg agc	953
Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser Arg Ser Arg Ser	
233 238 243 248	
cac agc cgg gga cat cgt cgg gct tcc cgg gac cga agt gcg aaa tac	1001
His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr	
249 254 259 264	
aag ttc tcc aga gag cgg gca tcc aga gag gag tcc tgg gag agc ggg	1049
Lys Phe Ser Arg Glu Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly	
265 270 275 280	
cgg agc gag cga ggg ccc ccg gac tgg agg ctt gag agc tcc aac ggg	1097
Arg Ser Glu Arg Gly Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly	
281 286 291 296	
aag atg gct tca cgg agg tca gaa gag aag gag gcc ggc gag atc tga	1145
Lys Met Ala Ser Arg Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
297 302 307 312	
acccgtctcc cgggtgctgt aaatagtctg ataaacgttc acacagtcta aaattaccct	1205
ttatatattgc tgaatacaaac tcattcttttg tagttttaaaa tttctattgt tttggagcta	1265
gctgtgagtt tctagaagtg tacagagttg ctctgtgtt cccgggtcat gttgagtagg	1325
aataaataaa tctgatgctg cctctgaaa aaaaaaaaa	1363

<210> 69
 <211> 3552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30)..(3218)

<400> 69

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	Met Arg Leu Leu Ser Met Pro Gly	
	1 5	
gcc cag gga gct gca gca gca ggg tct gaa ccc cct cca gcc acc acg	101	
Ala Gln Gly Ala Ala Ala Ala Gly Ser Glu Pro Pro Pro Ala Thr Thr		
9 14 19 24		
agc cca gag gga cag ccc aag gtc cac cga gcc cgc aaa acc atg tcc	149	
Ser Pro Glu Gly Gln Pro Lys Val His Arg Ala Arg Lys Thr Met Ser		
25 30 35 40		
aaa cca gga aat gga cag ccc ccg gtc cct gag aag cgg ccc cct gaa	197	
Lys Pro Gly Asn Gly Gln Pro Pro Val Pro Glu Lys Arg Pro Pro Glu		
41 46 51 56		
ata cag cat ttc cgc atg agt gat gat gtc cac tca ctg gga aag gtg	245	
Ile Gln His Phe Arg Met Ser Asp Asp Val His Ser Leu Gly Lys Val		
57 62 67 72		
acc tca gat ctg gcc aaa agg agg aag ctg aac tca gga ggt ggc ctg	293	
Thr Ser Asp Leu Ala Lys Arg Arg Lys Leu Asn Ser Gly Gly Gly Leu		
73 78 83 88		
tcg gag gag tta ggt tct gcc cgg cgt tca gga gaa gtg acc ctg acg	341	
Ser Glu Glu Leu Gly Ser Ala Arg Arg Ser Gly Glu Val Thr Leu Thr		
89 94 99 104		
aaa ggg gac ccc ggg tcc ctg gag gag tgg gag acg gtg gtg ggt gat	389	
Lys Gly Asp Pro Gly Ser Leu Glu Glu Trp Glu Thr Val Val Gly Asp		
105 110 115 120		
gac ttc agt ctc tac tat gat tcc tac tct gtg gat gag cgc gtg gac	437	
Asp Phe Ser Leu Tyr Tyr Asp Ser Tyr Ser Val Asp Glu Arg Val Asp		
121 126 131 136		
tcc gac agc aag tct gaa gtt gaa gct cta act gaa caa cta agt gaa	485	
Ser Asp Ser Lys Ser Glu Val Glu Ala Leu Thr Glu Gln Leu Ser Glu		
137 142 147 152		
gag gag gag gag gaa gag gag gaa gaa gaa gaa gag gaa gag gag gag	533	
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu		
153 158 163 168		
gaa gag gaa gaa gaa gag gaa gat gag gag tca ggg aat cag tca gat	581	
Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Ser Gly Asn Gln Ser Asp		
169 174 179 184		
agg agt ggt tcc agt ggc cgg cgc aag gcc aag aag aaa tgg cga aaa	629	
Arg Ser Gly Ser Ser Glu Arg Arg Lys Ala Lys Lys Lys Trp Arg Lys		
185 190 195 200		

gac agc cca tgg gtg aag ccg tct cgg aaa cgg cgc aag cgg gag cct	677
Asp Ser Pro Trp Val Lys Pro Ser Arg Lys Arg Arg Lys Arg Glu Pro	
201 206 211 216	
ccg cgg gcc aag gag cca cga gga gtg aat ggt gtg ggc tcc tca ggc	725
Pro Arg Ala Lys Glu Pro Arg Gly Val Asn Gly Val Gly Ser Ser Gly	
217 222 227 232	
ccc agt gag tac atg gag gtc cct ctg ggg tcc ctg gag ctg ccc agc	773
Pro Ser Glu Tyr Met Glu Val Pro Leu Gly Ser Leu Glu Leu Pro Ser	
233 238 243 248	
gag ggg acc ctc tcc ccc aac cac gct ggg gtg tcc aat gac aca tct	821
Glu Gly Thr Leu Ser Pro Asn His Ala Gly Val Ser Asn Asp Thr Ser	
249 254 259 264	
tcg ctg gag aca gag cga ggg ttt gag gag ttg ccc ctg tgc agc tgc	869
Ser Leu Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser Cys	
265 270 275 280	
cgc atg gag gca ccc aag att gac cgc atc agc gag agg gcg ggg cac	917
Arg Met Glu Ala Pro Lys Ile Asp Arg Ile Ser Glu Arg Ala Gly His	
281 286 291 296	
aag tgc atg gcc act gag agt gtg gac gga gag ctg tca ggc tgc aat	965
Lys Cys Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser Gly Cys Asn	
297 302 307 312	
gcc gcc atc ctc aag cgg gag acc atg agg cca tcc agc cgt gtg gcc	1013
Ala Ala Ile Leu Lys Arg Glu Thr Met Arg Pro Ser Ser Arg Val Ala	
313 318 323 328	
ctg atg gtg ctc tgt gag acc cac cgc gcc cgc atg gtc aaa cac cac	1061
Leu Met Val Leu Cys Glu Thr His Arg Ala Arg Met Val Lys His His	
329 334 339 344	
tgc tgc ccg ggc tgc ggc tac ttc tgc acg gcg ggc acc ttc ctg gag	1109
Cys Cys Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu	
345 350 355 360	
tgc cac cct gac ttc cgt gtg gcc cac cgc ttc cac aag gcc tgt gtg	1157
Cys His Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val	
361 366 371 376	
tct cag ctg aat ggg atg gtc ttc tgt ccc cac tgt ggg gag gat gct	1205
Ser Gln Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Ala	
377 382 387 392	
tct gaa gct caa gag gtg acc atc ccc cgg ggt gac ggg gtg acc cca	1253
Ser Glu Ala Gln Glu Val Thr Ile Pro Arg Gly Asp Gly Val Thr Pro	
393 398 403 408	
ccg gcc ggc act gca gct cct gca ccc cca ccc ctg tcc cag gat gtc	1301
Pro Ala Gly Thr Ala Pro Ala Pro Pro Pro Leu Ser Gln Asp Val	
409 414 419 424	
ccc ggg aga gca gac act tct cag ccc agt gcc cgg atg cga ggg cat	1349

Pro Gly Arg Ala Asp Thr Ser Gln Pro Ser Ala Arg Met Arg Gly His	
425 430 435 440	
ggg gaa ccc cgg cgc ccg ccc tgc gat ccc ctg gct gac acc att gac	1397
Gly Glu Pro Arg Arg Pro Pro Cys Asp Pro Leu Ala Asp Thr Ile Asp	
441 446 451 456	
agc tca ggg ccc tcc ctg acc ctg ccc aat ggg ggc tgc ctt tca gcc	1445
Ser Ser Gly Pro Ser Leu Thr Leu Pro Asn Gly Gly Cys Leu Ser Ala	
457 462 467 472	
gtg ggg ctg cca ctg ggg cca ggc cgg gag gcc ctg gaa aag gcc ctg	1493
Val Gly Leu Pro Leu Gly Pro Gly Arg Glu Ala Leu Glu Lys Ala Leu	
473 478 483 488	
gtc atc cag gag tca gag agg cgg aag aag ctc cgt ttc cac cct cgg	1541
Val Ile Gln Glu Ser Glu Arg Arg Lys Lys Leu Arg Phe His Pro Arg	
489 494 499 504	
cag ttg tac ctg tcc gtg aag cag ggc gag ctg cag aag gtg atc ctg	1589
Gln Leu Tyr Leu Ser Val Lys Gln Gly Glu Leu Gln Lys Val Ile Leu	
505 510 515 520	
atg ctg ttg gac aac ctg gac ccc aac ttc cag agc gac cag cag agc	1637
Met Leu Leu Asp Asn Leu Asp Pro Asn Phe Gln Ser Asp Gln Gln Ser	
521 526 531 536	
aag cgc acg ccc ctg cat gca gcc gcc cag aag ggc tcc gtg gag atc	1685
Lys Arg Thr Pro Leu His Ala Ala Ala Gln Lys Gly Ser Val Glu Ile	
537 542 547 552	
tgc cat gtg ctg ctg cag gct gga gcc aac ata aat gca gtg gac aaa	1733
Cys His Val Leu Leu Gln Ala Gly Ala Asn Ile Asn Ala Val Asp Lys	
553 558 563 568	
cag cag cgg acg cca ctg atg gag gcc gtg gtg aac aac cac ctg gag	1781
Gln Gln Arg Thr Pro Leu Met Glu Ala Val Val Asn Asn His Leu Glu	
569 574 579 584	
gta gcc cgt tac atg gtg cag cgt ggt ggc tgt gtc tat agc aag gag	1829
Val Ala Arg Tyr Met Val Gln Arg Gly Gly Cys Val Tyr Ser Lys Glu	
585 590 595 600	
gag gac ggt tcc acc tgc ctc cac cac gca gcc aaa atc ggg aac ttg	1877
Glu Asp Gly Ser Thr Cys Leu His His Ala Ala Lys Ile Gly Asn Leu	
601 606 611 616	
gag atg gtc agc ctg ctg ctg agc aca gga cag gtg gac gtc aac gcc	1925
Glu Met Val Ser Leu Leu Leu Ser Thr Gly Gln Val Asp Val Asn Ala	
617 622 627 632	
cag gac agt ggg ggg tgg acg ccc atc atc tgg gct gca gag cac aag	1973
Gln Asp Ser Gly Gly Trp Thr Pro Ile Ile Trp Ala Ala Glu His Lys	
633 638 643 648	
cac atc gag gtg atc cgc atg cta ctg acg cgg ggc gcc gac gtc acc	2021
His Ile Glu Val Ile Arg Met Leu Leu Thr Arg Gly Ala Asp Val Thr	

649	654	659	664	
ctc act gac aac gag	gag aac atc tgc ctg	cac tgg gcc tcc ttc acg		2069
Leu Thr Asp Asn Glu	Glu Asn Ile Cys Leu	His Trp Ala Ser Phe Thr		
665	670	675	680	
ggc agc gcc gcc atc	gcc gaa gtc ctt ctg	aat gcg cgc tgt gac ctc		2117
Gly Ser Ala Ala Ile	Ala Glu Val Leu Leu	Asn Ala Arg Cys Asp Leu		
681	686	691	696	
cat gct gtc aac tac	cat ggg gac acc ccc	ctg cac atc gca gct cgg		2165
His Ala Val Asn Tyr	His Gly Asp Thr Pro	Leu His Ile Ala Ala Arg		
697	702	707	712	
gag agc tac cat gac	tgc gtg ctg tta ttc	ctg tca cgt ggg gcc aac		2213
Glu Ser Tyr His Asp	Cys Val Leu Leu Phe	Leu Ser Arg Gly Ala Asn		
713	718	723	728	
cct gag ctg cgg aac	aaa gag ggg gac aca	gca tgg gac ctg act ccc		2261
Pro Glu Leu Arg Asn	Lys Glu Gly Asp Thr	Ala Trp Asp Leu Thr Pro		
729	734	739	744	
gag cgc tcc gac gtg	tgg ttt gcg ctt caa	ctc aac cgc aag ctc cga		2309
Glu Arg Ser Asp Val	Trp Phe Ala Leu Gln	Leu Asn Arg Lys Leu Arg		
745	750	755	760	
ctt ggg gtg gga aat	cgg gcc atc cgc aca	gag aag atc atc tgc cgg		2357
Leu Gly Val Gly Asn	Arg Ala Ile Arg Thr	Glu Lys Ile Ile Cys Arg		
761	766	771	776	
gac gtg gct cgg ggc	tat gag aac gtg ccc	att ccc tgt gtc aac ggt		2405
Asp Val Ala Arg Gly	Tyr Glu Asn Val Pro	Ile Pro Cys Val Asn Gly		
777	782	787	792	
gtg gat ggg gag ccc	tgc cct gag gat tac	aag tac atc tca gag aac		2453
Val Asp Gly Glu Pro	Cys Pro Glu Asp Tyr	Lys Tyr Ile Ser Glu Asn		
793	798	803	808	
tgc gag acg tcc acc	atg aac atc gat cgc	aac atc acc cac ctg cag		2501
Cys Glu Thr Ser Thr	Met Asn Ile Asp Arg	Asn Ile Thr His Leu Gln		
809	814	819	824	
cac tgc acg tgt gtg	gac gac tgc tct agc	tcc aac tgc ctg tgc ggc		2549
His Cys Thr Cys Val	Asp Asp Cys Ser Ser	Ser Asn Cys Leu Cys Gly		
825	830	835	840	
cag ctc agc atc cgg	tgc tgg tat gac aag	gat ggg cga ttg ctc cag		2597
Gln Leu Ser Ile Arg	Cys Trp Tyr Asp Lys	Asp Gly Arg Leu Leu Gln		
841	846	851	856	
gaa ttt aac aag att	gag cct ccg ctg att	ttc gag tgt aac cag gcg		2645
Glu Phe Asn Lys Ile	Glu Pro Pro Leu Ile	Phe Glu Cys Asn Gln Ala		
857	862	867	872	
tgc tca tgc tgg aga	aac tgc aag aac cgg	gtc gta cag agt ggc atc		2693
Cys Ser Cys Trp Arg	Asn Cys Lys Asn Arg	Val Val Gln Ser Gly Ile		
873	878	883	888	

aag gtg cgg cta cag ctc tac cga aca gcc aag atg ggc tgg ggg gtc	2741
Lys Val Arg Leu Gln Leu Tyr Arg Thr Ala Lys Met Gly Trp Gly Val	
889 894 899 904	
cgc gcc ctg cag acc atc cca cag ggg acc ttc atc tgc gag tat gtc	2789
Arg Ala Leu Gln Thr Ile Pro Gln Gly Thr Phe Ile Cys Glu Tyr Val	
905 910 915 920	
ggg gag ctg atc tct gat gct gag gct gat gtg aga gag gat gat tct	2837
Gly Glu Leu Ile Ser Asp Ala Glu Ala Asp Val Arg Glu Asp Asp Ser	
921 926 931 936	
tac ctc ttc gac tta gac aac aag gat gga gag gtg tac tgc ata gat	2885
Tyr Leu Phe Asp Leu Asp Asn Lys Asp Gly Glu Val Tyr Cys Ile Asp	
937 942 947 952	
gcc cgt tac tat ggc aac atc agc cgc ctc ctc tgc cac ctg tgt gac	2933
Ala Arg Tyr Tyr Gly Asn Ile Ser Arg Leu Leu Cys His Leu Cys Asp	
953 958 963 968	
ccc aac atc att ccc gtc cgg gtc ttc atg ctg cac caa gac ctg cga	2981
Pro Asn Ile Ile Pro Val Arg Val Phe Met Leu His Gln Asp Leu Arg	
969 974 979 984	
ttt cca cgc atc gcc ttc ttc agt tcc cga gac atc cgg act ggg gag	3029
Phe Pro Arg Ile Ala Phe Phe Ser Ser Arg Asp Ile Arg Thr Gly Glu	
985 990 995 1000	
gag cta ggg ttt gac tat ggc gac cgc ttc tgg gac atc aaa agc aaa	3077
Glu Leu Gly Phe Asp Tyr Gly Asp Arg Phe Trp Asp Ile Lys Ser Lys	
1001 1006 1011 1016	
tat ttc acc tgc caa tgt ggc tct gag aag tgc aag cac tca gcc gaa	3125
Tyr Phe Thr Cys Gln Cys Gly Ser Glu Lys Cys Lys His Ser Ala Glu	
1017 1022 1027 1032	
gcc att gcc ctg gag cag agc cgt ctg gcc cgc ctg gac cca cac cct	3173
Ala Ile Ala Leu Glu Gln Ser Arg Leu Ala Arg Leu Asp Pro His Pro	
1033 1038 1043 1048	
gag ctg ctg ccc gag ctc ggc tcc ctg ccc cct gtc aac aca tga gaa	3221
Glu Leu Leu Pro Glu Leu Gly Ser Leu Pro Pro Val Asn Thr *	
1049 1054 1059	
cgaccacac cctctctccc cagcatggat ggccacagct cagccgcctc ctctgccacc	3281
agctgctcgc agcccatgcc tgggggtgct gccatcttct ctccccacca ccctttcaca	3341
cattcctgac cagagatccc agccaggccc tggaggtctg acagcccctc cctcccagag	3401
ctggttcctc cctgggaggg caacttcagg gctggccacc ccccggtgtc cccatcctca	3461
gttgaagttt gatgaattga agtcgggcct ctatgccaac tggttccttt tggttctcaat	3521
aaatgttggg tttggtaata aaaaaaaaaa a	3552

<210> 70
 <211> 1925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (510)..(1562)

<220>
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 <222> (1)...(1925)
 <223> n = a,t,c or g

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 ccccgatgg cctcagccac ggaggacccc gttctggagc gttatttcaa aggccacaaa 180
 gctgcgatca cctccttgga cctcagcccc aacggcaagc aacttgctac tgcttcttgg 240
 gatacctttc tcatgctatg gaatttcaag ccacatgcta gagcttacag atatgtgggt 300
 cacaaggatg ttgtaaccag cgtgcagttt tctccacatg gaaacttatt ggcgtctgcc 360
 tcacgagaca gaaccgtgag actctggatt cctgataaga gaggaaaatt ctcagaattt 420
 aaagctcata cagctccagt tcgaagtgta gacttttcag ctgatggcca gtttctagct 480
 acagcttctg aagacaaatc cataaaagt atg gag cat gta tcg cca gcg ctt 533
 Met Glu His Val Ser Pro Ala Leu
 1 5
 cct gta ttc ctt gta tcg aca tac aca ctg ggt acg ctg tgc cca att 581
 Pro Val Phe Leu Val Ser Thr Tyr Thr Leu Gly Thr Leu Cys Pro Ile
 9 14 19 24
 tca ccc gat gga aga cta att gtg tca tgt agt gag gat aaa act att 629
 Ser Pro Asp Gly Arg Leu Ile Val Ser Cys Ser Glu Asp Lys Thr Ile
 25 30 35 40
 aaa att tgg gat acc aca aat aag caa tgt gtt aat aac ttc tca gat 677
 Lys Ile Trp Asp Thr Thr Asn Lys Gln Cys Val Asn Asn Phe Ser Asp
 41 46 51 56
 tcc gtt gga ttt gca aat ttt gtg gac ttt aac cct agt ggt aca tgc 725
 Ser Val Gly Phe Ala Asn Phe Val Asp Phe Asn Pro Ser Gly Thr Cys
 57 62 67 72
 ata gct tca gca ggt tct gat caa act gtg aaa gtc tgg gat gta aga 773
 Ile Ala Ser Ala Gly Ser Asp Gln Thr Val Lys Val Trp Asp Val Arg
 73 78 83 88

gtg aac aaa tta cta cag cat tac caa gtt cac agc ggt gga gtt aat	821
Val Asn Lys Leu Leu Gln His Tyr Gln Val His Ser Gly Gly Val Asn	
89 94 99 104	
tgc ata tca ttc cat cct tgc ggt aac tat ctc atc aca gct tct tca	869
Cys Ile Ser Phe His Pro Ser Gly Asn Tyr Leu Ile Thr Ala Ser Ser	
105 110 115 120	
gat ggt acc ctt aag att ctg gac ctc tta gaa gga agg ctc atc tat	917
Asp Gly Thr Leu Lys Ile Leu Asp Leu Leu Glu Gly Arg Leu Ile Tyr	
121 126 131 136	
aca ctt caa gga cat acg gga cct gtc ttt act gtt tca ttt tca aaa	965
Thr Leu Gln Gly His Thr Gly Pro Val Phe Thr Val Ser Phe Ser Lys	
137 142 147 152	
ggg gga gag cta ttt gca tca gga ggt gca gac aca cag gtc tta tta	1013
Gly Gly Glu Leu Phe Ala Ser Gly Gly Ala Asp Thr Gln Val Leu Leu	
153 158 163 168	
tgg agg act aac ttt gat gaa ttg cat tgt aaa ggt ctt acc aaa aga	1061
Trp Arg Thr Asn Phe Asp Glu Leu His Cys Lys Gly Leu Thr Lys Arg	
169 174 179 184	
aat ctc aaa aga tta cat ttt gat tca cca cca cat ctt ctt gat atc	1109
Asn Leu Lys Arg Leu His Phe Asp Ser Pro Pro His Leu Leu Asp Ile	
185 190 195 200	
tac cca aga aca cca cat ccc cat gag gaa aaa gtt gag act gta gaa	1157
Tyr Pro Arg Thr Pro His Pro His Glu Glu Lys Val Glu Thr Val Glu	
201 206 211 216	
att aat cca aag ctt gag gta atc gat ttg cag atc tct act ccc cct	1205
Ile Asn Pro Lys Leu Glu Val Ile Asp Leu Gln Ile Ser Thr Pro Pro	
217 222 227 232	
gtt atg gat atc ctt tct ttt gat tct acc aca aca aca gaa acc agt	1253
Val Met Asp Ile Leu Ser Phe Asp Ser Thr Thr Thr Glu Thr Ser	
233 238 243 248	
ggg agg act ctg cca gac aag ggt gaa gag gcc tgt gga tat ttc ttg	1301
Gly Arg Thr Leu Pro Asp Lys Gly Glu Glu Ala Cys Gly Tyr Phe Leu	
249 254 259 264	
aac cct tcc tta atg tca cca gaa tgt ttg cca aca acc acg aaa aag	1349
Asn Pro Ser Leu Met Ser Pro Glu Cys Leu Pro Thr Thr Thr Lys Lys	
265 270 275 280	
aaa aca gaa gac atg agt gac ctc ccc tgt gaa agt caa agg agc ata	1397
Lys Thr Glu Asp Met Ser Asp Leu Pro Cys Glu Ser Gln Arg Ser Ile	
281 286 291 296	
cct ctc gct gtg act gat gct tta gag cat att atg gaa caa ctc aat	1445
Pro Leu Ala Val Thr Asp Ala Leu Glu His Ile Met Glu Gln Leu Asn	
297 302 307 312	

ggt ttg aca cag act gtt tca atc ttg gag cag cga ctg act ttg aca	1493
Val Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr	
313 318 323 328	
gag gat aag ctg aaa gac tgc ctt gaa aat cag caa aag ctt ttc agt	1541
Glu Asp Lys Leu Lys Asp Cys Leu Glu Asn Gln Gln Lys Leu Phe Ser	
329 334 339 344	
gct gtc caa cag aaa agc tga at aaaaaattca ttttcatttg ttgggcagag	1594
Ala Val Gln Gln Lys Ser *	
345 350	
gccaataaaa tgaacaaatg tacatacact caggaaggta gtacaagata ctccatacaa	1654
cacaaccatg tgctatztat catggcattt cttaaaaggg tgagcaacag aacaaaaggc	1714
agaaaaggca tacctaagga ctaatttaaa cacatatcaa tgtgaaggac taatttaaat	1774
tactatcatt tatgattgca gtaataaagt gataagcatt caagcaactc tgtatatttcc	1834
ccatattaat ttaaatgtcc attntcattt ataggccana tcctgccaag aaaagaaccc	1894
agatctctgg atttcactgt taagtcattt a	1925

<210> 71
 <211> 956
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (484) .. (837)

<400> 71

agaggggggc cccttcccgg cggggtttta ggccttggga aaggatttcg gggccccctc	60
gctccccggg aagcgttttg gccccaccg gaatggtgtc atctggttaa gaagcgcaag	120
tggcgctttg gagaaaccaa ccaagacccc ggggggggggt tgggccccaa tcctaattac	180
ccttctgtcc ccaacttcca gttagccaaa atataaagaa ggcaaatacct gtactgttgg	240
caaaaacagc caccacaaaag ttgttaaaaa gcaaaacaaa acacctcaag cttaaatttt	300
tgaaaaacaa tcctcacaca aagatactat caacaaatca cacaccaatt tatcttagaa	360
ggatcaagag atgaaaaaca gcaaaggata ttttcgtaat atgctagaat ctttgaatat	420
aatactgaag ttggcaacca aaagcaattc agaagttcaa cttagaacta atggctgtat	480
ccg atg gca ctg tct att tta gat att aaa atg tca cca tct tgg tat	528
Met Ala Leu Ser Ile Leu Asp Ile Lys Met Ser Pro Ser Trp Tyr	
1 5 10	

ttt cac atg gct ata ggc att ata aac tgg aac act act gcg ggt tta	576
Phe His Met Ala Ile Gly Ile Ile Asn Trp Asn Thr Thr Ala Gly Leu	
16 21 26 31	
tct ggc act ctg tat cca aaa gtc ccc caa aag tac ata ctc ttt gac	624
Ser Gly Thr Leu Tyr Pro Lys Val Pro Gln Lys Tyr Ile Leu Phe Asp	
32 37 42 47	
tct gta att ctg ctt cta ggc atg tta aga aaa ata cgt cag gta tgc	672
Ser Val Ile Leu Leu Leu Gly Met Leu Arg Lys Ile Arg Gln Val Cys	
48 53 58 63	
caa aat gta tac atg aaa ggg tgt tca cca ata aca tta ttt aaa ata	720
Gln Asn Val Tyr Met Lys Gly Cys Ser Pro Ile Thr Leu Phe Lys Ile	
64 69 74 79	
gtt cac tac tgg cca ggc gca gta gct cat gcc tat aat cct agc act	768
Val His Tyr Trp Pro Gly Ala Val Ala His Ala Tyr Asn Pro Ser Thr	
80 85 90 95	
ttg gga ggc caa gtt ggg ggc aaa tca cct gag gtc agg agt tcg aga	816
Leu Gly Gly Gln Val Gly Gly Lys Ser Pro Glu Val Arg Ser Ser Arg	
96 101 106 111	
cca gcc tgg act aca tgg tga aa ccccatctct actaaaagaa caaaaattag	869
Pro Ala Trp Thr Thr Trp *	
112 117	
gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttggggtt tgggtggggta	929
tcttcatcgt cgaatcgta gttatat	956

<210> 72
 <211> 1615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (215)..(1507)

agttcggaat tcccggcacg acccacgcga tcgcggacgc gtgggccgga atgttaccta	60
tgatgaagca ggtggacccc gtgaggctgt cagcaaactt caagaattat gtcattctatg	120
gctgaagcca gagatccact caaaagagca gatactggaa ctgctgggtgc tggagcagtt	180
cctgactatt ctgccaggg agacacagac ccag atg cag aag cac cat cca	232
Met Gln Lys His His Pro	
1	
cag agc att gag gag gct gtg gct ctg gta gaa cac ttg cag agg gaa	280
Gln Ser Ile Glu Glu Ala Val Ala Leu Val Glu His Leu Gln Arg Glu	

7	12	17	22	
tct ggt caa aca tgg aat ggg gtt gca gtc cat gag ctg gga aag gag				328
Ser Gly Gln Thr Trp Asn Gly Val Ala Val His Glu Leu Gly Lys Glu				
23	28	33	38	
gca gtg ctc ttg gga gaa aca gca gag gcc tca agt ttc ggg ctg aag				376
Ala Val Leu Leu Gly Glu Thr Ala Glu Ala Ser Ser Phe Gly Leu Lys				
39	44	49	54	
cca aca gag tcc caa cca gtg ggc gta tcc caa gat gaa gaa ttt tgg				424
Pro Thr Glu Ser Gln Pro Val Gly Val Ser Gln Asp Glu Glu Phe Trp				
55	60	65	70	
aat aca tac gag ggt ctg caa gaa cag ctc agc agg aat act cat aaa				472
Asn Thr Tyr Glu Gly Leu Gln Glu Gln Leu Ser Arg Asn Thr His Lys				
71	76	81	86	
gag act gag cct gtg tat gag agg gct gtg cct act caa cag att cta				520
Glu Thr Glu Pro Val Tyr Glu Arg Ala Val Pro Thr Gln Gln Ile Leu				
87	92	97	102	
gct ttt cct gag caa aca aac acc aaa gac tgg aca gtg aca cct gag				568
Ala Phe Pro Glu Gln Thr Asn Thr Lys Asp Trp Thr Val Thr Pro Glu				
103	108	113	118	
cac gtc ttg cct gag tcc cag agc ttg ttg aca ttt gaa gaa gtg gcc				616
His Val Leu Pro Glu Ser Gln Ser Leu Leu Thr Phe Glu Glu Val Ala				
119	124	129	134	
atg tat ttt tcc cag gaa gaa tgg gag tta ttg gat ccc act cag aag				664
Met Tyr Phe Ser Gln Glu Glu Trp Glu Leu Leu Asp Pro Thr Gln Lys				
135	140	145	150	
gcc ctc tac aat gat gta atg cag gaa aac tat gag act gtc atc tct				712
Ala Leu Tyr Asn Asp Val Met Gln Glu Asn Tyr Glu Thr Val Ile Ser				
151	156	161	166	
cta gca ttg ttt gtg ctc ccc aaa cct aaa gtg atc tcc tgt cta gag				760
Leu Ala Leu Phe Val Leu Pro Lys Pro Lys Val Ile Ser Cys Leu Glu				
167	172	177	182	
caa ggg gaa gag cca tgg gtt caa gta tcc ccg gag ttt aag gat agt				808
Gln Gly Glu Glu Pro Trp Val Gln Val Ser Pro Glu Phe Lys Asp Ser				
183	188	193	198	
gcc gga aaa tct cct aca ggg tta aag ctc aaa aac gac act gaa aat				856
Ala Gly Lys Ser Pro Thr Gly Leu Lys Leu Lys Asn Asp Thr Glu Asn				
199	204	209	214	
cat cag cct gcg tct ctt tct gac tta gaa ata caa gca tca gca ggc				904
His Gln Pro Ala Ser Leu Ser Asp Leu Glu Ile Gln Ala Ser Ala Gly				
215	220	225	230	
gtc ata tca aaa aag gcc aaa gta aaa gtt ccc cag aaa aca gca ggc				952
Val Ile Ser Lys Lys Ala Lys Val Lys Val Pro Gln Lys Thr Ala Gly				
231	236	241	246	

aaa gaa aat cat ttt gat atg cac aga gtg gga aaa tgg cac caa gat	1000
Lys Glu Asn His Phe Asp Met His Arg Val Gly Lys Trp His Gln Asp	
247 252 257 262	
ttt cca gtg aag aaa aga aag aaa ctt tca acc tgg aaa caa gag ctg	1048
Phe Pro Val Lys Lys Arg Lys Lys Leu Ser Thr Trp Lys Gln Glu Leu	
263 268 273 278	
ctc aaa ctt atg gat cgt cac aag aaa gat tgt gca aga gag aag cct	1096
Leu Lys Leu Met Asp Arg His Lys Lys Asp Cys Ala Arg Glu Lys Pro	
279 284 289 294	
ttt aaa tgt cag gaa tgt ggg aaa acc ttc aga gtt agc tct gac ctt	1144
Phe Lys Cys Gln Glu Cys Gly Lys Thr Phe Arg Val Ser Ser Asp Leu	
295 300 305 310	
att aag cac caa aga att cac act gaa gag aaa ccc tat aaa tgt caa	1192
Ile Lys His Gln Arg Ile His Thr Glu Glu Lys Pro Tyr Lys Cys Gln	
311 316 321 326	
cag tgt gat aag agg ttt aga tgg agt tca gat ctt aat aag cac tta	1240
Gln Cys Asp Lys Arg Phe Arg Trp Ser Ser Asp Leu Asn Lys His Leu	
327 332 337 342	
aca aca cac caa gga ata aaa cca tat aaa tgt tca tgg tgt ggg aaa	1288
Thr Thr His Gln Gly Ile Lys Pro Tyr Lys Cys Ser Trp Cys Gly Lys	
343 348 353 358	
agc ttc agt caa aat aca aat tta cat aca cac caa aga act cat aca	1336
Ser Phe Ser Gln Asn Thr Asn Leu His Thr His Gln Arg Thr His Thr	
359 364 369 374	
gga gaa aag ccc ttc aca tgt cat gaa tgt gga aaa aaa ttc agt cag	1384
Gly Glu Lys Pro Phe Thr Cys His Glu Cys Gly Lys Lys Phe Ser Gln	
375 380 385 390	
aac tcc cac ctt att aaa cac cgg aga acc cac aca ggt gag cag cca	1432
Asn Ser His Leu Ile Lys His Arg Arg Thr His Thr Gly Glu Gln Pro	
391 396 401 406	
tat act tgt agc ata tgc agg aga aac ttc agc agg cgg tca agc ctt	1480
Tyr Thr Cys Ser Ile Cys Arg Arg Asn Phe Ser Arg Arg Ser Ser Leu	
407 412 417 422	
ctt aga cac cag aaa ctc cac ctg tga agaga agcttgtcca gtgtcctcat	1532
Leu Arg His Gln Lys Leu His Leu *	
423 428	
tctgaagaca ttcaccaaatt ggagcttggc actaaaattt atgtaaagaa aaatcacaaa	1592
cctttgaaaa ttttacatca gaa	1615

<210> 73

<211> 2531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (221)..(2314)

<400> 73

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tgccctggcgc gctccgcacc tggaggtgcc ttgcccctct cctgcccacc tcggaatttc	120
cctgtggctc ctttgatcct tcgagtctcc agctcctctc ccttccacct gtttccccca	180
agaaaggcag gatcctgggc cctgctacgt ttctggggcc atg gct ggt ctg ggc	235
Met Ala Gly Leu Gly	
1	
ccc ggc gta ggc gat tca gag ggg gga ccc cgg ccc ctg ttt tgc aga	283
Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe Cys Arg	
6 11 16 21	
aag ggg gct ctg agg cag aag gtg gtc cac gaa gtc aag agc cac aag	331
Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser His Lys	
22 27 32 37	
ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac tgc acc	379
Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr	
38 43 48 53	
gac ttc atc tgg ggt atc gga aag cag ggc ctg caa tgt caa gtc tgc	427
Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val Cys	
54 59 64 69	
agc ttt gtg gtt cat cga cga tgc cac gaa ttt gtg acc ttc gag tgt	475
Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys	
70 75 80 85	
cca ggc gct ggg aag ggc ccc cag acg gac gac ccc cgg aac aaa cac	523
Pro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His	
86 91 96 101	
aag ttc cgc ctg cat agc tac agc agc ccc acc ttc tgc gac cac tgt	571
Lys Phe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys	
102 107 112 117	
ggc tcc ctc ctc tac ggg ctt gtg cac cag ggc atg aaa tgc tcc tgc	619
Gly Ser Leu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys	
118 123 128 133	
tgc gag atg aac gtg cac cgg cgc tgt gtg cgt agc gtg ccc tcc ctg	667
Cys Glu Met Asn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu	
134 139 144 149	
tgc ggt gtg gac cac acc gag cgc cgc ggg cgc ctg cag ctg gag atc	715
Cys Gly Val Asp His Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile	

150	155	160	165	
cgg gct ccc aca gca gat gag atc cac gta act gtt ggc gag gcc cgt				763
Arg Ala Pro Thr Ala Asp Glu Ile His Val Thr Val Gly Glu Ala Arg				
166	171	176	181	
aac cta att cct atg gac ccc aat ggt ctc tct gat ccc tat gtg aaa				811
Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys				
182	187	192	197	
ctg aag ctc atc cca gac cct cgg aac ctg acg aaa cag aag acc cga				859
Leu Lys Leu Ile Pro Asp Pro Arg Asn Leu Thr Lys Gln Lys Thr Arg				
198	203	208	213	
acg gtg aaa gcc acg cta aac cct gtg tgg aat gag acc ttt gtg ttc				907
Thr Val Lys Ala Thr Leu Asn Pro Val Trp Asn Glu Thr Phe Val Phe				
214	219	224	229	
aac ctg aag cca ggg gat gtg gag cgc cgg ctc agc gtg gag gtg tgg				955
Asn Leu Lys Pro Gly Asp Val Glu Arg Arg Leu Ser Val Glu Val Trp				
230	235	240	245	
gac tgg gac cgg acc tcc cgc aac gac ttc atg ggg gcc atg tcc ttt				1003
Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met Gly Ala Met Ser Phe				
246	251	256	261	
ggc gtc tcg gag ctg ctc aag gcg ccc gtg gat ggc tgg tac aag tta				1051
Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp Gly Trp Tyr Lys Leu				
262	267	272	277	
ctg aac cag gag gag ggc gag tat tac aat gtg ccg gtg gcc gat gct				1099
Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro Val Ala Asp Ala				
278	283	288	293	
gac aac tgc agc ctc ctc cag aag ttt gag gct tgt aac tac ccc ctg				1147
Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn Tyr Pro Leu				
294	299	304	309	
gaa ttg tat gag cgg gtg cgg atg ggc ccc tct tcc tct ccc atc ccc				1195
Glu Leu Tyr Glu Arg Val Arg Met Gly Pro Ser Ser Ser Pro Ile Pro				
310	315	320	325	
tcc cct tcc cct agt ccc acc gac ccc aag cgc tgc ttc ttc ggg gcg				1243
Ser Pro Ser Pro Ser Pro Thr Asp Pro Lys Arg Cys Phe Phe Gly Ala				
326	331	336	341	
agt cca gga cgc ctg cac atc tcc gac ttc agc ttc ctc atg gtt cta				1291
Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu				
342	347	352	357	
gga aaa ggc agt ttt ggg aag gtg atg ctg gcc gag cgc agg ggc tct				1339
Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser				
358	363	368	373	
gat gag ctc tac gcc atc aag atc ttg aaa aag gac gtg atc gtc cag				1387
Asp Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln				
374	379	384	389	

gac gac gat gtg gac tgc acg ctg gtg gag aaa cgt gtg ctg gcg ctg	1435
Asp Asp Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu	
390 395 400 405	
ggg ggc cgg ggt cct ggc ggc cgg ccc cac ttc ctc acc cag ctc cac	1483
Gly Gly Arg Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His	
406 411 416 421	
tcc acc ttc cag acc ccg gac cgc ctg tat ttc gtg atg gag tac gtc	1531
Ser Thr Phe Gln Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val	
422 427 432 437	
acc ggg gga gac ttg atg tac cac att caa cag ctg ggc aag ttt aag	1579
Thr Gly Gly Asp Leu Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys	
438 443 448 453	
gag ccc cat gca gcg ttc tac gcg gca gaa atc gct atc ggc ctc ttc	1627
Glu Pro His Ala Ala Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe	
454 459 464 469	
ttc ctt cac aat cag ggc atc atc tac agg gac ctg aag ctg gac aat	1675
Phe Leu His Asn Gln Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn	
470 475 480 485	
gtg atg ctg gat gct gag gga cac atc aag atc act gac ttt ggc atg	1723
Val Met Leu Asp Ala Glu Gly His Ile Lys Ile Thr Asp Phe Gly Met	
486 491 496 501	
tgt aag gag aac gtc ttc ccc ggg acg aca acc cgc acc ttc tgc ggg	1771
Cys Lys Glu Asn Val Phe Pro Gly Thr Thr Thr Arg Thr Phe Cys Gly	
502 507 512 517	
acc ccg gac tac ata gcc ccg gag atc att gcc tac cag ccc tat ggg	1819
Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr Gln Pro Tyr Gly	
518 523 528 533	
aag tct gtc gat tgg tgg tcc ttt gga gtt ctg ctg tat gag atg ttg	1867
Lys Ser Val Asp Trp Trp Ser Phe Gly Val Leu Leu Tyr Glu Met Leu	
534 539 544 549	
gca gga cag cct ccc ttc gat ggg gag gac gag gag gag ctg ttt cag	1915
Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Glu Glu Leu Phe Gln	
550 555 560 565	
gcc atc atg gaa caa act gtc acc tac ccc aag tcg ctt tcc cgg gaa	1963
Ala Ile Met Glu Gln Thr Val Thr Tyr Pro Lys Ser Leu Ser Arg Glu	
566 571 576 581	
gcc gtg gcc atc tgc aag ggg ttc ctg acc aag cac cca ggg aag cgc	2011
Ala Val Ala Ile Cys Lys Gly Phe Leu Thr Lys His Pro Gly Lys Arg	
582 587 592 597	
ctg ggc tca ggg cct gat ggg gaa cct acc atc cgt gca cat ggc ttt	2059
Leu Gly Ser Gly Pro Asp Gly Glu Pro Thr Ile Arg Ala His Gly Phe	
598 603 608 613	

ttc cgc tgg att gac tgg gag cgg ctg gaa cga ttg gag atc ccg cct	2107
Phe Arg Trp Ile Asp Trp Glu Arg Leu Glu Arg Leu Glu Ile Pro Pro	
614 619 624 629	
cct ttc aga ccc cgc ccg tgt ggc cgc agc ggc gag aac ttt gac aag	2155
Pro Phe Arg Pro Arg Pro Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys	
630 635 640 645	
ttc ttc acg cgg gcg gcg cca gcg ctg acc cct cca gac cgc cta gtc	2203
Phe Phe Thr Arg Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val	
646 651 656 661	
ctg gcc agc atc gac cag gcc gat ttc cag ggc ttc acc tac gtg aac	2251
Leu Ala Ser Ile Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn	
662 667 672 677	
ccc gac ttc gtg cac ccg gat gcc cgc agc ccc acc agc cca gtg cct	2299
Pro Asp Phe Val His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro	
678 683 688 693	
gtg ccc gtc atg taa tctcaaccgc cgccactagg tgtccccaac gtcccctccg	2354
Val Pro Val Met *	
694	
ccgtgccggc ggcagcccca cttcaccccc aacttcacca cccctgtcc cattctagat	2414
cctgcacccc agcattocag ctctgcccc gcgggttcta gacgcccctc ccaagcgttc	2474
ctggccttct gaactccata cagcctctac agccgtcccg cgttcaagac ttgagcg	2531

<210> 74
 <211> 5359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (4556)..(4729)

<400> 74	
tttattgaac atttattctg ttcaaaacat tcccaaaggc aacagaagat acaaataaat	60
ctctgccccat gaaaagggtgt ggggggcatt agaaggcggt ctcttcggtg taatgaagta	120
atgagagaag aaaaagtagt ttgaagctat ggagtaaggg actttgagta tcccaggctc	180
aaaaagttgg gacttgaaca gtacgggggt gctgctgaaa acgtttgagg gaggtaatga	240
catgatcgaa gctatacttg agaaagggtga atctgataaa gtatgagtga aaaagagact	300
gaaggtctag aaattagatt gaggctaatt acaaaatcca cataaatagg aggacttgaa	360
cgaaggggca cttagaagag gacaggagat agtaaaaggc attcaatgat gagagcacac	420

actacagggg agcatgaggg aggttggaaa agataatgaa aggattaccg agcttcactg	480
acgatgtgtt tgaaatgagc aggaatcttg tagtgatcct aatccgtggg tttctggagc	540
atctcacagc ctaggaacat acaagggggg catctccctg gaatgtaaat tgactaagag	600
gaattcaata atgggtcaa atgaatgcagaa ttttagagtc ttgcttagta ttctcaccac	660
atctcgttta atctactcat actctttttc tcttactgct gacactagat ggaaaaactc	720
ttaattaaaa gtatttcaca aaatgtgctc gttttcagtc attccgtttc cactccagcc	780
tggtgtgttg tttttttgaa ataataat taaagtaatt tctttttgca ggatggcata	840
gtcaatccaa caataagaaa agatttgaaa actggaccga aattctactg ctgtccaatt	900
gaaggctgcc ccagaggccc tgagagaccg ttttctcagt tttctctcgt aaaacagcac	960
tttatgaaaa tgcattgctga gaagaagcac aaatgtagta agtgcagcaa ttcgtacggg	1020
acagaatggg acctgaaaag acatgcagag gactgtggca agaccttccg gtgcacatgc	1080
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Gly Pro Val Ala Leu Ala Arg Pro Gly Pro Arg Pro Arg Gly Pro Arg
79 84 89 94

cca ctg ccc gcc agg ccc cgt gat ggg gcc cct gag cca ggc ctc aca	1416
Pro Leu Pro Ala Arg Pro Arg Asp Gly Ala Pro Glu Pro Gly Leu Thr	
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Leu Pro Asp Leu Pro Glu Gln Phe Ser Pro Pro Asp Val Ala Pro Pro	
111 116 121 126	
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Leu Leu Val Lys Leu Val Glu Ala Ile Glu Arg Thr Gly Leu Asp Ser	
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Glu Ser His Tyr Arg Pro Glu Leu Pro Ala Pro Arg Thr Asp Trp Ser	
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Leu Ser Asp Val Asp Gln Trp Asp Thr Ala Ala Leu Ala Asp Gly Ile	
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Lys Ser Phe Leu Leu Ala Leu Pro Ala Pro Leu Val Thr Pro Glu Ala	
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Ser Ala Glu Ala Arg Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly	
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Pro Ala Leu Glu Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu	
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Arg Phe Leu Leu Gln His Leu Gly Arg Val Ala Ser Arg Ala Pro Ala	
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Leu Gly Pro Ala Val Arg Ala Leu Gly Ala Thr Phe Gly Pro Leu Leu	
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Leu Arg Ala Pro Pro Pro Pro Ser Ser Pro Pro Pro Gly Gly Ala Pro	
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Asp Gly Ser Glu Pro Ser Pro Asp Phe Pro Ala Leu Leu Val Glu Lys	
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Leu Leu Gln Glu His Leu Glu Glu Gln Glu Val Ala Pro Pro Ala Leu	
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Pro Pro Lys Pro Pro Lys Ala Lys Pro Ala Ser Thr Val Leu Ala Asn	
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Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Ser	Lys	Ile	Gln	Gly	Glu	Tyr	Thr		
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Arg	Asp	Gly	His	Tyr	Gly	Phe	Ser	Glu	Pro	Leu	Thr	Phe	Cys	Ser	Val		
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Val	Asp	Leu	Ile	Asn	His	Tyr	Arg	His	Glu	Ser	Leu	Ala	Gln	Tyr	Asn		
399					404					409					414		
gcc	aag	ctg	gac	aca	cgg	ctc	ctc	tac	cct	gtg	tcc	aaa	tac	cag	cag	2376	
Ala	Lys	Leu	Asp	Thr	Arg	Leu	Leu	Tyr	Pro	Val	Ser	Lys	Tyr	Gln	Gln		
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gac	cag	att	gtc	aag	gag	gac	agc	gtg	gag	gca	gtg	ggc	gcc	cag	ctt	2424	
Asp	Gln	Ile	Val	Lys	Glu	Asp	Ser	Val	Glu	Ala	Val	Gly	Ala	Gln	Leu		
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act	gca	att	gag	gcc	ttc	aat	gag	act	atc	aag	atc	ttt	gaa	gag	cag	2568	
Thr	Ala	Ile	Glu	Ala	Phe	Asn	Glu	Thr	Ile	Lys	Ile	Phe	Glu	Glu	Gln		
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Ser	Gln	Thr	Gln	Glu	Lys	Cys	Ser	Lys	Glu	Tyr	Leu	Glu	Arg	Phe	Arg		
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cgg	ctc	aag	tcc	cgc	att	gcc	gag	atc	cat	gag	agc	cgc	acg	aag	ctg	2712	
Arg	Leu	Lys	Ser	Arg	Ile	Ala	Glu	Ile	His	Glu	Ser	Arg	Thr	Lys	Leu		
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gac cag tac ctc gtg tgg ctc acc cag aaa ggc gcc cgg cag aag aaa				2856
Asp Gln Tyr Leu Val Trp Leu Thr Gln Lys Gly Ala Arg Gln Lys Lys				
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Ile Asn Glu Trp Leu Gly Ile Lys Asn Glu Thr Glu Asp Gln Tyr Ala				
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ctc atg gag gac gag gac gat ctc ccg cac cac gag gaa cgc act tgg				2952
Leu Met Glu Asp Glu Asp Asp Leu Pro His His Glu Glu Arg Thr Trp				
607	612	617	622	
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Tyr Val Gly Lys Ile Asn Arg Thr Gln Ala Glu Glu Met Leu Ser Gly				
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Tyr Ala Cys Ser Val Val Val Asp Gly Asp Thr Lys His Cys Val Ile				
655	660	665	670	
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Tyr Arg Thr Ala Thr Gly Phe Gly Phe Ala Glu Pro Tyr Asn Leu Tyr				
671	676	681	686	
ggg tcg ctg aag gag ctg gtg ctg cac tac cag cac gcc tcg ctg gtg				3192
Gly Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Ala Ser Leu Val				
687	692	697	702	
cag cac aac gac gcg ctc acc gtc acc ctg gcg cac cca gtg cgc gcc				3240
Gln His Asn Asp Ala Leu Thr Val Thr Leu Ala His Pro Val Arg Ala				
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Pro Gly Pro Gly Pro Pro Pro Ala Ala Arg *				
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 ggcaaccaag taatcttaaa tctggggaaa gaaagatgcc agctgagaga aacaggactc 240
 aagctttact tacctggg atg gac tct gcc aga cac cat ata agc cac tct 291
 Met Asp Ser Ala Arg His His Ile Ser His Ser
 1 5
 act tct gca ggc ccc atc cct tcc cag aaa gaa gag gaa atg act gag 339
 Thr Ser Ala Gly Pro Ile Pro Ser Gln Lys Glu Glu Glu Met Thr Glu
 12 17 22 27
 tcc cag gga aca gta aca ttc aaa gat gtg gct atc gac ttc act cag 387
 Ser Gln Gly Thr Val Thr Phe Lys Asp Val Ala Ile Asp Phe Thr Gln
 28 33 38 43
 gag gag tgg aag aga ttg gat cct gct cag aga aaa ctg tac cgg aat 435
 Glu Glu Trp Lys Arg Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asn
 44 49 54 59
 gtg atg cta gaa aac tat aac aac tta atc aca gta ggc tat ccg ttc 483
 Val Met Leu Glu Asn Tyr Asn Asn Leu Ile Thr Val Gly Tyr Pro Phe
 60 65 70 75

acc aaa cct gat gtg att ttc aaa ttg gag caa gaa gaa gaa cca tgg	531
Thr Lys Pro Asp Val Ile Phe Lys Leu Glu Gln Glu Glu Glu Pro Trp	
76 81 86 91	
gtg atg gag gaa gaa gta tta agg aga cac tgg caa gga gaa ata tgg	579
Val Met Glu Glu Glu Val Leu Arg Arg His Trp Gln Gly Glu Ile Trp	
92 97 102 107	
gga gtt gat gag cat cag aaa aac cag gac aga ctt ttg aga caa gtt	627
Gly Val Asp Glu His Gln Lys Asn Gln Asp Arg Leu Leu Arg Gln Val	
108 113 118 123	
gaa gtt aaa ttc cag aaa aca ctg act gaa gaa aaa ggc aat gaa tgt	675
Glu Val Lys Phe Gln Lys Thr Leu Thr Glu Glu Lys Gly Asn Glu Cys	
124 129 134 139	
caa aag aaa ttt gca aat gta ttt cct ctg aac tct gat ttt ttc cct	723
Gln Lys Lys Phe Ala Asn Val Phe Pro Leu Asn Ser Asp Phe Phe Pro	
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tcc aga cac aat ctc tat gag tat gac tta ttt gga aag tgt tta gaa	771
Ser Arg His Asn Leu Tyr Glu Tyr Asp Leu Phe Gly Lys Cys Leu Glu	
156 161 166 171	
cat aat ttt gac tgt cat aat aat gtg aaa tgc ctt atg aga aag gag	819
His Asn Phe Asp Cys His Asn Asn Val Lys Cys Leu Met Arg Lys Glu	
172 177 182 187	
cat tgt gaa tat aat gaa cct gtg aaa tca tat ggt aat agc tca tcc	867
His Cys Glu Tyr Asn Glu Pro Val Lys Ser Tyr Gly Asn Ser Ser Ser	
188 193 198 203	
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His Phe Val Ile Thr Pro Phe Lys Cys Asn His Cys Gly Lys Gly Phe	
204 209 214 219	
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Asn Gln Thr Leu Asp Leu Ile Arg His Leu Arg Ile His Thr Gly Glu	
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Lys Leu Ile Lys His Tyr Lys Ile His Ser Arg Glu Gln Ser Tyr Lys	
252 257 262 267	
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Cys Asn Glu Cys Gly Lys Ala Phe Ile Lys Met Ser Asn Leu Ile Arg	
268 273 278 283	
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His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Lys Glu Cys	
284 289 294 299	

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Glu Lys Ser Phe Ser	Gln Lys Ser Asn Leu Ile Asp His Glu Lys Ile	
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cat act gga gag aaa cct tat gaa tgt aat gag tgt gga aaa gca ttc	1251	
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332	337 342 347	
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348	353 358 363	
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Cys Asp Lys Cys Gly	Lys Ala Phe Ser Gln Phe Ser Met Leu Ile Ile	
380	385 390 395	
cat gtt aga att cat aca ggt gaa aaa ccc tat gaa tgt aat gag tgt	1491	
His Val Arg Ile His	Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys	
396	401 406 411	
gga aaa gcc ttc tct caa agc tca gcc ctt act gta cat atg aga agt	1539	
Gly Lys Ala Phe Ser	Gln Ser Ser Ala Leu Thr Val His Met Arg Ser	
412	417 422 427	
cac act ggt gag aaa ccc tat gaa tgt aag gaa tgc aga aaa gcc ttc	1587	
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Ser His Lys Lys Asn	Phe Ile Thr His Gln Lys Ile His Thr Arg Glu	
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Lys Pro Tyr Glu Cys	Asn Glu Cys Gly Lys Ala Phe Ile Gln Met Ser	
460	465 470 475	
aat ctt gtt aga cac cag aga att cat act ggg gaa aaa ccc tat ata	1731	
Asn Leu Val Arg His	Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile	
476	481 486 491	
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Cys Lys Glu Cys Gly	Lys Ala Phe Ser Gln Asn Ser Asn Leu Ile Ala	
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cat gaa aaa att cat tct gga gag aaa ccc tat gaa tgc aat gaa tgt	1827	
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Gly Lys Ala Phe Ser Gln Lys Gln Asn Phe Ile Thr His Gln Lys Val	
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His Thr Gly Glu Lys Pro Tyr Asp Cys Asn Glu Cys Gly Lys Ala Phe	
540 545 550 555	
tct caa att gca tcc ctt acc ctt cat ttg aga agt cat aca ggg gaa	1971
Ser Gln Ile Ala Ser Leu Thr Leu His Leu Arg Ser His Thr Gly Glu	
556 561 566 571	
aag cct tat gaa tgt gat aaa tgt ggt aaa gcc ttc tct cag tgc tca	2019
Lys Pro Tyr Glu Cys Asp Lys Cys Gly Lys Ala Phe Ser Gln Cys Ser	
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Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Arg Thr Ser Leu Ile Val	
604 609 614 619	
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His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Ala Phe	
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agc cac aag aaa aac ttc att aca cac cag aaa att cat act aga gag	2307
Ser His Lys Lys Asn Phe Ile Thr His Gln Lys Ile His Thr Arg Glu	
668 673 678 683	
aaa cct tta agt gta atc att gtg gaa aag gct tca atc aga ctt tgg	2355
Lys Pro Leu Ser Val Ile Ile Val Glu Lys Ala Ser Ile Arg Leu Trp	
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Thr Ser Ser Asp Ile *	
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 Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser
 49 54 59 64
 ggt gtg ggc aag acg gcg ctg gtg gcc aag ctg gct ggc ctg gag gtg 658
 Gly Val Gly Lys Thr Ala Leu Val Ala Lys Leu Ala Gly Leu Glu Val
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 cct gtg gtg cac cac gag acc acc ggc atc cag acc acc gtg gta ttt 706
 Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe
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 Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met
 113 118 123 128
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Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg	
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Ala Asp Val Ala His Ile Leu Asn Gly Leu Ala Glu Gln Leu Trp His	
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Gln Asp Gln Val Ala Ala Gly Leu Leu Pro Asn Pro Pro Glu Ser Ala	
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Pro Glu *	
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Leu Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala	
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Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn	
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Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met	
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Glu Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met	
228 233 238 243	
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Tyr Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala	
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Ile Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn	
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Leu Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln	
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Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser	
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 atg ggg gac aag aaa gat gac aag gac tca ccc aag aag aac aag ggc 165
 Met Gly Asp Lys Lys Asp Lys Asp Ser Pro Lys Lys Asn Lys Gly
 1 5 10 15

 aag gag cgc cgg gac ctg gat gac ctc aag aag gag gtg gct atg aca 213
 Lys Glu Arg Arg Asp Leu Asp Asp Leu Lys Lys Glu Val Ala Met Thr
 17 22 27 32

 gag cac aag atg tca gtg gaa gag gtc tgc cgg aaa tac aac aca gac 261
 Glu His Lys Met Ser Val Glu Glu Val Cys Arg Lys Tyr Asn Thr Asp
 33 38 43 48

 tgt gtg cag ggt ttg acc cac agc aaa gcc cag gag atc ctg gcc cgg 309
 Cys Val Gln Gly Leu Thr His Ser Lys Ala Gln Glu Ile Leu Ala Arg
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ggg gct atc ctc tgc ttc ctg gcc tac ggt atc cag gcg ggc acc gag	453
Gly Ala Ile Leu Cys Phe Leu Ala Tyr Gly Ile Gln Ala Gly Thr Glu	
97 102 107 112	
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Asp Asp Pro Ser Gly Asp Asn Leu Tyr Leu Gly Ile Val Leu Ala Ala	
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Val Val Ile Ile Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala Lys Ser	
129 134 139 144	
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Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln Ala Leu	
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Val Ile Arg Glu Gly Glu Lys Met Gln Val Asn Ala Glu Glu Val Val	
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Val Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro Ala Asp	
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Leu Arg Ile Ile Ser Ala His Gly Cys Lys Val Asp Asn Ser Ser Leu	
193 198 203 208	
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Asn Pro Leu Glu Thr Arg Asn Ile Thr Phe Phe Ser Thr Asn Cys Val	
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Glu Gly Thr Ala Arg Gly Val Val Val Ala Thr Gly Asp Arg Thr Val	
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Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val	
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Ala Val Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Gly	
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Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala	
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Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu	
321 326 331 336	
acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag	1173
Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu	
337 342 347 352	
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Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp Lys Thr	
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Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp Phe Asp	
369 374 379 384	
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Phe Asp Lys Ser Ser His Thr Trp Val Ala Leu Ser His Ile Ala Gly	
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Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val	
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Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu	
497 502 507 512	
cta cag ggc aag gag cag cct ctg gac gag gaa atg aag gag gcc ttc	1701

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Phe	Cys	His	Tyr	Tyr	Leu	Pro	Glu	Glu	Gln	Phe	Pro	Lys	Gly	Phe	Ala		
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Phe	Asp	Cys	Asp	Asp	Val	Asn	Phe	Thr	Thr	Asp	Asn	Leu	Cys	Phe	Val		
561					566					571					576		
ggc	ctc	atg	tcc	atg	atc	gac	cca	ccc	cgg	gca	gcc	gtc	cct	gac	gcg	1893	
Gly	Leu	Met	Ser	Met	Ile	Asp	Pro	Pro	Arg	Ala	Ala	Val	Pro	Asp	Ala		
577					582					587					592		
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Val	Gly	Lys	Cys	Arg	Ser	Ala	Gly	Ile	Lys	Val	Ile	Met	Val	Thr	Gly		
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Asp	His	Pro	Ile	Thr	Ala	Lys	Ala	Ile	Ala	Lys	Gly	Val	Gly	Ile	Ile		
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Phe	Glu	Gly	Asn	Glu	Thr	Val	Glu	Asp	Ile	Ala	Ala	Arg	Leu	Asn	Ile		
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ccc	gtc	agc	cag	gtt	aac	ccc	cgg	gat	gcc	aag	gcc	tgc	gtg	atc	cac	2085	
Pro	Val	Ser	Gln	Val	Asn	Pro	Arg	Asp	Ala	Lys	Ala	Cys	Val	Ile	His		
641					646					651					656		
ggc	acc	gac	ctc	aag	gac	ttc	acc	tcc	gag	caa	atc	gac	gag	atc	ctg	2133	
Gly	Thr	Asp	Leu	Lys	Asp	Phe	Thr	Ser	Glu	Gln	Ile	Asp	Glu	Ile	Leu		
657					662					667					672		
cag	aat	cac	acc	gag	atc	gtc	ttc	gcc	cgc	aca	tcc	ccc	cag	cag	aag	2181	
Gln	Asn	His	Thr	Glu	Ile	Val	Phe	Ala	Arg	Thr	Ser	Pro	Gln	Gln	Lys		
673					678					683					688		
ctc	atc	att	gtg	gag	ggc	tgt	cag	aga	cag	ggg	gca	att	gtg	gct	gtg	2229	
Leu	Ile	Ile	Val	Glu	Gly	Cys	Gln	Arg	Gln	Gly	Ala	Ile	Val	Ala	Val		
689					694					699					704		
acc	ggg	gat	ggg	gtg	aac	gac	tcc	ccc	gct	ctg	aag	aag	gcc	gac	att	2277	
Thr	Gly	Asp	Gly	Val	Asn	Asp	Ser	Pro	Ala	Leu	Lys	Lys	Ala	Asp	Ile		
705					710					715					720		
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Gly	Val	Ala	Met	Gly	Ile	Ala	Gly	Ser	Asp	Val	Ser	Lys	Gln	Ala	Ala		
721					726					731					736		
gac	atg	atc	ctg	ctg	gac	gac	aac	ttt	gcc	tcc	atc	gtc	aca	ggg	gtg	2373	
Asp	Met	Ile	Leu	Leu	Asp	Asp	Asn	Phe	Ala	Ser	Ile	Val	Thr	Gly	Val		

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Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr				
753	758	763	768	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc				2469
Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile				
769	774	779	784	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc				2517
Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile				
785	790	795	800	
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct				2565
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala				
801	806	811	816	
gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac				2613
Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp				
817	822	827	832	
aaa ttg gct gag gag cca atg ggg cga agc tac cat ctg tgg gat tat				2661
Lys Leu Ala Glu Glu Pro Met Gly Arg Ser Tyr His Leu Trp Asp Tyr				
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gac tga acgcctctaa gtcagaatcc cgcccaggcg gaacgatacg gcagcgccgc				2717
Asp *				
849				
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cggaattcaa aacggacctg gagg atg ttg atc tcc aag aac atg ccc tgg	171
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Arg Arg Leu Gln Gly Ile Ser Phe Gly Met Tyr Ser Ala Glu Glu Leu	
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Lys Lys Leu Ser Val Lys Ser Ile Thr Asn Pro Arg Tyr Leu Asp Ser	
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Cys Ser Gly His Leu Gly His Ile Glu Leu Pro Leu Thr Val Tyr Asn	
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cct ctc ctc ttc gat aag ctg tac ctg ctg ctt cgg ggc tct tgt tta	459
Pro Leu Leu Phe Asp Lys Leu Tyr Leu Leu Leu Arg Gly Ser Cys Leu	
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Asn Cys His Met Leu Thr Cys Pro Arg Ala Val Ile His Leu Leu Leu	
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Cys Gln Leu Arg Val Leu Glu Val Gly Ala Leu Gln Ala Val Tyr Glu	
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gaa cac aac agc aag ttg act atc aca ttt cca gcc atg gtg cac agg	843
Glu His Asn Ser Lys Leu Thr Ile Thr Phe Pro Ala Met Val His Arg	
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Ile Gly Lys Arg Gly Tyr Leu Thr Pro Thr Ser Ala Arg Glu His Leu	
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378 383 388 393	
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Arg Ser Val Ile Cys Pro Asp Met Tyr Ile Asn Thr Asn Glu Ile Gly	
442 447 452 457	

att ccc atg gtg ttt gcc aca aaa ctg acc tac cca cag cca gtt acc	1563
Ile Pro Met Val Phe Ala Thr Lys Leu Thr Tyr Pro Gln Pro Val Thr	
458 463 468 473	
cca tgg aat gtt cag gaa ctt agg caa gcg gtc atc aac ggc cct aat	1611
Pro Trp Asn Val Gln Glu Leu Arg Gln Ala Val Ile Asn Gly Pro Asn	
474 479 484 489	
gtg cac cca gga gcc tcc atg gtc atc aat gag gac ggc agc cgc aca	1659
Val His Pro Gly Ala Ser Met Val Ile Asn Glu Asp Gly Ser Arg Thr	
490 495 500 505	
gcc ctg agc gct gtg gac atg acc cag cga gag gcc gtg gcc aag cag	1707
Ala Leu Ser Ala Val Asp Met Thr Gln Arg Glu Ala Val Ala Lys Gln	
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Leu Leu Thr Pro Ala Thr Gly Ala Pro Lys Pro Gln Gly Thr Lys Ile	
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gtg tgc cgg cat gtg aag aat ggg gac att ctg cta ctg aac cga cag	1803
Val Cys Arg His Val Lys Asn Gly Asp Ile Leu Leu Leu Asn Arg Gln	
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Pro Thr Leu His Arg Pro Ser Ile Gln Ala His Arg Ala Arg Ile Leu	
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Pro Glu Glu Lys Val Leu Arg Leu His Tyr Ala Asn Cys Lys Ala Tyr	
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Asn Ala Asp Phe Asp Gly Asp Glu Met Asn Ala His Phe Pro Gln Ser	
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Glu Leu Gly Arg Ala Glu Ala Tyr Val Leu Ala Cys Thr Asp Gln Gln	
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Gly Arg Val Lys Leu Leu Ser Pro Ser Ile Leu Lys Pro Phe Pro Leu	
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Glu	Asp	His	Ile	Pro	Leu	Asn	Leu	Ser	Gly	Lys	Ala	Lys	Ile	Thr	Gly	
698					703					708					713	
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Lys	Ala	Trp	Val	Lys	Glu	Thr	Pro	Arg	Ser	Val	Pro	Gly	Phe	Asn	Pro	
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gac	tcg	atg	tgc	gag	tcc	cag	gtg	atc	atc	agg	gaa	ggg	gag	ctg	ctc	2379
Asp	Ser	Met	Cys	Glu	Ser	Gln	Val	Ile	Ile	Arg	Glu	Gly	Glu	Leu	Leu	
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tgc	gga	gtg	ctg	gac	aag	gcg	cac	tat	ggg	agc	tcc	gcc	tac	ggc	ctg	2427
Cys	Gly	Val	Leu	Asp	Lys	Ala	His	Tyr	Gly	Ser	Ser	Ala	Tyr	Gly	Leu	
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Val	His	Cys	Cys	Tyr	Glu	Ile	Tyr	Gly	Gly	Glu	Thr	Ser	Gly	Lys	Val	
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cta	acc	tgc	ctg	gcc	cgc	ctc	ttc	acc	gcc	tac	ctg	cag	ctc	tac	aga	2523
Leu	Thr	Cys	Leu	Ala	Arg	Leu	Phe	Thr	Ala	Tyr	Leu	Gln	Leu	Tyr	Arg	
778					783					788					793	
ggc	ttc	acc	ttg	ggc	gtg	gaa	gac	att	ttg	gtg	aag	cca	aag	gca	gat	2571
Gly	Phe	Thr	Leu	Gly	Val	Glu	Asp	Ile	Leu	Val	Lys	Pro	Lys	Ala	Asp	
794					799					804					809	
gtc	aag	agg	caa	cgt	atc	att	gaa	gaa	tcc	acc	cac	tgc	ggg	ccc	cag	2619
Val	Lys	Arg	Gln	Arg	Ile	Ile	Glu	Glu	Ser	Thr	His	Cys	Gly	Pro	Gln	
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gct	gtc	agg	gct	gca	tta	aac	ctg	cca	gaa	gcc	gca	tca	tat	gat	gag	2667
Ala	Val	Arg	Ala	Ala	Leu	Asn	Leu	Pro	Glu	Ala	Ala	Ser	Tyr	Asp	Glu	
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Val	Arg	Gly	Lys	Trp	Gln	Asp	Ala	His	Leu	Gly	Lys	Asp	Gln	Arg	Asp	
842					847					852					857	
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Phe	Asn	Met	Ile	Asp	Leu	Lys	Phe	Lys	Glu	Glu	Val	Asn	His	Tyr	Ser	
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Thr	Val	Asn	Thr	Met	Gln	Ile	Ser	Cys	Leu	Leu	Gly	Gln	Ile	Glu	Leu	

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Glu Gly Arg Ser Thr Pro Leu Met Ala Ser Gly Lys Ser Leu Pro Cys				
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Phe Glu Pro Tyr Glu Phe Thr Pro Arg Ala Gly Gly Phe Val Thr Gly				
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Arg Phe Leu Thr Gly Ile Lys Pro Pro Glu Phe Phe Phe His Cys Met				
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Ala Gly Arg Glu Gly Leu Val Asp Thr Ala Val Lys Thr Ser Arg Ser				
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Gly Tyr Leu Gln Arg Cys Ile Ile Lys His Leu Glu Gly Leu Val Val				
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Gln Tyr Asp Leu Thr Val Arg Asp Ser Asp Gly Ser Val Val Gln Phe				
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Leu Tyr Gly Glu Asp Gly Leu Asp Ile Pro Lys Thr Gln Phe Leu Gln				
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Pro Lys Gln Phe Pro Phe Leu Ala Ser Asn Tyr Glu Val Ile Met Lys				
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Ser Gln His Leu His Glu Val Leu Ser Arg Ala Asp Pro Lys Lys Ala				
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Leu His His Phe Arg Ala Ile Lys Lys Trp Gln Ser Lys His Pro Asn				
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Thr Leu Leu Arg Arg Gly Ala Phe Leu Ser Tyr Ser Gln Lys Ile Gln				
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Glu Ala Val Lys Ala Leu Lys Leu Glu Ser Glu Asn Arg Asn Gly Arg				
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Arg Pro Trp Asp Ser Gly Arg Met Leu Arg Met Trp Tyr Glu Leu Asp				
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Glu Glu Ser Arg Arg Lys Tyr Gln Lys Lys Ala Ala Ala Cys Pro Asp				
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Pro Ser Leu Ser Val Trp Arg Pro Asp Ile Tyr Phe Ala Ser Val Ser	
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Glu Thr Phe Glu Thr Lys Val Asp Asp Tyr Ser Gln Glu Trp Ala Ala	
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Gln Thr Glu Lys Ser Tyr Glu Lys Ser Glu Leu Ser Leu Asp Arg Leu	
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Arg Thr Leu Leu Gln Leu Lys Trp Gln Arg Ser Leu Cys Glu Pro Gly	
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Gln Met Thr Leu Asn Thr Phe His Phe Ala Gly Arg Gly Glu Met Asn	
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Val Thr Leu Gly Ile Pro Arg Leu Arg Glu Ile Leu Met Val Ala Ser	
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Ala Asn Ile Lys Thr Pro Met Met Ser Val Pro Val Leu Asn Thr Lys	
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Lys Ala Leu Lys Arg Val Lys Ser Leu Lys Lys Gln Leu Thr Arg Val	
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Cys Leu Gly Glu Val Leu Gln Lys Ile Asp Val Gln Glu Ser Phe Cys	
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Asp Ile Leu Arg Phe Met Glu Thr Arg Phe Phe Lys Leu Leu Met Glu	
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Ser Ile Lys Lys Lys Asn Asn Lys Ala Ser Ala Phe Arg Asn Val Asn	
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Glu Glu Arg Glu Gly Glu Glu Asn Asp Asp Glu Asp Met Gln Glu Glu	
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Ala Met Glu Arg Arg Val Gln Ala Val Arg Glu Ile His Pro Phe Ile	
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Val Lys Leu Pro Leu Met Lys Ile Asn Phe Asp Met Ser Ser Leu Val	
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Val Ser Leu Ala His Gly Ala Val Ile Tyr Ala Thr Lys Gly Ile Thr	
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Arg Cys Leu Leu Asn Glu Thr Thr Asn Asn Lys Asn Glu Lys Glu Leu	
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Tyr Tyr Ile Leu Ala Asp Pro Trp Arg Gln Glu Trp Glu Lys Gly Val
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Gln Val Pro Ala Gly Ala Glu Ala Ile Pro Glu Pro Val Val Arg Ile
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Met Leu Gly Glu Gly Ser Gln Pro Asp Trp Pro Gly Gly Ser Arg Tyr							
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Asp Leu Asp Glu Ile Asp Ala Tyr Trp Leu Glu Leu Ile Asn Ser Glu							
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Leu Lys Glu Met Glu Arg Pro Glu Leu Asp Glu Leu Thr Leu Glu Arg							
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Val Leu Glu Glu Leu Glu Thr Leu Cys His Gln Asn Met Ala Arg Ala							
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Ile Glu Thr Gln Glu Gly Leu Gly Ile Glu Tyr Asp Glu Asp Val Val							
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Cys Asp Val Cys Arg Ser Pro Glu Gly Glu Asp Gly Asn Glu Met Val							
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Phe Cys Asp Lys Cys Asn Val Cys Val His Gln Ala Cys Tyr Gly Ile							
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Gln Phe Leu Lys His Gln Gln Thr His Asn Ile Glu Lys Ala His Glu	
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gag aaa gct tac ttc tat atg tct tgc ctt gtt aaa cat aag aga ata	1641
Glu Lys Ala Tyr Phe Tyr Met Ser Cys Leu Val Lys His Lys Arg Ile	
436 441 446 451	
cac tca agg gag aaa cgg ggg gat tca gtg aag gtg gaa aat cct tcc	1689
His Ser Arg Glu Lys Arg Gly Asp Ser Val Lys Val Glu Asn Pro Ser	
452 457 462 467	
aca gca agt cac agc tta agt cct agt gaa cat gtg cag ggg aaa agc	1737
Thr Ala Ser His Ser Leu Ser Pro Ser Glu His Val Gln Gly Lys Ser	
468 473 478 483	
cct gtt aat atg gta act gtg gca atg gtg gca ggg cag tgt gag ttt	1785
Pro Val Asn Met Val Thr Val Ala Met Val Ala Gly Gln Cys Glu Phe	
484 489 494 499	
gcc cac atc ctg cat tca tga ta aacagtttgc tgtttgatca tatagcctcc	1838
Ala His Ile Leu His Ser *	
500 505	
agcggaaatgc tgagtttgtc atgtcccatg ggcctttggc tccctgcact aatatgtata	1898
gtaggggttta caagatatga aatatatattt acttttttat atcttataaa cctcactacc	1958
cctcccacaa tattgtttttt catttaactat cttgatcata gagtttggct ggggaggggg	2018
gcagtttttaa aggcttccac ttggtgttcc tcagaatgat atctcttact ccggggggcca	2078
aggtaggggt tagcttttgt tctctttgta gtttagattg tatctcttgc cttgttcaag	2138
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tgtggcgaat gctttgacct caaagtcaac cccacaggac ttccctgaat cttgtggagc	180
tggctgcaac atcactgaac agagcataga gaccctctcc ttgccacccg gcccttccca	240
cctggtttggg gacaaatcac aaggtggtag aagttgccag ggacagataa c atg gca	297

Met Ala

1

gcc agc ggg aag acc agc aag tcc gaa ccg aac cat gtt atc ttc aag	345
Ala Ser Gly Lys Thr Ser Lys Ser Glu Pro Asn His Val Ile Phe Lys	
3 8 13 18	
aag atc tcc cgg gac aaa tcg gtg acc atc tac ctg ggg aac aga gac	393
Lys Ile Ser Arg Asp Lys Ser Val Thr Ile Tyr Leu Gly Asn Arg Asp	
19 24 29 34	
tac ata gac cat gtc agc caa gtc cag cct gtg gat ggt gtc gtg ttg	441
Tyr Ile Asp His Val Ser Gln Val Gln Pro Val Asp Gly Val Val Leu	
35 40 45 50	
gtt gat cct gat ctt gtg aag gga aag aaa gtg tat gtc act ctg acc	489
Val Asp Pro Asp Leu Val Lys Gly Lys Lys Val Tyr Val Thr Leu Thr	
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Cys Ala Phe Arg Tyr Gly Gln Glu Asp Ile Asp Val Ile Gly Leu Thr	
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Phe Arg Arg Asp Leu Tyr Phe Ser Arg Val Gln Val Tyr Pro Pro Val	
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ggg gcc gcg agc acc ccc aca aaa ctg caa gag agc ctg ctt aaa aag	633
Gly Ala Ala Ser Thr Pro Thr Lys Leu Gln Glu Ser Leu Leu Lys Lys	
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ctg ggg agc aac acg tac ccc ttt ctc ctg acg ttt cct gac tac ttg	681
Leu Gly Ser Asn Thr Tyr Pro Phe Leu Leu Thr Phe Pro Asp Tyr Leu	
115 120 125 130	
ccc tgt tca gtg atg ttg cag cca gct cca caa gat tca ggg aag tcc	729
Pro Cys Ser Val Met Leu Gln Pro Ala Pro Gln Asp Ser Gly Lys Ser	
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Cys Gly Val Asp Phe Glu Val Lys Ala Phe Ala Thr Asp Ser Thr Asp	
147 152 157 162	
gcc gaa gag gac aaa atc ccc aag aag agc tcc gtg cga tta ctg atc	825
Ala Glu Glu Asp Lys Ile Pro Lys Lys Ser Ser Val Arg Leu Leu Ile	
163 168 173 178	
cgc aaa gta cag cat gcc cca ctt gag atg ggt ccc cag ccc cga gct	873
Arg Lys Val Gln His Ala Pro Leu Glu Met Gly Pro Gln Pro Arg Ala	
179 184 189 194	
gag gcg gcc tgg cag ttc ttc atg tct gac aag ccc ctg cac ctt gcg	921
Glu Ala Ala Trp Gln Phe Phe Met Ser Asp Lys Pro Leu His Leu Ala	
195 200 205 210	
gtc tct ctc aac aaa gag atc tat ttc cat ggg gag ccc atc cct gtg	969
Val Ser Leu Asn Lys Glu Ile Tyr Phe His Gly Glu Pro Ile Pro Val	

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acc gtg act gtc acc aat aac aca gag aag acc gtg aag aag att aaa				1017
Thr Val Thr Val Thr Asn Asn Thr Glu Lys Thr Val Lys Lys Ile Lys				
227	232	237	242	
gca ttc gtg gaa cag gtg gcc aat gtg gtt ctc tac tcg agt gat tat				1065
Ala Phe Val Glu Gln Val Ala Asn Val Val Leu Tyr Ser Ser Asp Tyr				
243	248	253	258	
tac gtc aag ccc gtg gct atg gag gaa gcg caa gaa aaa gtg cca cca				1113
Tyr Val Lys Pro Val Ala Met Glu Glu Ala Gln Glu Lys Val Pro Pro				
259	264	269	274	
aac agc act ttg acc aag acg ctg acg ctg ctg ccc ttg ctg gct aac				1161
Asn Ser Thr Leu Thr Lys Thr Leu Thr Leu Leu Pro Leu Leu Ala Asn				
275	280	285	290	
aat cga gaa agg aga ggc att gcc ctg gat ggg aaa atc aag cac gag				1209
Asn Arg Glu Arg Arg Gly Ile Ala Leu Asp Gly Lys Ile Lys His Glu				
291	296	301	306	
gac aca aac ctt gcc tcc agc acc atc att aag gag ggc ata gac cgg				1257
Asp Thr Asn Leu Ala Ser Ser Thr Ile Ile Lys Glu Gly Ile Asp Arg				
307	312	317	322	
acc gtc ctg gga atc ctg gtg tct tac cag atc aag gtg aag ctc aca				1305
Thr Val Leu Gly Ile Leu Val Ser Tyr Gln Ile Lys Val Lys Leu Thr				
323	328	333	338	
gtg tca ggc ttt ctg gga gag ctc acc tcc agt gaa gtc gcc act gag				1353
Val Ser Gly Phe Leu Gly Glu Leu Thr Ser Ser Glu Val Ala Thr Glu				
339	344	349	354	
gtc cca ttc cgc ctc atg cac cct cag cct gag gac cca gct aag gaa				1401
Val Pro Phe Arg Leu Met His Pro Gln Pro Glu Asp Pro Ala Lys Glu				
355	360	365	370	
agt tat cag gat gca aat tta gtt ttt gag gag ttt gct cgc cat aat				1449
Ser Tyr Gln Asp Ala Asn Leu Val Phe Glu Glu Phe Ala Arg His Asn				
371	376	381	386	
ctg aaa gat gca gga gaa gct gag gag ggg aag aga gac aag aat gac				1497
Leu Lys Asp Ala Gly Glu Ala Glu Glu Gly Lys Arg Asp Lys Asn Asp				
387	392	397	402	
att gat gag tga aga tgctcggtca ggatgccgga aaatgacctg tagttaccag				1552
Ile Asp Glu *				
403				
tgcaacgagc aaagccccac agtttagtcc tttggagtta tgctgcgtat gaaaggatga				1612
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cggggcgggg ccgagtgcga acctgagccc caaatcccga ccaggcagg ggcggggccc      180
ggagcggggc cttggaggcc cagcccgcg gcgcagctct ccgcgtggcg tcacggcacc      240
gactgacggc caccaccc  atg gcc gca gac cag cgc ccg aag gcc gac acg      291
                   Met Ala Ala Asp Gln Arg Pro Lys Ala Asp Thr
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ctg gcc ctg agg caa cgg ctc atc agc tct tcc tgc aga ctc ttt ttt      339
Leu Ala Leu Arg Gln Arg Leu Ile Ser Ser Cys Arg Leu Phe Phe
 12                   17                   22                   27

ccc gag gat cct gtt aag att gtc cgg gcc caa ggg cag tac atg tac      387
Pro Glu Asp Pro Val Lys Ile Val Arg Ala Gln Gly Gln Tyr Met Tyr
 28                   33                   38                   43

gat gaa cag ggg gca gaa tac atc gat tgc atc agc aat gtg gcg cac      435
Asp Glu Gln Gly Ala Glu Tyr Ile Asp Cys Ile Ser Asn Val Ala His
 44                   49                   54                   59

gtt ggg cac tgc cac cct ctc gtg gtc caa gca gca cat gag cag aac      483
Val Gly His Cys His Pro Leu Val Val Gln Ala Ala His Glu Gln Asn
 60                   65                   70                   75

cag gtg ctc aac acc aac agc cgg tac ctg cat gac aac atc gtg gac      531
Gln Val Leu Asn Thr Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp
 76                   81                   86                   91

tat gcg cag agg ctg tca gag acc ctg ccg gag cag ctc tgt gtg ttc      579
Tyr Ala Gln Arg Leu Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe
 92                   97                   102                   107

tat ttc ctg aat tct ggg tca gaa gcc aat gac ctg gcc ctg agg ctg      627
Tyr Phe Leu Asn Ser Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu
108                   113                   118                   123

gct cgc cac tac acg gga cac cag gac gtg gtg gta tta gat cat gcg      675
Ala Arg His Tyr Thr Gly His Gln Asp Val Val Val Leu Asp His Ala
124                   129                   134                   139

tat cac ggc cac ctg agc tcc ctg att gac atc agt ccc tac aag ttc      723
Tyr His Gly His Leu Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe
140                   145                   150                   155

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Arg Asn Leu Asp Gly Gln Lys Glu Trp Val His Val Ala Pro Leu Pro	
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gac acc tac cgg ggc ccc tac cgg gag gac cac ccc aac cca gct atg	819
Asp Thr Tyr Arg Gly Pro Tyr Arg Glu Asp His Pro Asn Pro Ala Met	
172 177 182 187	
gcc tat gcc aac gag gtg aaa cgt gtg gtc agc agt gca cag gag aag	867
Ala Tyr Ala Asn Glu Val Lys Arg Val Val Ser Ser Ala Gln Glu Lys	
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Gly Arg Lys Ile Ala Ala Phe Phe Ala Glu Ser Leu Pro Ser Val Gly	
204 209 214 219	
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Gly Gln Ile Ile Pro Pro Ala Gly Tyr Phe Ser Gln Val Ala Glu His	
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Ile Arg Lys Ala Gly Gly Val Phe Val Ala Asn Glu Ile Gln Val Gly	
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Phe Gly Arg Val Gly Lys His Phe Trp Ala Phe Gln Leu Gln Gly Lys	
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Asp Phe Val Pro Asp Ile Val Thr Met Gly Lys Ser Ile Gly Asn Gly	
268 273 278 283	
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His Pro Val Ala Cys Val Ala Ala Thr Gln Pro Val Ala Arg Ala Phe	
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Glu Ala Thr Gly Val Glu Tyr Phe Asn Thr Phe Gly Gly Ser Pro Val	
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Ser Cys Ala Val Gly Leu Ala Val Leu Asn Val Leu Glu Lys Glu Gln	
316 321 326 331	
ctc cag gat cat gcc acc agt gta ggc agc ttc ctg atg cag ctc ctc	1299
Leu Gln Asp His Ala Thr Ser Val Gly Ser Phe Leu Met Gln Leu Leu	
332 337 342 347	
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Gly Gln Gln Lys Ile Lys His Pro Ile Val Gly Asp Val Arg Gly Val	
348 353 358 363	
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Gly Leu Phe Ile Gly Val Asp Leu Ile Lys Asp Glu Ala Thr Arg Thr	
364 369 374 379	

cca gca act gaa gag gct gcc tac ttg gta tca agg ctg aag gag aac	1443
Pro Ala Thr Glu Glu Ala Ala Tyr Leu Val Ser Arg Leu Lys Glu Asn	
380 385 390 395	
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Tyr Val Leu Leu Ser Thr Asp Gly Pro Gly Arg Asn Ile Leu Lys Phe	
396 401 406 411	
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Lys Pro Pro Met Cys Phe Ser Leu Asp Asn Ala Arg Gln Val Val Ala	
412 417 422 427	
aag ctg gat gcc att ctg act gac atg gaa gag aag gtg aga agt tgt	1587
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428 433 438 443	
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Glu Thr Leu Arg Leu Gln Pro *	
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Met Leu Ser Ser Arg Ala Glu Ala Ala Met Thr Ala	
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Ala Asp Arg Ala Ile Gln Arg Phe Leu Arg Thr Gly Ala Ala Val Arg	
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Tyr Lys Val Met Lys Asn Trp Gly Val Ile Gly Gly Ile Ala Ala Ala	
29 34 39 44	
ctt gca gca gga ata tat gtt att tgg ggt ccc att aca gaa aga aag	252
Leu Ala Ala Gly Ile Tyr Val Ile Trp Gly Pro Ile Thr Glu Arg Lys	
45 50 55 60	
aag cgt aga aaa ggg ctt gtg cct ggc ctt gtt aat tta ggg aac acc	300
Lys Arg Arg Lys Gly Leu Val Pro Gly Leu Val Asn Leu Gly Asn Thr	
61 66 71 76	
tgc ttc atg aac tcc ctg cta caa ggc ctg tct gcc tgt cct gct ttc	348
Cys Phe Met Asn Ser Leu Leu Gln Gly Leu Ser Ala Cys Pro Ala Phe	
77 82 87 92	
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Ile Gly Trp Leu Glu Glu Phe Thr Ser Gln Tyr Ser Arg Asp Gln Lys	
93 98 103 108	
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Glu Pro Pro Ser His Gln Tyr Leu Ser Leu Thr Leu Leu His Leu Leu	
109 114 119 124	
aaa gcc ttg tcc tgc caa gaa gtt act gat gat gag gtc tta cat gca	492
Lys Ala Leu Ser Cys Gln Glu Val Thr Asp Asp Glu Val Leu His Ala	
125 130 135 140	
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Ser Cys Leu Leu Asp Val Leu Arg Met Tyr Arg Trp Gln Ile Ser Ser	
141 146 151 156	
ttt gaa gaa cag gat gct cac gaa tta ttc cat gtc att acc tcg tca	588
Phe Glu Glu Gln Asp Ala His Glu Leu Phe His Val Ile Thr Ser Ser	
157 162 167 172	
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Leu Glu Asp Glu Arg Asp Arg Gln Pro Arg Val Thr His Leu Phe Asp	
173 178 183 188	
gtg cat tcc ctg gag cag cag tca gaa ata act ccc aaa caa att acc	684
Val His Ser Leu Glu Gln Gln Ser Glu Ile Thr Pro Lys Gln Ile Thr	
189 194 199 204	
tgc cgc aca aga ggg tca cct cac ccc aca tcc aat cac tgg aag tct	732
Cys Arg Thr Arg Gly Ser Pro His Pro Thr Ser Asn His Trp Lys Ser	
205 210 215 220	
caa cat cct ttt cat gga aga ctc act agt aat atg gtc tgc aaa cac	780
Gln His Pro Phe His Gly Arg Leu Thr Ser Asn Met Val Cys Lys His	
221 226 231 236	
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Cys Glu His Gln Ser Pro Val Arg Phe Asp Thr Phe Asp Ser Leu Ser	

237	242	247	252	
cta agt att cca gcc gcc aca tgg ggt cac cca ttg acc ctg gac cac				876
Leu Ser Ile Pro Ala Ala Thr Trp Gly His Pro Leu Thr Leu Asp His				
253	258	263	268	
tgc ctt cac cac ttc atc tca tca gaa tca gtg cgg gat gtt gtg tgt				924
Cys Leu His His Phe Ile Ser Ser Glu Ser Val Arg Asp Val Val Cys				
269	274	279	284	
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Asp Asn Cys Thr Lys Ile Glu Ala Lys Gly Thr Leu Asn Gly Glu Lys				
285	290	295	300	
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Val Glu His Gln Arg Thr Thr Phe Val Lys Gln Leu Lys Leu Gly Lys				
301	306	311	316	
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317	322	327	332	
cac ggc acg cct ctg aag cgg cat gag cac gtg cag ttc aat gag ttc				1116
His Gly Thr Pro Leu Lys Arg His Glu His Val Gln Phe Asn Glu Phe				
333	338	343	348	
ctg atg atg gac att tac aag tac cac ctc ctt gga cat aaa cct agt				1164
Leu Met Met Asp Ile Tyr Lys Tyr His Leu Leu Gly His Lys Pro Ser				
349	354	359	364	
caa cac aac cct aaa ctg aac aag aac cca ggg cct aca ctg gag ctg				1212
Gln His Asn Pro Lys Leu Asn Lys Asn Pro Gly Pro Thr Leu Glu Leu				
365	370	375	380	
cag gat ggg ccg gga gcc cca cac cag ttc tga atcagcca ggggccccca				1263
Gln Asp Gly Pro Gly Ala Pro His Gln Phe *				
381	386	391		
aaacacagat ttttatgaat ggcgcctgct ccccatcttt attgccaaacg ctgtcagcgc				1323
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ctccaaaccg cacaccaga cgcacacgca taccacagcg cccggcagtt atg tat	296
Met Tyr	
1	
tct ccg ctc tgt ctc acc cag gat gaa ttt cat cct ttc atc gaa gca	344
Ser Pro Leu Cys Leu Thr Gln Asp Glu Phe His Pro Phe Ile Glu Ala	
3 8 13 18	
ctt ctg ccc cac gtc cga gcc ttt gcc tac aca tgg ttc aac ctg cag	392
Leu Leu Pro His Val Arg Ala Phe Ala Tyr Thr Trp Phe Asn Leu Gln	
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Glu Glu Glu Arg Ala Val Lys Asp Glu Leu Leu Ser Glu Lys Pro Glu	
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gtc aag cag aag tgg gca tct cga ctt ctg gca aag ttg cgg aaa gat	536
Val Lys Gln Lys Trp Ala Ser Arg Leu Leu Ala Lys Leu Arg Lys Asp	
67 72 77 82	
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Ile Arg Pro Glu Tyr Arg Glu Asp Phe Val Leu Thr Val Thr Gly Lys	
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Lys Pro Pro Cys Cys Val Leu Ser Asn Pro Asp Gln Lys Gly Lys Met	
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Arg Arg Ile Asp Cys Leu Arg Gln Ala Asp Lys Val Trp Arg Leu Asp	
115 120 125 130	
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Leu Val Met Val Ile Leu Phe Lys Gly Ile Pro Leu Glu Ser Thr Asp	
131 136 141 146	
ggc gag cgc ctt gta aag tcc cca caa tgc tct aat cca ggc ctc tgt	776
Gly Glu Arg Leu Val Lys Ser Pro Gln Cys Ser Asn Pro Gly Leu Cys	
147 152 157 162	

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Val	Gln	Pro	His	His	Ile	Gly	Val	Ser	Val	Lys	Glu	Leu	Asp	Leu	Tyr	
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Leu	Ala	Tyr	Phe	Val	His	Ala	Ala	Asp	Ser	Ser	Gln	Ser	Glu	Ser	Pro	
179					184					189					194	
agc	cag	cca	agt	gac	gct	gac	att	aag	gac	cag	cca	gaa	aat	gga	cat	920
Ser	Gln	Pro	Ser	Asp	Ala	Asp	Ile	Lys	Asp	Gln	Pro	Glu	Asn	Gly	His	
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Leu	Gly	Phe	Gln	Asp	Ser	Phe	Val	Thr	Ser	Gly	Val	Phe	Ser	Val	Thr	
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Glu	Leu	Val	Arg	Val	Ser	Gln	Thr	Pro	Ile	Ala	Ala	Gly	Thr	Gly	Pro	
227					232					237					242	
aat	ttt	tct	ctc	tca	gat	ttg	gaa	agt	tct	tca	tac	tac	agc	atg	agt	1064
Asn	Phe	Ser	Leu	Ser	Asp	Leu	Glu	Ser	Ser	Ser	Tyr	Tyr	Ser	Met	Ser	
243					248					253					258	
cca	gga	gca	atg	agg	agg	tct	tta	ccc	agc	aca	tcc	tct	acg	agc	tcc	1112
Pro	Gly	Ala	Met	Arg	Arg	Ser	Leu	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Ser	
259					264					269					274	
aca	aag	cgc	ctc	aag	tct	gtg	gag	gat	gaa	atg	gac	agt	cct	ggg	gag	1160
Thr	Lys	Arg	Leu	Lys	Ser	Val	Glu	Asp	Glu	Met	Asp	Ser	Pro	Gly	Glu	
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gag	cca	ttt	tat	aca	ggc	caa	ggg	cgc	tcc	cca	gga	agt	ggc	agt	cag	1208
Glu	Pro	Phe	Tyr	Thr	Gly	Gln	Gly	Arg	Ser	Pro	Gly	Ser	Gly	Ser	Gln	
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Ser	Ser	Gly	Trp	His	Glu	Val	Glu	Pro	Gly	Met	Pro	Ser	Pro	Thr	Thr	
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ctg	aag	aag	tcg	gag	aag	tct	ggg	ttc	agc	agc	ccc	tcc	cct	tca	cag	1304
Leu	Lys	Lys	Ser	Glu	Lys	Ser	Gly	Phe	Ser	Ser	Pro	Ser	Pro	Ser	Gln	
323					328					333					338	
acc	tcc	tcc	ctg	gga	acg	gcg	ttc	aca	cag	cat	cac	cga	cct	gtc	att	1352
Thr	Ser	Ser	Leu	Gly	Thr	Ala	Phe	Thr	Gln	His	His	Arg	Pro	Val	Ile	
339					344					349					354	
aca	gga	ccc	aga	gca	agt	cca	cat	gca	aca	cca	tcg	act	ctt	cat	ttc	1400
Thr	Gly	Pro	Arg	Ala	Ser	Pro	His	Ala	Thr	Pro	Ser	Thr	Leu	His	Phe	
355					360					365					370	
ccg	aca	tca	ccc	att	atc	cag	cag	cct	ggg	cct	tac	ttc	tca	cac	cca	1448
Pro	Thr	Ser	Pro	Ile	Ile	Gln	Gln	Pro	Gly	Pro	Tyr	Phe	Ser	His	Pro	
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gcc atc cgc tat cac cct cag gag acg ctg aaa gaa ttt gtc caa ctt	1496
Ala Ile Arg Tyr His Pro Gln Glu Thr Leu Lys Glu Phe Val Gln Leu	
387 392 397 402	
gtc tgc cct gat gct ggt cag cag gct gga cag ccc aat ggg agc agc	1544
Val Cys Pro Asp Ala Gly Gln Gln Ala Gly Gln Pro Asn Gly Ser Ser	
403 408 413 418	
caa ggc aag gtg cac aac cca ttc ctt ccc acc cca atg ttg cca ccg	1592
Gln Gly Lys Val His Asn Pro Phe Leu Pro Thr Pro Met Leu Pro Pro	
419 424 429 434	
cca ccg cca cca ccg atg gcc agg cct gtg cct ctg ccg gtg cca gac	1640
Pro Pro Pro Pro Pro Met Ala Arg Pro Val Pro Leu Pro Val Pro Asp	
435 440 445 450	
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Thr Lys Pro Pro Thr Thr Ser Thr Glu Gly Gly Ala Ala Ser Pro Thr	
451 456 461 466	
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Ser Pro Thr Tyr Ser Thr Pro Ser Thr Ser Pro Ala Asn Arg Phe Val	
467 472 477 482	
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Ser Val Gly Pro Arg Asp Pro Ser Phe Val Asn Ile Pro Gln Gln Thr	
483 488 493 498	
cag tcc tgg tac ctg gga taa aa gttgcagcgt cccaccatcc accagacaga	1837
Gln Ser Trp Tyr Leu Gly *	
499 504	
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 <213> Homo sapiens

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 <222> (265) .. (2067)

<400> 94

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ctggccacct	gccatgccct	cagccggctc	caggacaccc	ccgtgggcga	ccccatggac	180
ttgaagatgg	tggagtctac	tggctgggtc	ctggaggaag	agccggctgc	agactcagca	240
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			Met Arg Pro Pro Leu Trp Glu Pro Gln			
			1 5			
ctg cag gca atg gag gag ccc ccg gtg cca gtc agc gtc ctc cac cgc						339
Leu Gln Ala Met Glu Glu Pro Pro Val Pro Val Ser Val Leu His Arg						
10 15 20 25						
ttc ccc ttc tct tgc gct ctg cag cgc atg agt gtg gtg gtg gcg tgg						387
Phe Pro Phe Ser Ser Ala Leu Gln Arg Met Ser Val Val Val Ala Trp						
26 31 36 41						
cca ggg gcc act cag ccc gag gcc tac gtc aaa ggc tcc ccg gag ctg						435
Pro Gly Ala Thr Gln Pro Glu Ala Tyr Val Lys Gly Ser Pro Glu Leu						
42 47 52 57						
gtg gca ggg ctc tgc aac ccc gag aca gtg ccc acc gac ttc gcc cag						483
Val Ala Gly Leu Cys Asn Pro Glu Thr Val Pro Thr Asp Phe Ala Gln						
58 63 68 73						
atg ctg cag agc tat aca gct gct ggc tac cgt gtc gtg gcc ctg gcc						531
Met Leu Gln Ser Tyr Thr Ala Ala Gly Tyr Arg Val Val Ala Leu Ala						
74 79 84 89						
agc aag cca ctg ccc act gtg ccc agc ctg gag gca gcc cag caa ctg						579
Ser Lys Pro Leu Pro Thr Val Pro Ser Leu Glu Ala Ala Gln Gln Leu						
90 95 100 105						
acg agg gac act gtg gaa gga gac ctg agc ctc ctg ggg ctg ctg gtc						627
Thr Arg Asp Thr Val Glu Gly Asp Leu Ser Leu Leu Gly Leu Leu Val						
106 111 116 121						
atg agg aac cta ctg aag ccg cag aca acg cca gtt atc cag gct ctg						675
Met Arg Asn Leu Leu Lys Pro Gln Thr Thr Pro Val Ile Gln Ala Leu						
122 127 132 137						
cga agg acc cgc atc cgc gcc gtc atg gtg aca ggg gac aac ctg cag						723
Arg Arg Thr Arg Ile Arg Ala Val Met Val Thr Gly Asp Asn Leu Gln						
138 143 148 153						
aca gcg gtg act gtg gcc ccg ggc tgt ggc atg gtg gcc ccc cag gag						771
Thr Ala Val Thr Val Ala Arg Gly Cys Gly Met Val Ala Pro Gln Glu						
154 159 164 169						
cat ctg atc atc gtc cac gcc acc cac cct gag ccg ggt cag cct gcc						819
His Leu Ile Ile Val His Ala Thr His Pro Glu Arg Gly Gln Pro Ala						
170 175 180 185						
tct ctc gag ttc ctg ccg atg gag tcc ccc aca gcc gtg aat ggc gtt						867

Ser	Leu	Glu	Phe	Leu	Pro	Met	Glu	Ser	Pro	Thr	Ala	Val	Asn	Gly	Val	
186					191					196					201	
aag	gat	cct	gac	cag	gct	gca	agc	tac	acc	gtg	gag	cca	gac	ccc	cga	915
Lys	Asp	Pro	Asp	Gln	Ala	Ala	Ser	Tyr	Thr	Val	Glu	Pro	Asp	Pro	Arg	
202					207					212					217	
tcc	agg	cac	ctg	gcc	ctc	agc	ggg	ccc	acc	ttt	ggg	atc	att	gtg	aag	963
Ser	Arg	His	Leu	Ala	Leu	Ser	Gly	Pro	Thr	Phe	Gly	Ile	Ile	Val	Lys	
218					223					228					233	
cac	ttc	ccc	aag	ctg	ctg	ccc	aag	gtc	ctg	gtc	cag	ggc	act	gtc	ttt	1011
His	Phe	Pro	Lys	Leu	Leu	Pro	Lys	Val	Leu	Val	Gln	Gly	Thr	Val	Phe	
234					239					244					249	
gcc	cgc	atg	gcc	cct	gag	cag	aag	aca	gag	ctg	gtg	tgc	gag	cta	cag	1059
Ala	Arg	Met	Ala	Pro	Glu	Gln	Lys	Thr	Glu	Leu	Val	Cys	Glu	Leu	Gln	
250					255					260					265	
aag	ctt	cag	tac	tgc	gtg	ggc	atg	tgc	gga	gac	ggg	gcc	aat	gac	tgt	1107
Lys	Leu	Gln	Tyr	Cys	Val	Gly	Met	Cys	Gly	Asp	Gly	Ala	Asn	Asp	Cys	
266					271					276					281	
ggg	gcc	ctg	aag	gcg	gct	gat	gtc	ggc	atc	tcg	ctg	tcc	cag	gca	gaa	1155
Gly	Ala	Leu	Lys	Ala	Ala	Asp	Val	Gly	Ile	Ser	Leu	Ser	Gln	Ala	Glu	
282					287					292					297	
gcc	tca	gtg	gtc	tca	ccc	ttc	acc	tcg	agc	atg	gcc	agt	att	gag	tgc	1203
Ala	Ser	Val	Val	Ser	Pro	Phe	Thr	Ser	Ser	Met	Ala	Ser	Ile	Glu	Cys	
298					303					308					313	
gtg	ccc	atg	gtc	atc	agg	gag	ggg	cgc	tgt	tcc	ctt	gac	act	tcg	ttc	1251
Val	Pro	Met	Val	Ile	Arg	Glu	Gly	Arg	Cys	Ser	Leu	Asp	Thr	Ser	Phe	
314					319					324					329	
agc	gtc	ttc	aag	tac	atg	gct	ctg	tac	agc	ctg	acc	cag	ttc	atc	tcc	1299
Ser	Val	Phe	Lys	Tyr	Met	Ala	Leu	Tyr	Ser	Leu	Thr	Gln	Phe	Ile	Ser	
330					335					340					345	
gtc	ctg	atc	ctc	tac	acg	atc	aac	acc	aac	ctg	ggg	gac	ctg	cag	ttc	1347
Val	Leu	Ile	Leu	Tyr	Thr	Ile	Asn	Thr	Asn	Leu	Gly	Asp	Leu	Gln	Phe	
346					351					356					361	
ctg	gcc	atc	gac	ctg	gtc	atc	acc	acc	aca	gtg	gca	gtg	ctc	atg	agc	1395
Leu	Ala	Ile	Asp	Leu	Val	Ile	Thr	Thr	Thr	Val	Ala	Val	Leu	Met	Ser	
362					367					372					377	
cgc	acg	ggg	cca	gcg	ctg	gtc	ctg	gga	cgg	gtg	cgg	cca	ccg	ggg	gcg	1443
Arg	Thr	Gly	Pro	Ala	Leu	Val	Leu	Gly	Arg	Val	Arg	Pro	Pro	Gly	Ala	
378					383					388					393	
ctg	ctc	agc	gtg	ccc	gtg	ctc	agc	agc	ctg	ctg	ctg	cag	atg	gtc	ctg	1491
Leu	Leu	Ser	Val	Pro	Val	Leu	Ser	Ser	Leu	Leu	Leu	Gln	Met	Val	Leu	
394					399					404					409	
gtg	acc	ggc	gtg	cag	cta	ggg	ggc	tac	ttc	ctg	acc	ctg	gcc	cag	cca	1539
Val	Thr	Gly	Val	Gln	Leu	Gly	Gly	Tyr	Phe	Leu	Thr	Leu	Ala	Gln	Pro	

410	415	420	425	
tgg ttc gtg cct ctg aac agg aca gtg gcc gca cca gac aac ctg ccc				1587
Trp Phe Val Pro Leu Asn Arg Thr Val Ala Ala Pro Asp Asn Leu Pro				
426	431	436	441	
aac tac gag aac acc gtg gtc ttc tct ctg tcc agc ttc cag tac ctc				1635
Asn Tyr Glu Asn Thr Val Val Phe Ser Leu Ser Ser Phe Gln Tyr Leu				
442	447	452	457	
atc ctg gct gca gcc gtg tcc aag ggg gcg ccc ttc cgc cgg ccg ctc				1683
Ile Leu Ala Ala Ala Val Ser Lys Gly Ala Pro Phe Arg Arg Pro Leu				
458	463	468	473	
tac acc aat gag cgt gct aga cca gtg cct ccc cgc ctg cct gcg ccg				1731
Tyr Thr Asn Glu Arg Ala Arg Pro Val Pro Pro Arg Leu Pro Ala Pro				
474	479	484	489	
cct ccg gcc caa gcg ggc ctc caa gaa gcg ctt caa gca gct gga acg				1779
Pro Pro Ala Gln Ala Gly Leu Gln Glu Ala Leu Gln Ala Ala Gly Thr				
490	495	500	505	
aga gct ggc cga gca gcc ctg gcc gcc gct gcc cgc cgg ccc cct gag				1827
Arg Ala Gly Arg Ala Ala Leu Ala Ala Ala Ala Arg Arg Pro Pro Glu				
506	511	516	521	
gta gtg cag gcc cac ggg cac ccc aga cac tgg aac tcc ctg cct ctg				1875
Val Val Gln Ala His Gly His Pro Arg His Trp Asn Ser Leu Pro Leu				
522	527	532	537	
agc cac caa ctg gac ccc tct cca gca aca cca ccg cca cca cct ccc				1923
Ser His Gln Leu Asp Pro Ser Pro Ala Thr Pro Pro Pro Pro Pro Pro				
538	543	548	553	
aca tcc ctg agg ttg gcg act gtc tac act cct ccc ccg aga cca ccc				1971
Thr Ser Leu Arg Leu Ala Thr Val Tyr Thr Pro Pro Pro Arg Pro Pro				
554	559	564	569	
cca ccc tgg gga agc gtt gac tac tgt ccc cta cct tgg acc atc ccg				2019
Pro Pro Trp Gly Ser Val Asp Tyr Cys Pro Leu Pro Trp Thr Ile Pro				
570	575	580	585	
cgt agg ggt ggc agc ccc cag ctc ccc tca gtg ctg ctg tca gtg tag				2067
Arg Arg Gly Gly Ser Pro Gln Leu Pro Ser Val Leu Leu Ser Val *				
586	591	596	601	
caaataaagt catgatattt tcctggcaaa aaaaaaaaaa				2106

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 <211> 1555
 <212> DNA
 <213> Homo sapiens

<220>

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 <222> (808) .. (966)

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 <222> (1) ... (1555)
 <223> n = a,t,c or g

<400> 95

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ccctgcatct ggagccaccc acctggagga actcatcggg cttcctctgt agacgggaaa      180
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ttgcaatgtt ctgagcccac ctgtcctcgg gctagtccca ttttcaaaag ttctgagtac      360
gcaggtgaga agacaccccc acaaaacccc aaaactagcc ttaggctgtt tttccccaac      420
acaacgcacc tccacacccc acaccgccag cagcccacct gggtagccaa agtgagctgc      480
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aggtgcttgt gggattctgc tggctggagc caggaggtaa gtgtgaacag ggaggccaaa      720
gatgaaagtt atctgaaaga gcccgtaccc cctataaaca cggcagagga atgtcttaag      780
agccaccaac agtaattccc tttccgg      atg tta aca ggt tat ttg tat ctt      831
                                Met Leu Thr Gly Tyr Leu Tyr Leu
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atg tgg cgt cgt aaa gca ttc tgg agt ggc aca caa cgt cat ccc ctt      879
Met Trp Arg Arg Lys Ala Phe Trp Ser Gly Thr Gln Arg His Pro Leu
  9                14                19                24

ccc ggt ggt ctg aag agg agg agg aga cca ggg agg ggt cct tgg cca      927
Pro Gly Gly Leu Lys Arg Arg Arg Arg Pro Gly Arg Gly Pro Trp Pro
  25                30                35                40

gcc cct ggc ggc caa ggg gtg ggt cct tct gct cta tag aaggcaggaa      976
Ala Pro Gly Gly Gln Gly Val Gly Pro Ser Ala Leu *
  41                46                51

gcccgccagc taaccgcccg ggtcaggggg agcaggcctg atctctccca agcctgtgac      1036
cgaggtcctg cctgatgtcc aaggggcccc tgtgccagta ccccaacttc ccacgcccc      1096
cagccttcct cacctccaga atcagccgcc caggtgcagc actatctcct ttctttttct      1156

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aaa ggc ctt ggc ctc ctc cag ctg ggt ctg ctc ctt cct ttg aac ccc	96
Lys Gly Leu Gly Leu Leu Gln Leu Gly Leu Leu Leu Pro Leu Asn Pro	
17 22 27 32	
atc ggt acc tat gcc cac acc ttt cag agc ttt cct gat cag tgt caa	144
Ile Gly Thr Tyr Ala His Thr Phe Gln Ser Phe Pro Asp Gln Cys Gln	
33 38 43 48	
cat gct gct ctt cct ctt aca aaa tgt acc atc aat aca gcc cag gca	192
His Ala Ala Leu Pro Leu Thr Lys Cys Thr Ile Asn Thr Ala Gln Ala	
49 54 59 64	
cat ggc tcc cac aaa gct agc cac tta tat agt atg ggt cac atc aaa	240
His Gly Ser His Lys Ala Ser His Leu Tyr Ser Met Gly His Ile Lys	
65 70 75 80	
aat gac tcc agc aca atc att cat aca gac ttc tct cac act aaa cct	288
Asn Asp Ser Ser Thr Ile Ile His Thr Asp Phe Ser His Thr Lys Pro	
81 86 91 96	
tta aac aag caa ggt tca gta gct aca gaa ctc tcc atc atc atc atc	336
Leu Asn Lys Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile Ile Ile	
97 102 107 112	
atc atc atc tgg ttg ctt ttg gca agg ttc agt agc tac aga act ctc	384
Ile Ile Ile Trp Leu Leu Leu Ala Arg Phe Ser Ser Tyr Arg Thr Leu	

113		118		123		128	
ctt cat cat cat cat cat ctg gtt gct ttt ggc aag caa ggt tca gta	432						
Leu His His His His His Leu Val Ala Phe Gly Lys Gln Gly Ser Val							
129		134		139		144	
gct aca gaa ctc tcc tcc tcc tcc tcc tcc tcc tca tca tca tca tca	480						
Ala Thr Glu Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser							
145		150		155		160	
tct ggt tgc ttt cag caa ggt tca gta gct aca gaa ctc tcc atc atc	528						
Ser Gly Cys Phe Gln Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile							
161		166		171		176	
atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg gca	576						
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala							
177		182		187		192	
agg ttc agt agc tac aga act ctc ctc ctc ctc ctc ctc ctc ctc ctc	624						
Arg Phe Ser Ser Tyr Arg Thr Leu Leu Leu Leu Leu Leu Leu Leu Leu							
193		198		203		208	
ctc ctc atc atc atc atc atc atc tgg ttg ctt tta gca agg ttc agt	672						
Leu Leu Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala Arg Phe Ser							
209		214		219		224	
agc tac aga act ctc ctc ctc ctc ctc ctc ctc ctc atc atc atc atc	720						
Ser Tyr Arg Thr Leu Leu Leu Leu Leu Leu Leu Leu Leu Ile Ile Ile Ile							
225		230		235		240	
atc tgg ttg ctt tca gca agg ttc agt agc tac aga act ctc ctt cat	768						
Ile Trp Leu Leu Ser Ala Arg Phe Ser Ser Tyr Arg Thr Leu Leu His							
241		246		251		256	
cat cat caa cat cat cat ctg gtt gct ttt ggc aag caa ggt tca gta	816						
His His Gln His His His Leu Val Ala Phe Gly Lys Gln Gly Ser Val							
257		262		267		272	
gct aca gaa ctc tcc tcc tcc tcc tcc tcc tcc tca tca tca tca tca	864						
Ala Thr Glu Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser							
273		278		283		288	
tct ggt tgc ttt cag caa ggt tca gta gct aca gaa ctc tcc atc atc	912						
Ser Gly Cys Phe Gln Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile							
289		294		299		304	
atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg gca	960						
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala							
305		310		315		320	
agg ttc agt agc tac aga act ctc ctt cat cat cat cat cat cat cat	1008						
Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His His							
321		326		331		336	
ctg gtt gct ttt ggc aag caa ggt tca gta gct aca gaa ctc tcc atc	1056						
Leu Val Ala Phe Gly Lys Gln Gly Ser Val Ala Thr Glu Leu Ser Ile							
337		342		347		352	

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Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu	
353 358 363 368	
gca agg ttc agt agc tac aga act ctc ctt cat cat cat cat cat cat	1152
Ala Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His	
369 374 379 384	
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His Leu Val Ala Phe Gly Lys Ala Leu Ala Arg Ile Ile Trp Leu Tyr	
385 390 395 400	
cga aac acc tat tcc ata ggt aac caa ttc cag tca aaa atg cca gag	1248
Arg Asn Thr Tyr Ser Ile Gly Asn Gln Phe Gln Ser Lys Met Pro Glu	
401 406 411 416	
tat tac tcc tca acc caa tgc cct atc tcc tta gtg gat tat aaa ctt	1296
Tyr Tyr Ser Ser Thr Gln Cys Pro Ile Ser Leu Val Asp Tyr Lys Leu	
417 422 427 432	
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Thr Thr Thr Thr Cys Leu Leu Trp Ile Gln Ser Pro Pro Lys Ser Glu	
433 438 443 448	
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Ser Ser Leu Pro Gly Tyr Lys Pro Pro Ser Pro Gly Ser Ser Met Leu	
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Asp Ser Ser Leu Thr Ser Thr Ser Ser Asp His Trp Val Ala Leu Leu	
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Ala Val Leu Gln Pro Ser Ser Arg Ser Asp Thr His Pro Leu Ser Gly	
481 486 491 496	
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Glu Pro Arg Pro Leu Leu Tyr Pro Leu Pro Asp Pro Ala Val Pro Phe	
497 502 507 512	
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Trp Thr Leu Arg Thr Pro Leu Ser Pro Arg Thr Pro Tyr Arg Leu Phe	
513 518 523 528	
ctc ctc cac tcc cac aac tcc gcc cga gct cca ctg cgc ctg tgc ggc	1632
Leu Leu His Ser His Asn Ser Ala Arg Ala Pro Leu Arg Leu Cys Gly	
529 534 539 544	
caa cga ggc cgc gcg cag gcg atc ggg gca gaa gag ctt ccg gtt cct	1680
Gln Arg Gly Arg Ala Gln Ala Ile Gly Ala Glu Glu Leu Pro Val Pro	
545 550 555 560	
gct gtc aat aag acg tgg acc tgc gag ccg ggg caa aag ggc ttc cgg	1728
Ala Val Asn Lys Thr Trp Thr Cys Glu Pro Gly Gln Lys Gly Phe Arg	
561 566 571 576	

tct gcg gga aac tgg agg cta gcg gtg ggc gtg gac cgt cga ggt gac	1776
Ser Ala Gly Asn Trp Arg Leu Ala Val Gly Val Asp Arg Arg Gly Asp	
577 582 587 592	
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Trp Arg Leu Ser Asp Leu Leu Leu Phe Ala Asp Gln Ala Ala Val Gly	
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aat gac gga tgc cca gac cct gtg ggc gga gta aag gaa tca tgc act	1872
Asn Asp Gly Cys Pro Asp Pro Val Gly Gly Val Lys Glu Ser Cys Thr	
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Asp Thr Arg Thr Leu Thr Glu Gly Arg Val Arg Leu Arg Ala Pro His	
625 630 635 640	
ctc gta gcc gaa agg agc gcg ttc cgg ggc agg cct ccg ggt act tcc	1968
Leu Val Ala Glu Arg Ser Ala Phe Arg Gly Arg Pro Pro Gly Thr Ser	
641 646 651 656	
cgc aga gga ccg ggc ttt ata ctc ttt gct cct ttt cct ccc cta aaa	2016
Arg Arg Gly Pro Gly Phe Ile Leu Phe Ala Pro Phe Pro Pro Leu Lys	
657 662 667 672	
gct gtg ctt gac ttc ttg gtg tac atg gat aaa ggc tac aat gaa gga	2064
Ala Val Leu Asp Phe Leu Val Tyr Met Asp Lys Gly Tyr Asn Glu Gly	
673 678 683 688	
aac att tta gaa ata ctc gcc tac ctg gta gtc cac aga tct tta gat	2112
Asn Ile Leu Glu Ile Leu Ala Tyr Leu Val Val His Arg Ser Leu Asp	
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ttc att ggc cag caa aat ctc aaa gga aga gaa aga gag aac aag aga	2160
Phe Ile Gly Gln Gln Asn Leu Lys Gly Arg Glu Arg Glu Asn Lys Arg	
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	Met Ser Trp Pro Pro Ser Gly Glu Ile Ala Ser Pro Pro					
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gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg gcc cca gat	217					
Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val Ala Pro Asp						
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Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser						
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acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc ccc cag tct	313					
Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly Pro Gln Ser						
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ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc tct gtc aaa	361					
Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys Ser Val Lys						
62 67 72 77						
gac cag acg cca ctc caa ctt tct gta gaa gat acc acc tct cca aat	409					
Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr Ser Pro Asn						
78 83 88 93						
acc aag ccg tgc cca cct act ccc acc acc cca gaa aca tcc cct cct	457					
Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr Ser Pro Pro						
94 99 104 109						
cct cct cct cct cct cct tca tct act cct tgt tca gct cac ctg acc	505					
Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala His Leu Thr						
110 115 120 125						
ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tgc gaa cag aaa	553					
Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser Glu Gln Lys						
126 131 136 141						
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Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu His Ile Ala						
142 147 152 157						
ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc gac ggg gcc	649					
Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro Asp Gly Ala						
158 163 168 173						
acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag ctg agc tgc	697					
Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu Leu Ser Cys						
174 179 184 189						
ctg cag gac gcc ata gac cac tca gct ttc atc atc cta ctt ctc acc	745					
Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu Leu Leu Thr						
190 195 200 205						

tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac caa gcc atg	793
Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn Gln Ala Met	
206 211 216 221	
atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc atc ccc ttc	841
Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val Ile Pro Phe	
222 227 232 237	
ctg ccc ctg gag agc tcc ccg gcc cgg ctc agc tcc gac acg gcc agc	889
Leu Pro Leu Glu Ser Ser Pro Ala Arg Leu Ser Ser Asp Thr Ala Ser	
238 243 248 253	
ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag atc ttc gcc	937
Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln Ile Phe Ala	
254 259 264 269	
agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag gcc cga aag	985
Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln Ala Arg Lys	
270 275 280 285	
gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg gaa cag agc	1033
Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg Glu Gln Ser	
286 291 296 301	
caa cac ctg gat ggt gag cgg atg cag gcg gcg gca ctg aac gca gcc	1081
Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu Asn Ala Ala	
302 307 312 317	
tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca cag atg gag	1129
Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala Gln Met Glu	
318 323 328 333	
cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg act ggg gcg	1177
Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly Thr Gly Ala	
334 339 344 349	
ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc ctg gga gcc	1225
Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro Leu Gly Ala	
350 355 360 365	
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Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro Pro Pro Leu	
366 371 376 381	
cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca cag cca gca	1321
His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro Gln Pro Ala	
382 387 392 397	
gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc ttc cct acg	1369
Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala Phe Pro Thr	
398 403 408 413	
gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc ctc att atc	1417
Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro Leu Ile Ile	
414 419 424 429	

cac cac gca cag atg gta cag ctg ggg ctg aac aac cac atg tgg aac	1465
His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His Met Trp Asn	
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cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag gca gaa tga	1513
Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu Ala Glu *	
446 451 456 461	
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ccatagagca ccccggtctg ccctgtgccc tgtggacagt ggaagatgag gtcattctgcc	1633
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attaagaagg aaatatctcc attgttcatt ggc atg gaa aaa tgt tca gtg gga	174
Met Glu Lys Cys Ser Val Gly	
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gga tta gag ttg act gaa cag act cct gct tta tta ggg aat atg gcc	222
Gly Leu Glu Leu Thr Glu Gln Thr Pro Ala Leu Leu Gly Asn Met Ala	
8 13 18 23	
atg gca act agt ctc atg gac ata ggg gat tca ttt ggt cat cca gct	270
Met Ala Thr Ser Leu Met Asp Ile Gly Asp Ser Phe Gly His Pro Ala	
24 29 34 39	
tgt cct tta gtc agt aga tct agg aac tca cca gtg gaa gat gat gat	318
Cys Pro Leu Val Ser Arg Ser Arg Asn Ser Pro Val Glu Asp Asp Asp	
40 45 50 55	
gat gat gat gat gtt gtg ttt att gaa tct ata caa cct cct tca att	366
Asp Asp Asp Asp Val Val Phe Ile Glu Ser Ile Gln Pro Pro Ser Ile	
56 61 66 71	

tct gct cca gca ata gct gat caa aga aac ttc ata ttt gca tca tca	414
Ser Ala Pro Ala Ile Ala Asp Gln Arg Asn Phe Ile Phe Ala Ser Ser	
72 77 82 87	
aaa aat gaa aag cct caa gga aat tat tct gta att cct cct tct tca	462
Lys Asn Glu Lys Pro Gln Gly Asn Tyr Ser Val Ile Pro Pro Ser Ser	
88 93 98 103	
aga gat ttg gca tct cag aaa gga aat ata agt gag aca att gtt att	510
Arg Asp Leu Ala Ser Gln Lys Gly Asn Ile Ser Glu Thr Ile Val Ile	
104 109 114 119	
gat gat gaa gag gac ata gaa aca aat gga gga gca gag aaa aag tct	558
Asp Asp Glu Glu Asp Ile Glu Thr Asn Gly Gly Ala Glu Lys Lys Ser	
120 125 130 135	
tcc tgt ttt atc gaa tgg gga ctt cct gga act aaa aac aaa acc aac	606
Ser Cys Phe Ile Glu Trp Gly Leu Pro Gly Thr Lys Asn Lys Thr Asn	
136 141 146 151	
gat ttg gat ttc tcc act tcc agt ctt tca aga agt aag acc aag act	654
Asp Leu Asp Phe Ser Thr Ser Ser Leu Ser Arg Ser Lys Thr Lys Thr	
152 157 162 167	
gga gta aga cct ttt aac cct ggt aga atg aat gtg gca gga gac tta	702
Gly Val Arg Pro Phe Asn Pro Gly Arg Met Asn Val Ala Gly Asp Leu	
168 173 178 183	
ttt cag aat gga gaa ttt gca act cat cat agt cct gat tct tgg atc	750
Phe Gln Asn Gly Glu Phe Ala Thr His His Ser Pro Asp Ser Trp Ile	
184 189 194 199	
tcc cag tca gct tca ttt ccc agt aat cag aaa cag cca ggg gtg gat	798
Ser Gln Ser Ala Ser Phe Pro Ser Asn Gln Lys Gln Pro Gly Val Asp	
200 205 210 215	
tct tta tca cca gtg gcc tta ctt cgt aag cag aat ttc cag cct aca	846
Ser Leu Ser Pro Val Ala Leu Leu Arg Lys Gln Asn Phe Gln Pro Thr	
216 221 226 231	
gcc caa caa caa ctt act aaa cca gct aaa atc act tgt gca aat tgc	894
Ala Gln Gln Gln Leu Thr Lys Pro Ala Lys Ile Thr Cys Ala Asn Cys	
232 237 242 247	
aaa aag cct tta cag aag gga cag aca gct tat caa cga aaa gga tca	942
Lys Lys Pro Leu Gln Lys Gly Gln Thr Ala Tyr Gln Arg Lys Gly Ser	
248 253 258 263	
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Ala His Leu Phe Cys Ser Thr Thr Cys Leu Ser Ser Phe Ser His Lys	
264 269 274 279	
cgt act caa aac aca cga agc ata ata tgt aaa aaa gat gca tct aca	1038
Arg Thr Gln Asn Thr Arg Ser Ile Ile Cys Lys Lys Asp Ala Ser Thr	
280 285 290 295	
aag aag gct aat gtc att ctt cca gta gaa tca agc aaa tcc ttc caa	1086

Lys	Lys	Ala	Asn	Val	Ile	Leu	Pro	Val	Glu	Ser	Ser	Lys	Ser	Phe	Gln	
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gaa	ttt	tat	agt	aca	tct	tgt	ttg	tct	ccc	tgt	gaa	aac	aac	tgg	aat	1134
Glu	Phe	Tyr	Ser	Thr	Ser	Cys	Leu	Ser	Pro	Cys	Glu	Asn	Asn	Trp	Asn	
312					317					322					327	
ctt	aaa	aaa	gga	gtt	ttt	aat	aag	tca	aga	tgt	aca	att	tgt	agt	aaa	1182
Leu	Lys	Lys	Gly	Val	Phe	Asn	Lys	Ser	Arg	Cys	Thr	Ile	Cys	Ser	Lys	
328					333					338					343	
tta	gca	gag	gtc	tgg	att	ttt	ata	cct	aag	ttg	ttg	ttt	agg	cta	aca	1230
Leu	Ala	Glu	Val	Trp	Ile	Phe	Ile	Pro	Lys	Leu	Leu	Phe	Arg	Leu	Thr	
344					349					354					359	
gtg	ata	att	tta	act	ttt	aag	tgc	tat	tat	gta	ctc	ttt	cat	cta	cat	1278
Val	Ile	Ile	Leu	Thr	Phe	Lys	Cys	Tyr	Tyr	Val	Leu	Phe	His	Leu	His	
360					365					370					375	
aat	gca	cgt	gtt	ctg	gat	gta	taa	catgaagctg	aaaggaagaa	taaggatatg						1332
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attaagaagg	aaatatctcc	attgttcatt	ggc	atg	gaa	aaa	174
				Met	Glu	Lys	
				1		5	
gga	tta	gag	ttg	act	gaa	cag	222
Gly	Leu	Glu	Leu	Thr	Glu	Gln	
8				13		18	23
atg	gca	act	agt	ctc	atg	gac	270
Met	Ala	Thr	Ser	Leu	Met	Asp	
24				29		34	39
tgt	cct	tta	gtc	agt	aga	tct	318
Cys	Pro	Leu	Val	Ser	Arg	Ser	
40				45		50	55

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Asp Asp Asp Asp Val Val Phe Ile Glu Ser Ile Gln Pro Pro Ser Ile	
56 61 66 71	
tct gct cca gca ata gct gat caa aga aac ttc ata ttt gca tca tca	414
Ser Ala Pro Ala Ile Ala Asp Gln Arg Asn Phe Ile Phe Ala Ser Ser	
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aaa aat gaa aag cct caa gga aat tat tct gta att cct cct tct tca	462
Lys Asn Glu Lys Pro Gln Gly Asn Tyr Ser Val Ile Pro Pro Ser Ser	
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Arg Asp Leu Ala Ser Gln Lys Gly Asn Ile Ser Glu Thr Ile Val Ile	
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Asp Asp Glu Glu Asp Ile Glu Thr Asn Gly Gly Ala Glu Lys Lys Ser	
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tcc tgt ttt atc gaa tgg gga ctt cct gga act aaa aac aaa acc aac	606
Ser Cys Phe Ile Glu Trp Gly Leu Pro Gly Thr Lys Asn Lys Thr Asn	
136 141 146 151	
gat ttg gat ttc tcc act tcc agt ctt tca aga agt aag acc aag act	654
Asp Leu Asp Phe Ser Thr Ser Ser Leu Ser Arg Ser Lys Thr Lys Thr	
152 157 162 167	
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Gly Val Arg Pro Phe Asn Pro Gly Arg Met Asn Val Ala Gly Asp Leu	
168 173 178 183	
ttt cag aat gga gaa ttt gca act cat cat agt cct gat gat gca tct	750
Phe Gln Asn Gly Glu Phe Ala Thr His His Ser Pro Asp Asp Ala Ser	
184 189 194 199	
aca aag aag gct aat gtc att ctt cca gta gaa tca agc aaa tcc ttc	798
Thr Lys Lys Ala Asn Val Ile Leu Pro Val Glu Ser Ser Lys Ser Phe	
200 205 210 215	
caa gaa ttt tat agg aca tct tgt ttg tct ccc tgt gaa aac aac tgg	846
Gln Glu Phe Tyr Arg Thr Ser Cys Leu Ser Pro Cys Glu Asn Asn Trp	
216 221 226 231	
aat ctt aaa aaa gga gtt ttt aat aag tca aga tgt aca att tgt agt	894
Asn Leu Lys Lys Gly Val Phe Asn Lys Ser Arg Cys Thr Ile Cys Ser	
232 237 242 247	
aaa tta gca gag gtc tgg att ttt ata cct aag ttg ttg ttt agg cta	942
Lys Leu Ala Glu Val Trp Ile Phe Ile Pro Lys Leu Leu Phe Arg Leu	
248 253 258 263	
aca gtg ata att tta act ttt aag tgc tat tat gga ctc ttt cat cta	990
Thr Val Ile Ile Leu Thr Phe Lys Cys Tyr Tyr Gly Leu Phe His Leu	
264 269 274 279	

cat aat gca cgt gtt ctg gat gta taa catga agctgaaagg aagaataagg 1042
 His Asn Ala Arg Val Leu Asp Val *
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 Tyr His Pro Phe Leu Pro His Arg Ala Pro Asp Phe Ala Met Ser Ala
 17 22 27 32

gtg ctg ggt cac cag ccg ccg ttc ttc ccc gcg ctg acg ctg cct ccc 144
 Val Leu Gly His Gln Pro Pro Phe Phe Pro Ala Leu Thr Leu Pro Pro
 33 38 43 48

aac ggc gcg gcg gcg ctc tcg ctg ccg ggc gcc ctg gcc aag ccg atc 192
 Asn Gly Ala Ala Ala Leu Ser Leu Pro Gly Ala Leu Ala Lys Pro Ile
 49 54 59 64

atg gat caa ttg gtg ggg gcg gcc gag acc ggc atc ccg ttc tcc tcc 240
 Met Asp Gln Leu Val Gly Ala Ala Glu Thr Gly Ile Pro Phe Ser Ser
 65 70 75 80

ctg ggg ccc cag gcg cat ctg agg cct ttg aag acc atg gag ccc gaa 288
 Leu Gly Pro Gln Ala His Leu Arg Pro Leu Lys Thr Met Glu Pro Glu
 81 86 91 96

gaa gag gtg gag gac gac ccc aag gtg cac ctg gag gct aaa gaa ctt 336
 Glu Glu Val Glu Asp Asp Pro Lys Val His Leu Glu Ala Lys Glu Leu
 97 102 107 112

tgg gat cag ttt cac aag cgg ggc acc gag atg gtc att acc aag tcg 384
 Trp Asp Gln Phe His Lys Arg Gly Thr Glu Met Val Ile Thr Lys Ser
 113 118 123 128

gga agg cga atg ttt cct cca ttt aaa gtg aga tgt tct ggg ctg gat 432
 Gly Arg Arg Met Phe Pro Pro Phe Lys Val Arg Cys Ser Gly Leu Asp
 129 134 139 144

aaa aaa gcc aaa tac att tta ttg atg gac att ata gct gct gat gac	480
Lys Lys Ala Lys Tyr Ile Leu Leu Met Asp Ile Ile Ala Ala Asp Asp	
145 150 155 160	
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Cys Arg Tyr Lys Phe His Asn Ser Arg Trp Met Val Ala Gly Lys Ala	
161 166 171 176	
gac ccc gaa atg cca aag agg atg tac att cac ccg gac agc ccc gct	576
Asp Pro Glu Met Pro Lys Arg Met Tyr Ile His Pro Asp Ser Pro Ala	
177 182 187 192	
act ggg gaa cag tgg atg tcc aaa gtc gtc act ttc cac aaa ctg aaa	624
Thr Gly Glu Gln Trp Met Ser Lys Val Val Thr Phe His Lys Leu Lys	
193 198 203 208	
ctc acc aac aac att tca gac aaa cat gga ttt act ata ttg aac tcc	672
Leu Thr Asn Asn Ile Ser Asp Lys His Gly Phe Thr Ile Leu Asn Ser	
209 214 219 224	
atg cac aaa tac cag ccc cgg ttc cac att gta aga gcc aat gac atc	720
Met His Lys Tyr Gln Pro Arg Phe His Ile Val Arg Ala Asn Asp Ile	
225 230 235 240	
ttg aaa ctc cct tat agt aca ttt cgg aca tac ttg ttc ccc gaa act	768
Leu Lys Leu Pro Tyr Ser Thr Phe Arg Thr Tyr Leu Phe Pro Glu Thr	
241 246 251 256	
gaa ttc atc gct gtg act gca tac cag aat gat aag ata acc cag tta	816
Glu Phe Ile Ala Val Thr Ala Tyr Gln Asn Asp Lys Ile Thr Gln Leu	
257 262 267 272	
aaa ata gac aac aac cct ttt gca aaa ggt ttc cgg gac act gga aat	864
Lys Ile Asp Asn Asn Pro Phe Ala Lys Gly Phe Arg Asp Thr Gly Asn	
273 278 283 288	
ggc cga aga gaa aaa aga aaa cag ctc acc ctg cag tcc atg agg gtg	912
Gly Arg Arg Glu Lys Arg Lys Gln Leu Thr Leu Gln Ser Met Arg Val	
289 294 299 304	
ttt gat gaa aga cac aaa aag gag aat ggg acc tct gat gag tcc tcc	960
Phe Asp Glu Arg His Lys Lys Glu Asn Gly Thr Ser Asp Glu Ser Ser	
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Ser Glu Gln Ala Ala Phe Asn Cys Phe Ala Gln Ala Ser Ser Pro Ala	
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Arg Pro Arg Asp Ser Gly Arg Leu Asp Lys Ala Ser Pro Asp Ser Arg	
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His Ser Pro Ala Thr Ile Ser Ser Ser Thr Arg Gly Leu Gly Ala Glu	
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Glu Arg Arg Ser Pro Val Arg Glu Gly Thr Ala Pro Ala Lys Val Glu	
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Gln Thr Asp Ala Ala Ala Ala His Leu Ala Gln Gly Pro Leu Pro Gly	
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Leu Cys Ala Glu Lys Glu Ala Ala Thr Ser Glu Leu Gln Ser Ile Gln				
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Arg Leu Val Ser Gly Leu Glu Ala Lys Pro Asp Arg Ser Arg Ser Ala				
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Ser Pro *				
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cttttctggg cgaggggagc ggcgcccggc ccccaaagcg agaagacaga cagccccggt    240

tctccgcagc cccaggtttg ctctcaagg acggaggggc ctctcagctc cggccgcctc     300

ctttccgccc cctgcaggcc ggccggagga aagctcaggg cccaggtcgg cccagggagc     360

acggaaccaa agagcgctag cgccggttcg gccgcctttc cagaaagccc gggccgaacg     420

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                        Met Ala Gln Val
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Leu Ile Val Gly Ala Gly Met Thr Gly Ser Leu Cys Ala Ala Leu Leu
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Arg Arg Gln Thr Ser Gly Pro Leu Tyr Leu Ala Val Trp Asp Lys Ala
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gag gac tca ggg gga aga atg act aca gcc tgc agt cct cat aat cct      620
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cag tgc aca gct gac ttg ggt gct cag tac atc acc tgc act cct cat      668
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tat gcc aaa aaa cac caa cgt ttt tat gat gaa ctg tta gcc tat ggc      716
Tyr Ala Lys Lys His Gln Arg Phe Tyr Asp Glu Leu Leu Ala Tyr Gly
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Val Leu Arg Pro Leu Ser Ser Pro Ile Glu Gly Met Val Met Lys Glu
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Ser Ser Met Ser Ala Ser Ala Asp Val Leu Ala Leu Ala Lys Ile Glu	
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Ile Lys Leu Ser Asp Ile Pro Glu Gly Lys Asn Met Ala Phe Lys Trp	
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Arg Gly Lys Pro Leu Phe Val Arg His Arg Thr Gln Lys Glu Ile Glu	
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Gln Glu Ala Ala Val Glu Leu Ser Gln Leu Arg Asp Pro Gln His Asp	
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Leu Asp Arg Val Lys Lys Pro Glu Trp Val Ile Leu Ile Gly Val Cys	
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Thr His Leu Gly Cys Val Pro Ile Ala Asn Ala Gly Asp Phe Gly Gly	
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Tyr Tyr Cys Pro Cys His Gly Ser His Tyr Asp Ala Ser Gly Arg Ile	
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Arg Leu Gly Pro Ala Pro Leu Asn Leu Glu Val Pro Thr Tyr Glu Phe	
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Gly His Lys Ala Cys Glu Cys Gln Glu Tyr Gly Pro Lys Pro Trp Lys	
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His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	
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His	Glu	Lys	Thr	Leu	Glu	Gly	Asn	Pro	Met	Lys	Ala	Ser	Asn	Val	Ala	
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aag	ctt	tca	ctt	ctt	cca	gtt	ctt	ttc	aat	atc	atg	aaa	gaa	ttc	aca	1879
Lys	Leu	Ser	Leu	Leu	Pro	Val	Leu	Phe	Asn	Ile	Met	Lys	Glu	Phe	Thr	
594					599					604					609	
ctg	ggg	aga	aac	cct	atc	agt	gta	agc	aat	gtg	cga	aag	cct	tta	ttt	1927
Leu	Gly	Arg	Asn	Pro	Ile	Ser	Val	Ser	Asn	Val	Arg	Lys	Pro	Leu	Phe	

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ctt cca ctt ctt ttc aat atc atg aaa gga ctc aca tgg gag aga aac				1975
Leu Pro Leu Leu Phe Asn Ile Met Lys Gly Leu Thr Trp Glu Arg Asn				
626	631	636	641	
cct atg agt gta tgc cat gtg gga aag cct tca ttt ttc tag ttgcttt				2024
Pro Met Ser Val Cys His Val Gly Lys Pro Ser Phe Phe *				
642	647	652		
cgatgtcatg aaaggactca cactggagag aagccctatg aatgtaagca atgcaggaaa				2084
gccttcagat cagcctcaca ccttcaaattg tatggaagga ctcacactgg agagaaaccc				2144
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ccgttgggcg tgcagcggcg ccagtcggcg gacgaggggc ccccgaggagtg tgcgtgactg				180
agacatgagc ctccaactgt gtggttgggc tcggtagcac atcgtgggac ttgggtgtgc				240
gcccacagat ggtttgccc tgcagtgacc agagcagccc aagccgccac catggtgaaa				300
ttgctagtgg ccaaaatcct gtgcatggtg ggcgtgttct tcttc				354
			atg ctg ctc	
			Met Leu Leu	
			1	

ggc tcc ctg ctc ccc gtg aag atc atc gag aca gat ttt gag aag gcc				402
Gly Ser Leu Leu Pro Val Lys Ile Ile Glu Thr Asp Phe Glu Lys Ala				
4	9	14	19	
cat cgc tcg aaa aag atc ctc tct ctc tgc aac acc ttt gga gga ggg				450
His Arg Ser Lys Lys Ile Leu Ser Leu Cys Asn Thr Phe Gly Gly Gly				
20	25	30	35	

gtg ttt ctg gcc acg tgc ttc aac gct ctg ctg ccc gct gtg agg gaa	498
Val Phe Leu Ala Thr Cys Phe Asn Ala Leu Leu Pro Ala Val Arg Glu	
36 41 46 51	
aag ctc cag aag gtc ctg agc ctc ggc cac atc agc acc gac tac ccg	546
Lys Leu Gln Lys Val Leu Ser Leu Gly His Ile Ser Thr Asp Tyr Pro	
52 57 62 67	
ctg gcc gaa acc atc ctc ctg ctg ggc ttc ttc atg acc gtc ttc ctg	594
Leu Ala Glu Thr Ile Leu Leu Leu Gly Phe Phe Met Thr Val Phe Leu	
68 73 78 83	
gag cag ctg atc ctg acc ttc cgc aag gag aag ccg tcc ttc atc gac	642
Glu Gln Leu Ile Leu Thr Phe Arg Lys Glu Lys Pro Ser Phe Ile Asp	
84 89 94 99	
ctg gag acc ttc aac gcc gga tcg gac gtg ggc agc gac tcg gag tat	690
Leu Glu Thr Phe Asn Ala Gly Ser Asp Val Gly Ser Asp Ser Glu Tyr	
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Glu Ser Pro Phe Met Gly Gly Ala Arg Gly His Ala Leu Tyr Val Glu	
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Pro His Gly His Gly Pro Ser Leu Ser Val Gln Gly Leu Ser Arg Ala	
132 137 142 147	
agc ccc gtg cgc ctg ctc agc ctg gcc ttc gcg ctg tcg gcc cac tcg	834
Ser Pro Val Arg Leu Leu Ser Leu Ala Phe Ala Leu Ser Ala His Ser	
148 153 158 163	
gtc ttt gag ggc ctg gcc ctg ggc ctg cag gag gag ggg gag aaa gtg	882
Val Phe Glu Gly Leu Ala Leu Gly Leu Gln Glu Glu Gly Glu Lys Val	
164 169 174 179	
gtg agc ctg ttc gtg ggg gtg gcc gtc cac gag aca ctg gtg gcc gtg	930
Val Ser Leu Phe Val Gly Val Ala Val His Glu Thr Leu Val Ala Val	
180 185 190 195	
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Ala Leu Gly Ile Ser Met Ala Arg Ser Ala Met Pro Leu Arg Asp Ala	
196 201 206 211	
gcc aag ctg gcg gtc acc gta agc gcc atg atc ccc ctg ggc atc ggc	1026
Ala Lys Leu Ala Val Thr Val Ser Ala Met Ile Pro Leu Gly Ile Gly	
212 217 222 227	
ctg ggc ctg ggc att gag agc gcc cag ggc gtg ccg ggc agc gtg gcg	1074
Leu Gly Leu Gly Ile Glu Ser Ala Gln Gly Val Pro Gly Ser Val Ala	
228 233 238 243	
tcc gtg ctg ctg cag ggc ctg gcg ggc ggc acc ttc ctc ttc atc acc	1122
Ser Val Leu Leu Gln Gly Leu Ala Gly Gly Thr Phe Leu Phe Ile Thr	
244 249 254 259	

ttc ctg gag atc ctg gcc aag gag ctg gag gag aag agt gac cgt ctg	1170
Phe Leu Glu Ile Leu Ala Lys Glu Leu Glu Glu Lys Ser Asp Arg Leu	
260 265 270 275	
ctc aag gtc ctc ttc ctg gtg ctg ggc tac acc gtc ctg gcc ggg atg	1218
Leu Lys Val Leu Phe Leu Val Leu Gly Tyr Thr Val Leu Ala Gly Met	
276 281 286 291	
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Val Phe Leu Lys Trp *	
292 297	
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ctgtggccct gggccaccac ctgtgcacaa ggggcctccc gggaccaggc tgtgcccccg	1392
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<400> 105

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cag ttt cct cat ctg gaa agt aga aat gat aac cgc acc tgc cac tgg	97	
Gln Phe Pro His Leu Glu Ser Arg Asn Asp Asn Arg Thr Cys His Trp		
13 18 23 28		
tgt gac aca gag att cat ata gtg aac gcc acc atc agt gac act gat	145	
Cys Asp Thr Glu Ile His Ile Val Asn Ala Thr Ile Ser Asp Thr Asp		
29 34 39 44		
tgc atg aaa tct gcc atg gtg gtg gcc ctt agt aag aga agt cag gag	193	
Cys Met Lys Ser Ala Met Val Val Ala Leu Ser Lys Arg Ser Gln Glu		
45 50 55 60		
gcg gag gct gct ttt ctg agt gtt tac aag caa tta att gaa gca cca	241	
Ala Glu Ala Ala Phe Leu Ser Val Tyr Lys Gln Leu Ile Glu Ala Pro		
61 66 71 76		
gcc ctg tgg gaa ctc aag ctc aag tcc agg cct gcc ctt gga gac tct	289	
Ala Leu Trp Glu Leu Lys Leu Lys Ser Arg Pro Ala Leu Gly Asp Ser		
77 82 87 92		

cg	gt	ca	ga	ca	ca	cat	ga	ca	aa	ac	ga	aa	ca	aa	ac		337
Arg	Val	Gln	Gln	Gly	Gln	His	Asp	Pro	Lys	Thr	Asp	Asn	Gln	Asn	Thr		
93					98					103					108		
ca	ca	aa	ga	gg	tt	aa	ga	ga	tg	ct	ga	ga	gc	tc	ga		385
Gln	Gln	Lys	Ala	Gly	Phe	Lys	Glu	Gly	Trp	Leu	Ala	Glu	Ala	Ser	Glu		
109					114					119					124		
ag	ga	gc	tt	ga	ct	gg	tt	aa	ga	cc	gt	cc	gt	tt	ga		433
Arg	Glu	Ala	Phe	Gly	Pro	Gly	Phe	Lys	Asp	Pro	Val	Pro	Val	Phe	Glu		
125					130					135					140		
gc	ga	cg	ag	ct	ga	ga	ag	ct	ca	cc	cc	ag	tt	ga	cc		481
Ala	Ala	Arg	Ser	Leu	Asp	Asp	Arg	Leu	Gln	Pro	Pro	Ser	Phe	Asp	Pro		
141					146					151					156		
ag	gg	ca	cc	cg	cg	ga	gc	ct	ca	ac	tg	tg	aa	ag	aa	cc	529
Ser	Gly	Gln	Pro	Arg	Arg	Asp	Leu	His	Thr	Ser	Trp	Lys	Arg	Asn	Pro		
157					162					167					172		
ga	ct	ct	ag	cc	aa	gc	ct	aa	gt	ac	ca	ga	ga	ct	ct		577
Glu	Leu	Leu	Ser	Pro	Lys	Ala	Leu	Lys	Ala	Thr	Gln	Ala	Glu	Leu	Leu		
173					178					183					188		
ga	ct	cg	cg	aa	ta	ga	ga	ga	ga	ga	tc	aa	ga	ga	ga		625
Glu	Leu	Arg	Arg	Lys	Tyr	Asp	Glu	Glu	Ala	Ala	Ser	Lys	Ala	Asp	Glu		
189					194					199					204		
gt	gg	ct	at	at	ac	aa	ct	ga	aa	gt	aa	ca	cg	gt	ga		673
Val	Gly	Leu	Ile	Met	Thr	Asn	Leu	Glu	Lys	Ala	Asn	Gln	Arg	Ala	Glu		
205					210					215					220		
gt	gc	ca	cg	ga	gt	ga	ag	ct	cg	ga	ca	ct	gc	tc	gt		721
Ala	Ala	Gln	Arg	Glu	Val	Glu	Ser	Leu	Arg	Glu	Gln	Leu	Ala	Ser	Val		
221					226					231					236		
aa	ag	tc	at	cg	ct	gt	tg	tg	tc	cc	ca	gg	cc	ag	gg		769
Asn	Ser	Ser	Ile	Arg	Leu	Ala	Cys	Cys	Ser	Pro	Gln	Gly	Pro	Ser	Gly		
237					242					247					252		
ga	aa	gt	aa	tt	ac	ct	tg	tg	tg	gg	cc	cg	ct	ga	gc	gc	817
Asp	Lys	Val	Asn	Phe	Thr	Leu	Cys	Ser	Gly	Pro	Arg	Leu	Glu	Ala	Ala		
253					258					263					268		
ct	gc	tc	aa	ga	ag	ga	at	ct	cg	ct	ct	aa	ga	gt	ca		865
Leu	Ala	Ser	Lys	Asp	Arg	Glu	Ile	Leu	Arg	Leu	Leu	Lys	Asp	Val	Gln		
269					274					279					284		
ca	ct	ca	ag	tc	ct	ca	ga	ct	ga	ga	ga	tc	gc	aa	ca		913
His	Leu	Gln	Ser	Ser	Leu	Gln	Glu	Leu	Glu	Glu	Ala	Ser	Ala	Asn	Gln		
285					290					295					300		
at	gc	ga	ct	ga	cg	ca	ct	ac	gc	aa	tc	ga	gc	at	ga		961
Ile	Ala	Asp	Leu	Glu	Arg	Gln	Leu	Thr	Ala	Lys	Ser	Glu	Ala	Ile	Glu		
301					306					311					316		
aa	ct	ga	ga	ag	ct	ca	gc	ca	tc	ga	ta	ga	ga	at	aa		1009

Lys 317	Leu	Glu	Glu	Lys	Leu 322	Gln	Ala	Gln	Ser	Asp 327	Tyr	Glu	Glu	Ile	Lys 332	
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Thr 333	Glu	Leu	Ser	Ile	Leu 338	Lys	Ala	Met	Lys	Leu 343	Ala	Ser	Ser	Thr	Cys 348	
agc	ctc	ccc	cag	ggc	atg	gcc	aag	cct	gaa	gac	tca	ctg	ctt	att	gca	1105
Ser 349	Leu	Pro	Gln	Gly	Met 354	Ala	Lys	Pro	Glu	Asp 359	Ser	Leu	Leu	Ile	Ala 364	
aag	gag	gcc	ttc	ttc	ccc	acg	cag	aaa	ttc	ctt	ctg	gag	aag	ccc	agc	1153
Lys 365	Glu	Ala	Phe	Phe	Pro 370	Thr	Gln	Lys	Phe	Leu 375	Leu	Glu	Lys	Pro	Ser 380	
ctc	ctg	gcc	agc	cct	gag	gaa	gac	cca	tca	gag	gac	gat	tcc	atc	aag	1201
Leu 381	Leu	Ala	Ser	Pro	Glu 386	Glu	Asp	Pro	Ser	Glu 391	Asp	Asp	Ser	Ile	Lys 396	
gat	tca	ctg	ggc	acg	gag	cag	tcc	tac	ccc	tcc	cct	cag	cag	ctc	cca	1249
Asp 397	Ser	Leu	Gly	Thr	Glu 402	Gln	Ser	Tyr	Pro	Ser 407	Pro	Gln	Gln	Leu	Pro 412	
cct	cca	cca	ggg	cca	gaa	gac	ccc	ctg	tct	ccc	agc	ccc	ggg	cag	ccc	1297
Pro 413	Pro	Pro	Gly	Pro	Glu 418	Asp	Pro	Leu	Ser	Pro 423	Ser	Pro	Gly	Gln	Pro 428	
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Leu 429	Leu	Gly	Pro	Ser	Leu 434	Gly	Pro	Asp	Gly	Thr 439	Arg	Thr	Phe	Ser	Leu 444	
tcc	ccc	ttc	ccc	agc	ctg	gca	tca	ggg	gag	aga	ctg	atg	atg	ccc	cca	1393
Ser 445	Pro	Phe	Pro	Ser	Leu 450	Ala	Ser	Gly	Glu	Arg 455	Leu	Met	Met	Pro	Pro 460	
gcc	gcc	ttc	aag	gga	gag	gcg	ggc	ggc	ctg	ctg	gtg	ttc	ccc	cca	gcc	1441
Ala 461	Ala	Phe	Lys	Gly	Glu 466	Ala	Gly	Gly	Leu	Leu 471	Val	Phe	Pro	Pro	Ala 476	
ttc	tat	ggc	gcc	aag	ccc	ccc	aca	gcc	cct	gcc	acc	ccg	gcc	cct	ggc	1489
Phe 477	Tyr	Gly	Ala	Lys	Pro 482	Pro	Thr	Ala	Pro	Ala 487	Thr	Pro	Ala	Pro	Gly 492	
cct	gag	cca	ctg	ggc	ggt	cct	gag	ccc	gcg	gat	ggt	ggt	ggg	ggc	gga	1537
Pro 493	Glu	Pro	Leu	Gly	Gly 498	Pro	Glu	Pro	Ala	Asp 503	Gly	Gly	Gly	Gly	Gly 508	
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Ala 509	Ala	Gly	Pro	Gly	Ala 514	Glu	Glu	Glu	Gln	Leu 519	Asp	Thr	Ala	Glu	Ile 524	
gcc	ttc	cag	gtg	aag	gag	cag	ctg	ctg	aaa	cac	aac	atc	ggg	cag	cgg	1633
Ala 525	Phe	Gln	Val	Lys	Glu 530	Gln	Leu	Leu	Lys	His 535	Asn	Ile	Gly	Gln	Arg 540	
gtg	ttt	ggg	cat	tac	gtg	ctg	ggg	ctg	tcg	cag	ggc	tcg	gtc	agc	gag	1681
Val	Phe	Gly	His	Tyr	Val	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Val	Ser	Glu	

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atc cta gcc cgg ccc aag ccc tgg cgc aag ctc acg gtg aag ggc aag				1729
Ile Leu Ala Arg Pro Lys Pro Trp Arg Lys Leu Thr Val Lys Gly Lys				
557	562	567	572	
gag ccc ttc atc aag atg aag cag ttc ctg tgc gat gag cag aat gta				1777
Glu Pro Phe Ile Lys Met Lys Gln Phe Leu Ser Asp Glu Gln Asn Val				
573	578	583	588	
ctg gcg ctc agg acc atc caa gtg cgg cag cga ggc agc atc acc ccg				1825
Leu Ala Leu Arg Thr Ile Gln Val Arg Gln Arg Gly Ser Ile Thr Pro				
589	594	599	604	
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Arg Ile Arg Thr Pro Glu Thr Gly Ser Asp Asp Ala Ile Lys Ser Ile				
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cta gag cag gcc aag aag gag atc gag tgc cag aag ggc ggc gag ccc				1921
Leu Glu Gln Ala Lys Lys Glu Ile Glu Ser Gln Lys Gly Gly Glu Pro				
621	626	631	636	
aag acc tcg gtg gcc ccg ctg agc atc gcc aac ggc acg acc ccc gcc				1969
Lys Thr Ser Val Ala Pro Leu Ser Ile Ala Asn Gly Thr Thr Pro Ala				
637	642	647	652	
agc acc tcg gag gac gcc atc aag agc atc ctg gag cag gca cgc cgt				2017
Ser Thr Ser Glu Asp Ala Ile Lys Ser Ile Leu Glu Gln Ala Arg Arg				
653	658	663	668	
gag atg cag gcg caa cag cag gcg ctg ctg gag atg gag gtg gcg ccc				2065
Glu Met Gln Ala Gln Gln Gln Ala Leu Leu Glu Met Glu Val Ala Pro				
669	674	679	684	
agg ggc cgc tcg gtg ccc ccc tcg ccc ccg gag cgg cca tca ctg gcc				2113
Arg Gly Arg Ser Val Pro Pro Ser Pro Pro Glu Arg Pro Ser Leu Ala				
685	690	695	700	
acc gcg agc cag aac ggg gcc ccg gcc ttg gtg aag cag gag gag ggc				2161
Thr Ala Ser Gln Asn Gly Ala Pro Ala Leu Val Lys Gln Glu Glu Gly				
701	706	711	716	
agc ggg ggc ccc gcg cag gcg ccg ctc ccg gtc ctg tcc ccc gcc gcc				2209
Ser Gly Gly Pro Ala Gln Ala Pro Leu Pro Val Leu Ser Pro Ala Ala				
717	722	727	732	
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Phe Val Gln Ser Ile Ile Arg Lys Val Lys Ser Glu Ile Gly Asp Ala				
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ggc tac ttc gac cac cac tgg gcc tcc gac cgc ggc ctg ctc agc cgc				2305
Gly Tyr Phe Asp His His Trp Ala Ser Asp Arg Gly Leu Leu Ser Arg				
749	754	759	764	
ccc tac gcc tcc gtg tcg ccc tcg ctg tcc tcc tcc tcc tct ggc				2353
Pro Tyr Ala Ser Val Ser Pro Ser Leu Ser Ser Ser Ser Ser Gly				
765	770	775	780	

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Tyr Ser Gly Gln Pro Asn Gly Arg Ala Trp Pro Arg Gly Asp Glu Ala	
781 786 791 796	
cct gtg ccc ccc gag gac gag gcg gcg gca ggg gcg gag gac gaa ccc	2449
Pro Val Pro Pro Glu Asp Glu Ala Ala Ala Gly Ala Glu Asp Glu Pro	
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Pro Arg Thr Gly Glu Leu Lys Ala Glu Gly Ala Thr Ala Glu Ala Gly	
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Ala Arg Leu Pro Tyr Tyr Pro Ala Tyr Val Pro Arg Thr Leu Lys Pro	
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acc gtg ccg ccg ctg acc ccc gag cag tac gag ctg tac atg tac cgt	2593
Thr Val Pro Pro Leu Thr Pro Glu Gln Tyr Glu Leu Tyr Met Tyr Arg	
845 850 855 860	
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Glu Val Asp Thr Leu Glu Leu Thr Arg Gln Val Lys Glu Lys Leu Ala	
861 866 871 876	
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Lys Asn Gly Ile Cys Gln Arg Ile Phe Gly Glu Lys Val Leu Gly Leu	
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Ser Gln Gly Ser Val Ser Asp Met Leu Ser Arg Pro Lys Pro Trp Ser	
893 898 903 908	
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Lys Leu Thr Gln Lys Gly Arg Glu Pro Phe Ile Arg Met Gln Leu Trp	
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ctc tct gac cag ctc ggc cag gca gtg ggc cag cag cct ggt gcc tcc	2833
Leu Ser Asp Gln Leu Gly Gln Ala Val Gly Gln Gln Pro Gly Ala Ser	
925 930 935 940	
cag gcc agt ccc aca gaa cca agg tcc tca cca tcc cca ccc ccc agc	2881
Gln Ala Ser Pro Thr Glu Pro Arg Ser Ser Pro Ser Pro Pro Pro Ser	
941 946 951 956	
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Pro Thr Glu Pro Glu Lys Ser Ser Gln Glu Pro Leu Ser Leu Ser Leu	
957 962 967 972	
gag agc agc aag gag aac cag cag cca gag ggc cgc tcc agc tcc tcg	2977
Glu Ser Ser Lys Glu Asn Gln Gln Pro Glu Gly Arg Ser Ser Ser Ser	
973 978 983 988	
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Leu Ser Gly Lys Met Tyr Ser Gly Ser Gln Ala Pro Gly Gly Ile Gln	
989 994 999 1004	

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Glu Ile Val Ala Met Ser Pro Glu Leu Asp Thr Tyr Ser Ile Thr Lys	
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Arg Val Lys Glu Val Leu Thr Asp Asn Asn Leu Gly Gln Arg Leu Phe	
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ggg gaa agc atc ctg ggt ctg aca cag ggc tcc gtg tct gac ctg ctg	3169
Gly Glu Ser Ile Leu Gly Leu Thr Gln Gly Ser Val Ser Asp Leu Leu	
1037 1042 1047 1052	
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Ser Arg Pro Lys Pro Trp His Lys Leu Ser Leu Lys Gly Arg Glu Pro	
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Phe Val Arg Met Gln Leu Trp Leu Asn Asp Pro His Asn Val Glu Lys	
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Leu Arg Asp Met Lys Lys Leu Glu Lys Lys Ala Tyr Leu Lys Arg Arg	
1085 1090 1095 1100	
tat ggc ctc atc agc acc ggc tca gac agt gag tcc ccg gcc acc cgc	3361
Tyr Gly Leu Ile Ser Thr Gly Ser Asp Ser Glu Ser Pro Ala Thr Arg	
1101 1106 1111 1116	
tca gag tgc ccc agc ccc tgc ctg cag ccc cag gac ctg agc ctc ctg	3409
Ser Glu Cys Pro Ser Pro Cys Leu Gln Pro Gln Asp Leu Ser Leu Leu	
1117 1122 1127 1132	
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Gln Ile Lys Lys Pro Arg Val Val Leu Ala Pro Glu Glu Lys Glu Ala	
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Leu Arg Lys Ala Tyr Gln Leu Glu Pro Tyr Pro Ser Gln Gln Thr Ile	
1149 1154 1159 1164	
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Glu Leu Leu Ser Phe Gln Leu Asn Leu Lys Thr Asn Thr Val Ile Asn	
1165 1170 1175 1180	
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Trp Phe His Asn Tyr Arg Ser Arg Met Arg Arg Glu Met Leu Val Glu	
1181 1186 1191 1196	
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Gly Thr Gln Asp Glu Pro Asp Leu Asp Pro Ser Gly Gly Pro Gly Ile	
1197 1202 1207 1212	
cta ccg cca ggc cac tcc cac cca gac ccc acc ccg cag agc cct gac	3697
Leu Pro Pro Gly His Ser His Pro Asp Pro Thr Pro Gln Ser Pro Asp	
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Leu	Phe	Val	Lys	Thr	Cys	Thr	Phe	His	Val	Ser	Gly	Glu	Pro	Ser	Thr		
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tgc	aga	gaa	ttt	ggg	aag	gac	ttc	ctg	gcc	aag	ttg	gga	ttt	ctc	cat		579
Cys	Arg	Glu	Phe	Gly	Lys	Asp	Phe	Leu	Ala	Lys	Leu	Gly	Phe	Leu	His		
91					96					101					106		
caa	cag	gct	gct	cac	act	ggg	gag	caa	tcc	aat	agc	aaa	agc	gac	ggg		627
Gln	Gln	Ala	Ala	His	Thr	Gly	Glu	Gln	Ser	Asn	Ser	Lys	Ser	Asp	Gly		
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Gly	Ala	Ile	Ser	His	Arg	Gly	Lys	Thr	His	Tyr	Asn	Cys	Gly	Glu	His		
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Thr	Lys	Ala	Phe	Ser	Gly	Lys	His	Thr	Leu	Val	Gln	Gln	Gln	Arg	Thr		
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ctc	act	aca	gaa	aga	tgt	tac	ata	tgc	agt	gaa	tgt	ggg	aaa	tcc	ttt		771
Leu	Thr	Thr	Glu	Arg	Cys	Tyr	Ile	Cys	Ser	Glu	Cys	Gly	Lys	Ser	Phe		
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Ser	Lys	Ser	Tyr	Ser	Leu	Asn	Asp	His	Trp	Arg	Leu	His	Thr	Gly	Glu		
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Lys	Pro	Tyr	Glu	Cys	Arg	Glu	Cys	Gly	Lys	Ser	Phe	Arg	Gln	Ser	Ser		
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Ser	Leu	Ile	Gln	His	Arg	Arg	Gly	His	Thr	Ala	Val	Arg	Pro	His	Glu		
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Gly	Asp	Glu	Cys	Gly	Lys	Leu	Phe	Ser	Asn	Pro	Ser	Asn	Leu	Ile	Lys		
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cat	cgg	aga	gtt	cac	act	ggg	gaa	agg	cca	tat	gag	tgc	agc	gaa	tgt		1011
His	Arg	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys		
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ggg	aaa	tcc	ttt	aac	caa	agg	tct	gca	ctc	ctt	caa	cat	cgg	gga	ggg		1059
Gly	Lys	Ser	Phe	Asn	Gln	Arg	Ser	Ala	Leu	Leu	Gln	His	Arg	Gly	Gly		
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cac	act	ggg	gag	agg	cct	tat	gag	tgc	agt	gaa	tgt	ggg	aag	ttt	ttt		1107
His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Phe	Phe		
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Pro	Tyr	Ser	Ser	Ser	Leu	Arg	Lys	His	Gln	Arg	Val	His	Thr	Gly	Ser		

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Gly Leu Ile Lys His Arg Arg Val His Thr Gly Glu Lys Pro Tyr Glu				
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Cys Thr Glu Cys Gly Lys Ser Phe Ser His Asn Ser Ser Leu Ile Lys				
331	336	341	346	
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His Gln Arg Ile His Ser Arg *				
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Met Lys Gly Ile Ser Gly Gly Val Arg	
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Val Ala Ala Leu Ala Ala Arg Ala Glu Arg Glu Glu Leu Pro Val Pro	
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Ala Met Glu Pro Gln Pro Thr Ala Trp Gly Ser Pro His Pro Glu Ala	
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Val Leu Gln Leu Glu Val Ala Pro Glu Ser Ser Gly Pro Cys Thr Asp	
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Thr Ala Lys Asp Gln Gln Ser Asp Lys Leu Pro Asp Leu Met Pro Pro	
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gct gta gcc act ggg ctc agc cct gga gct gag agc atc gct gga gat	472
Ala Val Ala Thr Gly Leu Ser Pro Gly Ala Glu Ser Ile Ala Gly Asp	
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aga cgt ggc aga gaa gag gtt gcg agc atg gcc cca gcc agc agc tcc	520
Arg Arg Gly Arg Glu Glu Val Ala Ser Met Ala Pro Ala Ser Ser Ser	
90 95 100 105	
cac gct gcc cct agt cct ggg cat gga gcg agc ctt ggt gtc aga gac	568
His Ala Ala Pro Ser Pro Gly His Gly Ala Ser Leu Gly Val Arg Asp	
106 111 116 121	
cag ggt gtg cag tct gag ctc ctc tac ctt act aaa gag agg cct ctt	616
Gln Gly Val Gln Ser Glu Leu Leu Tyr Leu Thr Lys Glu Arg Pro Leu	
122 127 132 137	
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Leu Phe Thr Arg Ala Thr Ala Leu Leu Pro Gln Asp Leu Phe Ile Leu	
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Pro Val Leu Gly Leu Ser Ile Cys Lys Leu Glu Val Leu Arg Ala Gly	
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Lys Gly Gly Cys Glu Glu Gly Phe Gly Gln Leu Leu Leu Leu Ser Glu	
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Val Ala Ser Ser Ser Arg His Gly Gly Leu Ser Thr Thr Gly Leu Leu	
186 191 196 201	
ggc tat ttg ccc ctg att tgc tcc ctg gta cgg gct ctt gtt aac agg	856
Gly Tyr Leu Pro Leu Ile Cys Ser Leu Val Arg Ala Leu Val Asn Arg	
202 207 212 217	
cag gca agg ggt gcg ggg acc agg caa ggg ctt caa agg gta cag tac	904
Gln Ala Arg Gly Ala Gly Thr Arg Gln Gly Leu Gln Arg Val Gln Tyr	
218 223 228 233	
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Gln Ile Phe Gln Thr Gln His Leu Cys Pro Gly Val Ser Lys Leu Ser	
234 239 244 249	
tct gcc cta gga ttt att cat act gtt aaa tta cca gtt tat gca aat	1000
Ser Ala Leu Gly Phe Ile His Thr Val Lys Leu Pro Val Tyr Ala Asn	
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Ala Leu Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val Ser Val Val
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cag gca ggg ctg act cag cca ccc tcg gtg tcc aag ggc ttg aga cag      153
Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
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acc gcc aca ctc acc tgc act ggg aac agc aac aat gtt ggc gac caa      201
Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asp Gln
  36                               41                               46                               51

gga gca tct tgg ctg cag cag cac cag ggc cac cct ccc aaa ctc ctc      249
Gly Ala Ser Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
  52                               57                               62                               67

tcc tac agg aat aac aac cgg ccc tca ggg atc tca gag aga tta tct      297
Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
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gca tcc agg tca gga aac aca gcc tcc ctg acc att act gga ctc cag      345
Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
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cct gag gac gag gct gac tat tac tgc tca gca tgg gac agc agc ctc      393
Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
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agt gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag      441
Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
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ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag      489
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
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ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac      537
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
  148                               153                               158                               163

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Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys	
164 169 174 179	

gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag tac	633
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr	
180 185 190 195	

gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag tcc cac	681
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His	
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aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag	729
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys	
212 217 222 227	

aca gtg gcc cct aca gaa tgt tca tag gttct caaccctcac ccccaccacg	781
Thr Val Ala Pro Thr Glu Cys Ser *	
228 233	

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Met Cys Val Arg Ser Cys Phe Gln Ser Pro	
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Arg Leu Gln Trp Val Trp Arg Thr Ala Phe Leu Lys His Thr Gln Arg	
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agg cac cag ggg tcc cac cga tgg aca cac ctt gga ggc agc acc tac	328
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Arg Ala Val Ile Phe Asp Met Gly Gly Val Leu Ile Pro Ser Pro Gly	
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Arg Val Ala Ala Glu Trp Glu Val Gln Asn Arg Ile Pro Ser Gly Thr	
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Ile Leu Lys Ala Leu Met Glu Gly Gly Glu Asn Gly Pro Trp Met Arg	
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Arg Leu Cys Ser Glu Met Leu Lys Thr Ser Val Pro Val Asp Ser Phe	
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Phe Ser Leu Leu Thr Ser Glu Arg Val Ala Lys Gln Phe Pro Val Met	
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act gag gcc ata act caa att cgg gca aaa ggt ctt cag act gca gtc	664
Thr Glu Ala Ile Thr Gln Ile Arg Ala Lys Gly Leu Gln Thr Ala Val	
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Leu Ser Asn Asn Phe Tyr Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu	
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Asp Arg Lys Gln Phe Asp Val Ile Val Glu Ser Cys Met Glu Gly Ile	
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Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly	
187 192 197 202	
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Leu Gln Pro Ser Glu Ser Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu	
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aaa gaa gct gcc aga ctt ggt att cac acc att aag gtt aat gac cca	904
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219 224 229 234	
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Glu Thr Ala Val Lys Glu Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg	
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Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys Thr Met Glu Ile Pro	
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Lys Asp Ser Leu Gln	Lys Tyr Leu Lys Asp	Leu Leu Gly Ile Gln Thr	
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299	304	309	314
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Pro Pro Gly Thr Leu	Leu Pro Ser Ala His	Ala Ile Glu Arg Glu Phe	
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Arg Ile Met Lys Ala	Leu Ala Asn Ala Gly	Val Pro Val Pro Asn Val	
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Met Glu Tyr Cys Pro	Gly Leu Ile Tyr Lys	Asp Pro Ser Leu Pro Gly	
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ttatgggtct ttcaactctc gtatatatatt aaatgcaatt ggagccccgc aggggaatacc	180
agatcaattt aaagcttgaa atcaaatagt tacaggactg aagtcaatat tttggtagat	240
gacagtcaat aaaaatgtaa attagataca ctacatctat tacaaccaac agcaacgagc	300

ttttcatgag ttaaaaagaa aaactcatgt cggccccgagc cctgggggcta cctgacctga	360
caaaactctt tacactccat gtgtcaaaaa gagaaaaaat ggcagttgga gttttaaccc	420
agactgtggg gccctggcca aggccagtgg cctatctctc aaaacaacta gatggggttc	480
caaaggctgg ccactatgtc taaggaccct ggcagcaaca gccctgttag cacaagaagc	540
agataaacta acccttgggc aaaacctgaa tataaaggcc ccccatgctg tggttaacttt	600
g atg act acc gaa gga cat cat tgg cta aca aat gct aga tta acc	646
Met Thr Thr Glu Gly His His Trp Leu Thr Asn Ala Arg Leu Thr	
1 5 10	
aag tac caa agc ttg cca tgt gaa aat ccc cac ata act att gaa gtc	694
Lys Tyr Gln Ser Leu Pro Cys Glu Asn Pro His Ile Thr Ile Glu Val	
16 21 26 31	
tgt aac acc cta aat ccc acc acc ctg ctc cca gta tca gag agc ccg	742
Cys Asn Thr Leu Asn Pro Thr Thr Leu Leu Pro Val Ser Glu Ser Pro	
32 37 42 47	
ggc gag cat aac tgt gta gag gtg ttg gac tca gtc tat tct agc aga	790
Gly Glu His Asn Cys Val Glu Val Leu Asp Ser Val Tyr Ser Ser Arg	
48 53 58 63	
cct gac ctt cgg gac cag cca tgg gca tca tca gta gac tgg gag tta	838
Pro Asp Leu Arg Asp Gln Pro Trp Ala Ser Ser Val Asp Trp Glu Leu	
64 69 74 79	
tac atg gac ggg agc agc ttc atc aac tca caa gga gaa aga tgt gca	886
Tyr Met Asp Gly Ser Ser Phe Ile Asn Ser Gln Gly Glu Arg Cys Ala	
80 85 90 95	
gga tat gcg gtg gta act ttg gat gct gtc att aaa gcc aaa ctg tgg	934
Gly Tyr Ala Val Val Thr Leu Asp Ala Val Ile Lys Ala Lys Leu Trp	
96 101 106 111	
cta cag ggc act tca gcc cag aag gct gag ctc att gct tta act cgg	982
Leu Gln Gly Thr Ser Ala Gln Lys Ala Glu Leu Ile Ala Leu Thr Arg	
112 117 122 127	
gct gta gaa ctc agt gaa ggg caa gag tca ctt gaa gaa ttg tta ggc	1030
Ala Val Glu Leu Ser Glu Gly Gln Glu Ser Leu Glu Glu Leu Leu Gly	
128 133 138 143	
cgg tac ttc tac gtc tca cac ttg cca gcc ttt gcc aaa gca gta gca	1078
Arg Tyr Phe Tyr Val Ser His Leu Pro Ala Phe Ala Lys Ala Val Ala	
144 149 154 159	
caa ctg tgc att aca tgc cga cag cac aat gcg agg caa agc ccc act	1126
Gln Leu Cys Ile Thr Cys Arg Gln His Asn Ala Arg Gln Ser Pro Thr	
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Val Ser Pro His Ile Gln Ala Tyr Gly Ala Ala Pro Phe Glu Asp Leu	
176 181 186 191	

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Gln Val Asp Phe Thr Glu Met Pro Lys Cys Gly Gly Asn Lys Tyr Leu	
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ctg gtt ctt acg tgt act tac tct ggg tgg gtg gag gct tat cca aca	1270
Leu Val Leu Thr Cys Thr Tyr Ser Gly Trp Val Glu Ala Tyr Pro Thr	
208 213 218 223	
cga act gaa aag gcc tac gaa gta acc cgt gtg ctt ctc cga gat ctt	1318
Arg Thr Glu Lys Ala Tyr Glu Val Thr Arg Val Leu Leu Arg Asp Leu	
224 229 234 239	
att cct agg ttt gga ctg ccc tta cga att ggc tca cat aac ggg ccg	1366
Ile Pro Arg Phe Gly Leu Pro Leu Arg Ile Gly Ser His Asn Gly Pro	
240 245 250 255	
gtg ttt gtg gct gac ttg gac tgt gtg gaa atc aat gtg gat act ggt	1414
Val Phe Val Ala Asp Leu Asp Cys Val Glu Ile Asn Val Asp Thr Gly	
256 261 266 271	
gtc att tgg gcc act tgg ata aaa aat gaa aag gat cca gtg cag ctt	1462
Val Ile Trp Ala Thr Trp Ile Lys Asn Glu Lys Asp Pro Val Gln Leu	
272 277 282 287	
cag aaa gga aaa agt ggc cct tcc tgt act aag gga caa tgt aac ccc	1510
Gln Lys Gly Lys Ser Gly Pro Ser Cys Thr Lys Gly Gln Cys Asn Pro	
288 293 298 303	
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Leu Glu Leu Val Ile Thr Asn Pro Leu Asp Pro Arg Trp Lys Lys Gly	
304 309 314 319	
gag cgt gtg acc tta gga atc aat ggg gct gga ctg aat ccc cga gta	1606
Glu Arg Val Thr Leu Gly Ile Asn Gly Ala Gly Leu Asn Pro Arg Val	
320 325 330 335	
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Asn Ile Leu Val Arg Gly Glu Val Tyr Lys Cys Ser Leu Glu Pro Val	
336 341 346 351	
ttt caa act ttc tat gat gaa cta aat gtg cca ata aca gaa ttt cca	1702
Phe Gln Thr Phe Tyr Asp Glu Leu Asn Val Pro Ile Thr Glu Phe Pro	
352 357 362 367	
gga aaa aca aga aat ttg ttt ttg caa tta gcc gag cat gta gcc cag	1750
Gly Lys Thr Arg Asn Leu Phe Leu Gln Leu Ala Glu His Val Ala Gln	
368 373 378 383	
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Ser Leu Thr Val Thr Ser Cys Tyr Val Cys Gly Gly Thr Val Ile Ala	
384 389 394 399	
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Asp Gln Trp Pro Trp Glu Ala Arg Glu Leu Val Pro Thr Asp Pro Val	
400 405 410 415	

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Pro Asp Glu Phe Pro Ala Gln Lys Asn His Pro Asp Asn Phe Trp Val	
416 421 426 431	
cta aaa gcc tca atc att aga caa tac tat ata gca aga gtg gag aag	1942
Leu Lys Ala Ser Ile Ile Arg Gln Tyr Tyr Ile Ala Arg Val Glu Lys	
432 437 442 447	
gac ttc acc ctt cct gta gga aga cta cat ggt gga gtt caa acc aca	1990
Asp Phe Thr Leu Pro Val Gly Arg Leu His Gly Gly Val Gln Thr Thr	
448 453 458 463	
cag aga aaa atc cat tca gta aat ttc caa agt tgc aga ccg ttt agg	2038
Gln Arg Lys Ile His Ser Val Asn Phe Gln Ser Cys Arg Pro Phe Arg	
464 469 474 479	
ccc acc cag aat ccc acc ggg act gga cag ccc cca ctg ggc tat act	2086
Pro Thr Gln Asn Pro Thr Gly Thr Gly Gln Pro Pro Leu Gly Tyr Thr	
480 485 490 495	
gga tat gtg gac ata gag cct aca cta agc tgc ctg aca agt agt tgt	2134
Gly Tyr Val Asp Ile Glu Pro Thr Leu Ser Cys Leu Thr Ser Ser Cys	
496 501 506 511	
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Val Ile Gly Thr Ile Lys Pro Ser Phe Phe Leu Leu Ser Ile Lys Thr	
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Gly Glu Leu Leu Gly Phe Pro Val Tyr Ala Ser Arg Glu Lys His Ser	
528 533 538 543	
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Tyr Lys Lys Leu Lys Gln *	
544 549	
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 actgagacgc agcctatagg tccgcaggcc agtcctccca ggaactgaaa tagtgaaat 239
 atg agt tgg cga gga aga tca aca tat agg cct agg cca aga aga agt 287
 Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Ser
 1 5 10 15
 tta cag cct cct gag ctg att ggg gct atg ctt gaa ccc act gat gaa 335
 Leu Gln Pro Pro Glu Leu Ile Gly Ala Met Leu Glu Pro Thr Asp Glu
 17 22 27 32
 gag cct aaa gaa gag aaa cca ccc act aaa agt cgg aat cct aca cct 383
 Glu Pro Lys Glu Glu Lys Pro Pro Thr Lys Ser Arg Asn Pro Thr Pro
 33 38 43 48
 gat cag aag aga gaa gat gat cag ggt gca gct gag att caa gtg cct 431
 Asp Gln Lys Arg Glu Asp Asp Gln Gly Ala Ala Glu Ile Gln Val Pro
 49 54 59 64
 gac ctg gaa gcc gat ctc cag gag cta tgt cag aca aag act ggg gat 479
 Asp Leu Glu Ala Asp Leu Gln Glu Leu Cys Gln Thr Lys Thr Gly Asp
 65 70 75 80
 gga tgt gaa ggt ggt act gat gtc aag ggg aag att cta cca aaa gca 527
 Gly Cys Glu Gly Gly Thr Asp Val Lys Gly Lys Ile Leu Pro Lys Ala

81	86	91	96	
gag cac ttt aaa atg cca gaa gca ggt gaa ggg aaa tca cag gtt taa				575
Glu His Phe Lys Met Pro Glu Ala Gly Glu Gly Lys Ser Gln Val *				
97	102	107	112	
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cgtccggtgg aa atg ccc gct ccc ggt gga acc cag gac acg tca gct	768
	Met Pro Ala Pro Gly Thr Gln Asp Thr Ser Ala
1 5 10	
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Leu Ser Gly Glu Asp Glu Glu Ser Leu Ser Thr Gln Thr Pro Thr Pro	
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Ser Arg Thr Ser Trp Gly Pro His Arg Ser Cys Tyr Pro Ser Cys Pro	
29 34 39 44	
gcc cgt gag tcc aac cgg cgc ctc tgg cca aga aag gcg agc tga acc	912
Ala Arg Glu Ser Asn Arg Arg Leu Trp Pro Arg Lys Ala Ser *	
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gctgctgacg ctgtttgcct tgtgtctgca caggcctcta ctaaactctc ccacacaatt	240
agtgtcttaa atat atg tac acg tat ata ttt tgt ccc aac tgt gtc agt	290
Met Tyr Thr Tyr Ile Phe Cys Pro Asn Cys Val Ser	
1 5 10	
tat aaa atg aaa act gac cac ttc tcc tta cgt tat ctt cac agt agc	338
Tyr Lys Met Lys Thr Asp His Phe Ser Leu Arg Tyr Leu His Ser Ser	
13 18 23 28	
tgt gca gaa gac aac aaa tcc agt gtt gat agc tca ggg cag gct gcc	386
Cys Ala Glu Asp Asn Lys Ser Ser Val Asp Ser Ser Gly Gln Ala Ala	
29 34 39 44	
cac ccc agc aaa ggg aag ttc ttc ccc cat ggg acc cac tgg ggg acc	434
His Pro Ser Lys Gly Lys Phe Phe Pro His Gly Thr His Trp Gly Thr	
45 50 55 60	
cag tgc cgc ggc cac atc tcc gtg ctt ggg tgg cag tgt agc tgc cca	482
Gln Cys Arg Gly His Ile Ser Val Leu Gly Trp Gln Cys Ser Cys Pro	
61 66 71 76	
tct acg ggg tgc cgg gtt ggc ttg ggc ctt gcc atg tgc cag acg cat	530

Ser	Thr	Gly	Cys	Arg	Val	Gly	Leu	Gly	Leu	Ala	Met	Cys	Gln	Thr	His		
77					82					87					92		
gca tac ata cac aca cac aca cac aca cac aca cac acc cca ccc gat 578																	
Ala	Tyr	Ile	His	Thr	His	Thr	His	Thr	His	Thr	His	Thr	Pro	Pro	Asp		
93					98					103					108		
tat gga gca cat cac acc gat ccc ttg cag agg tgg ggg ctg ggg ccc 626																	
Tyr	Gly	Ala	His	His	Thr	Asp	Pro	Leu	Gln	Arg	Trp	Gly	Leu	Gly	Pro		
109					114					119					124		
agg aca atc aga agc agg gcc cct ccc cca gct gtc tcg aga cca aag 674																	
Arg	Thr	Ile	Arg	Ser	Arg	Ala	Pro	Pro	Pro	Ala	Val	Ser	Arg	Pro	Lys		
125					130					135					140		
cca tcc agg gcc tct gag ccc tgg ggc atc acc cag aag cgc tgg gct 722																	
Pro	Ser	Arg	Ala	Ser	Glu	Pro	Trp	Gly	Ile	Thr	Gln	Lys	Arg	Trp	Ala		
141					146					151					156		
ccc agg ctg gca ccc agc aca cca gga gcc cag ggc gcg tgg gag atg 770																	
Pro	Arg	Leu	Ala	Pro	Ser	Thr	Pro	Gly	Ala	Gln	Gly	Ala	Trp	Glu	Met		
157					162					167					172		
cgc cag gga cgg tct ttc act cca gac cag gct gac taa taaatatgac 819																	
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173					178					183							
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gta tct gcc gct ctt cag ttt tca tta tct tgc att ttt ctg agg gaa	151					
Val Ser Ala Ala Leu Gln Phe Ser Leu Ser Cys Ile Phe Leu Arg Glu						
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Gly Lys Ala Thr Asp Glu Asp Met Gln Ser Leu Ala Ser Leu Met Ser						
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gaa gat gat gat gag aac aga gtg aac caa gaa gaa aag gca gct aaa	295					
Glu Asp Asp Asp Glu Asn Arg Val Asn Gln Glu Glu Lys Ala Ala Lys						
67 72 77 82						
att aca gag ctt atc aac aaa ctt aac ttt ttg gat gaa gca gaa aag	343					
Ile Thr Glu Leu Ile Asn Lys Leu Asn Phe Leu Asp Glu Ala Glu Lys						
83 88 93 98						
gac ttg gcc acc gtg aat tca aat cca ttt gat gat cct gat gct gca	391					
Asp Leu Ala Thr Val Asn Ser Asn Pro Phe Asp Asp Pro Asp Ala Ala						
99 104 109 114						
gaa tta aat cca ttt gga gat cct gac tca gaa gaa cct atc act gaa	439					
Glu Leu Asn Pro Phe Gly Asp Pro Asp Ser Glu Glu Pro Ile Thr Glu						
115 120 125 130						
aca gct tca cct aga aaa aca gaa gac tct ttt tat aat aac agc tat	487					
Thr Ala Ser Pro Arg Lys Thr Glu Asp Ser Phe Tyr Asn Asn Ser Tyr						
131 136 141 146						
aat ccc ttt aaa gag gtg cag act cca cag tat ttg aac cca ttc gat	535					
Asn Pro Phe Lys Glu Val Gln Thr Pro Gln Tyr Leu Asn Pro Phe Asp						
147 152 157 162						
gag cca gaa gca ttt gtg acc ata aag gat tct cct ccc cag tct aca	583					
Glu Pro Glu Ala Phe Val Thr Ile Lys Asp Ser Pro Pro Gln Ser Thr						

163		168		173		178	
aaa aga aaa aat ata	aga cct gtg gat atg	agc aag tac ctc tat	gct	631			
Lys Arg Lys Asn Ile	Arg Pro Val Asp Met	Ser Lys Tyr Leu Tyr	Ala				
179	184	189	194				
gat agt tct aaa act	gaa gaa gaa gaa ttg	gat gaa tca aat cct	ttt	679			
Asp Ser Ser Lys Thr	Glu Glu Glu Glu Leu	Asp Glu Ser Asn Pro	Phe				
195	200	205	210				
tat gaa cct aaa tca	act cct cct cca aat	aat ttg gta aat cct	gtt	727			
Tyr Glu Pro Lys Ser	Thr Pro Pro Pro Asn	Asn Leu Val Asn Pro	Val				
211	216	221	226				
caa gaa cta gaa act	gaa agg cga gtg aaa	aga aag gcc ccg gct	cca	775			
Gln Glu Leu Glu Thr	Glu Arg Arg Val Lys	Arg Lys Ala Pro Ala	Pro				
227	232	237	242				
cca gtc ctc tca cca	aaa aca gga gta tta	aat gaa aac aca gtt	tct	823			
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243	248	253	258				
gca gga aaa gat ctc	tct act tct cct aag	cca agc cct ata cca	agt	871			
Ala Gly Lys Asp Leu	Ser Thr Ser Pro Lys	Pro Ser Pro Ile Pro	Ser				
259	264	269	274				
cct gtt ttg ggg cga	aag cca aat gct agt	cag tct ttg ctt gta	tgg	919			
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275	280	285	290				
tgt aaa gaa gtt aca	aag aac tac cga gga	gta aaa atc acc aat	ttt	967			
Cys Lys Glu Val Thr	Lys Asn Tyr Arg Gly	Val Lys Ile Thr Asn	Phe				
291	296	301	306				
act aca tcg tgg aga	aat ggt tta tct ttt	tgt gca ata tta cac	cac	1015			
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307	312	317	322				
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Phe Arg Pro Asp Leu	Ile Asp Tyr Lys Ser	Leu Asn Pro Gln Asp	Ile				
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cat ttg gag cga act ctg gag caa aac aaa ggc aag atg gcc aag aaa	3127
His Leu Glu Arg Thr Leu Glu Gln Asn Lys Gly Lys Met Ala Lys Lys	
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gag gag aaa tgt gtt ctt cag tag ccatcagatc agaaagaatc tctcccaaca	3181
Glu Glu Lys Cys Val Leu Gln *	
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aacattttgt ttggctggat tgtactactt tacctctact ttaccaccac cacccttttc	3301
ctccctcctt tccaaataat atacagaact ccaaaatagc ttcattttaag gatttttttg	3361
tgagttaaca atttccttga aatcctgtga aatagatttg cacagacacc ttgtgagtga	3421
ttggtattgg aggtgttcaa gaaactgttc gaaaaagaac aaaaacactt cctcgttat	3481
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<400> 117

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Arg Arg Thr Ala Leu Ile Leu Gly Ser Gly Leu Leu Ser Phe Val Ala
  2                               7                               12                               17

ttc tgg aac tca gtg aca tgg cat ctt cag aga ttt tgg ggt gct tct      152
Phe Trp Asn Ser Val Thr Trp His Leu Gln Arg Phe Trp Gly Ala Ser
 18                               23                               28                               33

ggc tac ttt tgg caa gcc cag tgg gag agg ctg ctg act aca ttt gaa      200
Gly Tyr Phe Trp Gln Ala Gln Trp Glu Arg Leu Leu Thr Thr Phe Glu
 34                               39                               44                               49

ggg aag gag tgg atc ctc ttc ttt ata ggt gcc atc caa gtg cct tgt      248
Gly Lys Glu Trp Ile Leu Phe Phe Ile Gly Ala Ile Gln Val Pro Cys
 50                               55                               60                               65

ctc ttc ttc tgg agc ttc aat ggg ctt cta ttg gtg gtt gac aca aca      296
Leu Phe Phe Trp Ser Phe Asn Gly Leu Leu Leu Val Val Asp Thr Thr
 66                               71                               76                               81

gga aaa cct aac ttc atc tct cgc tac cga att cag gtc ggc aag aat      344
Gly Lys Pro Asn Phe Ile Ser Arg Tyr Arg Ile Gln Val Gly Lys Asn
 82                               87                               92                               97

gaa cct gtg gat cct gtg aaa ctg cac cag tgc atg ata tct ttc ccc      392
Glu Pro Val Asp Pro Val Lys Leu His Gln Cys Met Ile Ser Phe Pro
 98                               103                               108                               113

atg gtg gtc ttc ctc tat ccc ttc ctc aaa tgg tgg aga gac ccc tgc      440
Met Val Val Phe Leu Tyr Pro Phe Leu Lys Trp Trp Arg Asp Pro Cys
114                               119                               124                               129

cgc cgt gag cta ccc acc ttc cac tgg ttc ctc ctg gag ctg gcc atc      488
Arg Arg Glu Leu Pro Thr Phe His Trp Phe Leu Leu Glu Leu Ala Ile
130                               135                               140                               145

ttc acg ctg atc gag gaa gtc ttg ttc tac tat tca cac cgg ctc ctt      536
Phe Thr Leu Ile Glu Glu Val Leu Phe Tyr Tyr Ser His Arg Leu Leu
146                               151                               156                               161

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His His Pro Thr Phe Tyr Lys Lys Ile His Lys Lys His His Glu Trp	
162 167 172 177	
aca gct ccc att ggc gtg atc tct ctc tat gcc cac cct ata gag cat	632
Thr Ala Pro Ile Gly Val Ile Ser Leu Tyr Ala His Pro Ile Glu His	
178 183 188 193	
gca gtc tcc aac atg cta ccg gtg ata gtg ggc cca tta gta atg ggc	680
Ala Val Ser Asn Met Leu Pro Val Ile Val Gly Pro Leu Val Met Gly	
194 199 204 209	
tcc cac ttg tcc tcc atc acc atg tgg ttt tcc ttg gcc ctc atc atc	728
Ser His Leu Ser Ser Ile Thr Met Trp Phe Ser Leu Ala Leu Ile Ile	
210 215 220 225	
acc acc atc tcc cac tgt ggc tac cac ctt ccc ttc ctg cct tcg cct	776
Thr Thr Ile Ser His Cys Gly Tyr His Leu Pro Phe Leu Pro Ser Pro	
226 231 236 241	
gaa ttc cac gac tac cac cat ctc aag ttc aac cag tgc tat ggg gtg	824
Glu Phe His Asp Tyr His His Leu Lys Phe Asn Gln Cys Tyr Gly Val	
242 247 252 257	
ctg ggt gtg ctg gac cac ctc cat ggg act gac acc atg ttc aag cag	872
Leu Gly Val Leu Asp His Leu His Gly Thr Asp Thr Met Phe Lys Gln	
258 263 268 273	
acc aag gcc tac gag aga cat gtc ctc ctg ctg ggc ttc acc ccg ctc	920
Thr Lys Ala Tyr Glu Arg His Val Leu Leu Leu Gly Phe Thr Pro Leu	
274 279 284 289	
tct gag agc atc cca gac tcc cca aag agg atg gag tga gagacagcct	969
Ser Glu Ser Ile Pro Asp Ser Pro Lys Arg Met Glu *	
290 295 300	
aagtgtcatc ctggctgtcc ctcagccatg ggatgcagac acggcttcct gattgcacct	1029
aacaatttgc ctccttcggc cacacgccct aatgatggca ccaccagggt agaggggaagg	1089
tcggcttccc ggaaaagcag ggccaaggat gaggctttct tcaaactact gcccttgatg	1149
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agataactcc tttgtggcct gggcaggatg cagagaatga caaggctgaa aggaggggga	1329
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aaggcgccg	gacccggagg	aaccggaaaa	aacagaactc	agcgaaagag	agctggcagt	180
agcagtggc	gtgtcccagg	agaacgatga	ggagaacgaa	gagcgctggg	ttggaccttt	240
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tgataatctc	cccagtgc	cc atg tat	gag cgc agt	tac atg cat	aga gat	352
		Met Tyr Glu Arg Ser Tyr Met His Arg Asp				
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gtt atc acc cat	gtg gta tgc acc	aaa aca gat	ttt att att act	gcc		400
Val Ile Thr His	Val Val Cys Thr	Lys Thr Asp Phe	Ile Ile Thr Ala			
11	16	21	26			
agt cat gat gga	cat gtc aag ttc	tgg aaa aaa ata	gaa gag gga att			448
Ser His Asp Gly	His Val Lys Phe	Trp Lys Lys Ile	Glu Glu Gly Ile			
27	32	37	42			
gaa ttt gtt aaa	cat ttt cgt agt	cac ctg gga gtt	att gag agt att			496
Glu Phe Val Lys	His Phe Arg Ser	His Leu Gly Val	Ile Glu Ser Ile			
43	48	53	58			
gca gtt agc tct	gag gga gca ttg	ttc tgt tct gtg	ggg gat gat aaa			544
Ala Val Ser Ser	Glu Gly Ala Leu	Phe Cys Ser Val	Gly Asp Asp Lys			
59	64	69	74			
gca atg aag gtg	ttt gat gta gtg	aac ttt gac atg	atc aac atg ctg			592
Ala Met Lys Val	Phe Asp Val Val	Asn Phe Asp Met	Ile Asn Met Leu			
75	80	85	90			
aaa ctt ggc tat	ttt cct gga cag	tgt gag tgg atc	tat tgc cca ggg			640
Lys Leu Gly Tyr	Phe Pro Gly Gln	Cys Glu Trp Ile	Tyr Cys Pro Gly			
91	96	101	106			
gat gca att tct	tca gtt gct gct	tcc gaa aag agt	aca gga aaa att			688
Asp Ala Ile Ser	Ser Val Ala Ala	Ser Glu Lys Ser	Thr Gly Lys Ile			
107	112	117	122			
ttc att tat gat	ggc cga gga gat	aac cag cca ctt	cat att ttt gac			736
Phe Ile Tyr Asp	Gly Arg Gly Asp	Asn Gln Pro Leu	His Ile Phe Asp			
123	128	133	138			
aaa ctc cat aca	tca cct ctt act	cag ata cgg cta	aac cca gtt tac			784
Lys Leu His Thr	Ser Pro Leu Thr	Gln Ile Arg Leu	Asn Pro Val Tyr			
139	144	149	154			

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Lys Ala Val Val Ser Ser Asp Lys Ser Gly Met Ile Glu Tyr Trp Thr	
155 160 165 170	
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Gly Pro Pro His Glu Tyr Lys Phe Pro Lys Asn Val Asn Trp Glu Tyr	
171 176 181 186	
aaa act gac act gat tta tat gaa ttt gcc aag tgt aag gct tat cca	928
Lys Thr Asp Thr Asp Leu Tyr Glu Phe Ala Lys Cys Lys Ala Tyr Pro	
187 192 197 202	
acc agc gta tgt ttt tca cca gat ggg aag aaa ata gct act att ggt	976
Thr Ser Val Cys Phe Ser Pro Asp Gly Lys Lys Ile Ala Thr Ile Gly	
203 208 213 218	
tct gat aga aaa gtt aga att ttc aga ttt gta act gga aaa ctc atg	1024
Ser Asp Arg Lys Val Arg Ile Phe Arg Phe Val Thr Gly Lys Leu Met	
219 224 229 234	
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Arg Val Phe Asp Glu Ser Leu Ser Met Phe Thr Glu Leu Gln Gln Met	
235 240 245 250	
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Arg Gln Gln Leu Pro Asp Met Glu Phe Gly Arg Arg Met Ala Val Glu	
251 256 261 266	
cgt gag ttg gag aag gtt gat gct gta aga tta att aat ata gtt ttt	1168
Arg Glu Leu Glu Lys Val Asp Ala Val Arg Leu Ile Asn Ile Val Phe	
267 272 277 282	
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Asp Glu Thr Gly His Phe Val Leu Tyr Gly Thr Met Leu Gly Ile Lys	
283 288 293 298	
gtt ata aat gta gag aca aac cgg tgt gtg cgg att tta ggc aaa caa	1264
Val Ile Asn Val Glu Thr Asn Arg Cys Val Arg Ile Leu Gly Lys Gln	
299 304 309 314	
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Glu Asn Ile Arg Val Met Gln Leu Ala Leu Phe Gln Gly Ile Ala Lys	
315 320 325 330	
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Lys His Arg Ala Ala Thr Thr Ile Glu Met Lys Ala Ser Glu Asn Pro	
331 336 341 346	
gtt ctt cag aat att caa gct gac cca aca ata gtc tgt aca tca ttc	1408
Val Leu Gln Asn Ile Gln Ala Asp Pro Thr Ile Val Cys Thr Ser Phe	
347 352 357 362	
aaa aag aat aga ttt tat atg ttt acc aaa cga gaa cca gaa gat acg	1456
Lys Lys Asn Arg Phe Tyr Met Phe Thr Lys Arg Glu Pro Glu Asp Thr	
363 368 373 378	
aaa agt gca gat tct gat cga gat gtt ttt aat gag aaa cct tct aaa	1504

Lys Ser Ala Asp Ser Asp Arg Asp Val Phe Asn Glu Lys Pro Ser Lys	
379 384 389 394	
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Glu Glu Val Met Ala Ala Thr Gln Ala Glu Gly Pro Lys Arg Val Ser	
395 400 405 410	
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Asp Ser Ala Ile Ile His Thr Ser Met Gly Asp Ile His Thr Lys Leu	
411 416 421 426	
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Phe Pro Val Glu Cys Pro Lys Thr Val Glu Asn Phe Cys Val His Ser	
427 432 437 442	
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Arg Asn Gly Tyr Tyr Asn Gly His Thr Phe His Arg Ile Ile Lys Gly	
443 448 453 458	
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Phe Met Ile Gln Thr Gly Asp Pro Thr Gly Thr Gly Met Gly Gly Glu	
459 464 469 474	
agc ata tgg gga gga gaa ttt gaa gat gaa ttt cat tca aca tta cga	1792
Ser Ile Trp Gly Gly Glu Phe Glu Asp Glu Phe His Ser Thr Leu Arg	
475 480 485 490	
cat gac agg cca tac aca ctc agc atg gct aac gcg gga tca aat act	1840
His Asp Arg Pro Tyr Thr Leu Ser Met Ala Asn Ala Gly Ser Asn Thr	
491 496 501 506	
aat gga tcc cag ttt ttc ata acg gta gta cca acg cct tgg ctt gat	1888
Asn Gly Ser Gln Phe Phe Ile Thr Val Val Pro Thr Pro Trp Leu Asp	
507 512 517 522	
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Asn Lys His Thr Val Phe Gly Arg Val Thr Lys Gly Met Glu Val Val	
523 528 533 538	
cag agg atc tcc aac gtc aaa gtc aat ccc aaa aca gat aag ccc tat	1984
Gln Arg Ile Ser Asn Val Lys Val Asn Pro Lys Thr Asp Lys Pro Tyr	
539 544 549 554	
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Glu Asp Val Ser Ile Ile Asn Ile Thr Val Lys *	
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      Met Ala Ala Ser Arg Lys Pro Pro Arg Val Arg Val
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Asn His Gln Asp Phe Gln Leu Arg Asn Leu Arg Ile Ile Glu Pro Asn
      13              18              23              28

gag gtg aca cac tca gga gac aca ggt gtg gaa aca gac ggc aga atg      207
Glu Val Thr His Ser Gly Asp Thr Gly Val Glu Thr Asp Gly Arg Met
      29              34              39              44

cct cca aag gtg act tca gag ctg ctt cgg cag ctg aga caa gcc atg      255
Pro Pro Lys Val Thr Ser Glu Leu Leu Arg Gln Leu Arg Gln Ala Met
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agg aac tct gag tat gtg acc gaa ccg atc cag gcc tac atc atc cca      303
Arg Asn Ser Glu Tyr Val Thr Glu Pro Ile Gln Ala Tyr Ile Ile Pro
      61              66              71              76

tcg gga gat gct cat cag agt gag tat att gct cca tgt gac tgt cgg      351
Ser Gly Asp Ala His Gln Ser Glu Tyr Ile Ala Pro Cys Asp Cys Arg
      77              82              87              92

cgg gct ttt gtc tct gga ttc gat ggc tct gcg ggc aca gcc atc atc      399
Arg Ala Phe Val Ser Gly Phe Asp Gly Ser Ala Gly Thr Ala Ile Ile
      93              98              103              108

aca gaa gag cat gca gcc atg tgg act gac ggg cgc tac ttt ctg cag      447
Thr Glu Glu His Ala Ala Met Trp Thr Asp Gly Arg Tyr Phe Leu Gln
      109              114              119              124

gct gcc aag caa atg gac agc aac tgg aca ctt atg aag atg ggt ctg      495
Ala Ala Lys Gln Met Asp Ser Asn Trp Thr Leu Met Lys Met Gly Leu
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aag gac aca cca act cag gaa gac tgg ctg gtg agt gtg ctt cct gaa      543
Lys Asp Thr Pro Thr Gln Glu Asp Trp Leu Val Ser Val Leu Pro Glu
      141              146              151              156

gga tcc agg gtt ggt gtg gac ccc ttg atc att cct aca gat tat tgg      591

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aag	aaa	atg	gcc	aaa	gtt	ctg	aga	agt	gcc	ggc	cat	cac	ctc	att	cct	639
Lys	Lys	Met	Ala	Lys	Val	Leu	Arg	Ser	Ala	Gly	His	His	Leu	Ile	Pro	
173					178					183					188	
gtc	aag	gag	aac	ctc	gtt	gac	aaa	atc	tgg	aca	gac	cgt	cct	gag	cgc	687
Val	Lys	Glu	Asn	Leu	Val	Asp	Lys	Ile	Trp	Thr	Asp	Arg	Pro	Glu	Arg	
189					194					199					204	
cct	tgc	aag	cct	ctc	ctc	aca	ctg	ggc	ctg	gat	tac	aca	ggc	atc	tcc	735
Pro	Cys	Lys	Pro	Leu	Leu	Thr	Leu	Gly	Leu	Asp	Tyr	Thr	Gly	Ile	Ser	
205					210					215					220	
tgg	aag	gac	aag	gtt	gca	gac	ctt	cgg	ttg	aaa	atg	gct	gag	agg	aac	783
Trp	Lys	Asp	Lys	Val	Ala	Asp	Leu	Arg	Leu	Lys	Met	Ala	Glu	Arg	Asn	
221					226					231					236	
gtc	atg	tgg	ttt	gtg	gtc	act	gcc	ttg	gat	gag	att	gcg	tgg	cta	ttt	831
Val	Met	Trp	Phe	Val	Val	Thr	Ala	Leu	Asp	Glu	Ile	Ala	Trp	Leu	Phe	
237					242					247					252	
aat	ctc	cga	gga	tca	gat	gtg	gag	cac	aat	cca	gta	ttt	ttc	tcc	tac	879
Asn	Leu	Arg	Gly	Ser	Asp	Val	Glu	His	Asn	Pro	Val	Phe	Phe	Ser	Tyr	
253					258					263					268	
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Ala	Ile	Ile	Gly	Leu	Glu	Thr	Ile	Met	Leu	Phe	Ile	Asp	Gly	Asp	Arg	
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ata	gac	gcc	ccc	agt	gtg	aag	gag	cac	ctg	ctt	ctt	gac	ttg	ggc	ctg	975
Ile	Asp	Ala	Pro	Ser	Val	Lys	Glu	His	Leu	Leu	Leu	Asp	Leu	Gly	Leu	
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Val	Ser	Asp	Lys	Ala	Ser	Tyr	Ala	Val	Ser	Glu	Thr	Ile	Pro	Lys	Asp	
333					338					343					348	
cac	cgc	tgc	tgt	atg	cct	tac	acc	ccc	atc	tgc	atc	gcc	aaa	gct	gtg	1167
His	Arg	Cys	Cys	Met	Pro	Tyr	Thr	Pro	Ile	Cys	Ile	Ala	Lys	Ala	Val	
349					354					359					364	
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Lys	Asn	Ser	Ala	Glu	Ser	Glu	Gly	Met	Arg	Arg	Ala	His	Ile	Lys	Asp	
365					370					375					380	
gct	gtt	gct	ctc	tgt	gaa	ctc	ttt	aac	tgg	ctg	gag	aaa	gag	gtt	ccc	1263
Ala	Val	Ala	Leu	Cys	Glu	Leu	Phe	Asn	Trp	Leu	Glu	Lys	Glu	Val	Pro	

381		386		391		396	
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Lys Gly Gly Val Thr Glu Ile Ser Ala Ala Asp	Lys Ala Glu Glu Phe						
397	402	407	412				
cgc agg caa cag gca gag ttt gtg gac ctg agc ttc cca aca att tcc	1359						
Arg Arg Gln Gln Ala Asp Phe Val Asp Leu Ser Phe Pro Thr Ile Ser							
413	418	423	428				
agt acg gga ccc aac ggc gcc atc att cac tac gcg cca gtc cct gag	1407						
Ser Thr Gly Pro Asn Gly Ala Ile Ile His Tyr Ala Pro Val Pro Glu							
429	434	439	444				
acg aat agg acc ttg tcc ctg gat gag gtg tac ctt att gac tcg ggt	1455						
Thr Asn Arg Thr Leu Ser Leu Asp Glu Val Tyr Leu Ile Asp Ser Gly							
445	450	455	460				
gct caa tac aag gat ggc acc aca gat gtg acg cgg aca atg cat ttt	1503						
Ala Gln Tyr Lys Asp Gly Thr Thr Asp Val Thr Arg Thr Met His Phe							
461	466	471	476				
ggg acc cct aca gcc tac gag aag gaa tgc ttc aca tat gtc ctc aag	1551						
Gly Thr Pro Thr Ala Tyr Glu Lys Glu Cys Phe Thr Tyr Val Leu Lys							
477	482	487	492				
ggc cac ata gct gtg agt gca gcc gtt ttc ccg act gga acc aaa ggt	1599						
Gly His Ile Ala Val Ser Ala Ala Val Phe Pro Thr Gly Thr Lys Gly							
493	498	503	508				
cac ctt ctt gac tcc ttt gcc cgt tca gct tta tgg gat tca ggc cta	1647						
His Leu Leu Asp Ser Phe Ala Arg Ser Ala Leu Trp Asp Ser Gly Leu							
509	514	519	524				
gat tac ttg cac ggg act gga cat ggt gtt ggg tct ttt ttg aat gtc	1695						
Asp Tyr Leu His Gly Thr Gly His Gly Val Gly Ser Phe Leu Asn Val							
525	530	535	540				
cat gag ggt cct tgc ggc atc agt tac aaa aca ttc tct gat gag ccc	1743						
His Glu Gly Pro Cys Gly Ile Ser Tyr Lys Thr Phe Ser Asp Glu Pro							
541	546	551	556				
ttg gag gca ggc atg att gtc act gat gag ccc ggg tac tat gaa gat	1791						
Leu Glu Ala Gly Met Ile Val Thr Asp Glu Pro Gly Tyr Tyr Glu Asp							
557	562	567	572				
ggg gct ttt gga att cgc att gag aat gtt gtc ctt gtg gtt cct gtg	1839						
Gly Ala Phe Gly Ile Arg Ile Glu Asn Val Val Leu Val Val Pro Val							
573	578	583	588				
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Lys Thr Lys Tyr Asn Phe Asn Asn Arg Gly Ser Leu Thr Phe Glu Pro							
589	594	599	604				
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605	610	615	620				

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Thr Asp Lys Glu Cys Asp Trp Leu Asn Asn Tyr His Leu Thr Cys Arg	
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Asp Val Ile Gly Lys Glu Leu Gln Lys Gln Gly Arg Gln Glu Ala Leu	
637 642 647 652	
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Glu Trp Leu Ile Arg Glu Thr Gln Pro Ile Ser Lys Gln His *	
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Met Pro Glu Asn Pro Ala	
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Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp Arg Leu Lys Met Lys	
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Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu Lys Leu Ser Met Phe	
23 28 33 38	
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Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr Leu Gln	
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Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn His Ile Pro Ser Asp	
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Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly Leu Leu Val Phe Thr	
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Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg Pro Ser Asn Asn Ser	
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Thr Val Ser Gly Leu Phe Pro Trp Thr Pro Lys Leu Gly Asn Glu Asp	
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Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly Leu Gly Phe Ser Val Val	
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Val Gln Pro Gly Ser Val Ala Asp Arg Asp Gln Arg Leu Lys Glu Asn	
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Asp Gln Ile Leu Ala Ile Asn His Thr Pro Leu Asp Gln Asn Ile Ser	
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His Gln Gln Ala Ile Ala Leu Leu Gln Gln Thr Thr Gly Ser Leu Arg	
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Leu Ile Val Ala Arg Glu Pro Val His Thr Lys Ser Ser Thr Ser Ser	
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Ser Leu Asn Asp Thr Thr Leu Pro Glu Thr Val Cys Trp Gly His Val	
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Val Gly Gly Lys Thr Ser Gly Val Val Val Arg Thr Ile Val Pro Gly	
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Gly Leu Ala Asp Arg Asp Gly Arg Leu Gln Thr Gly Asp His Ile Leu	
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Ser Leu Gly Ile Arg Ile Val Gly Tyr Val Gly Thr Ser His Thr Gly	
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Glu Ala Ser Gly Ile Tyr Val Lys Ser Ile Ile Pro Gly Ser Ala Ala	
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Tyr His Asn Gly His Ile Gln Val Asn Asp Lys Ile Val Ala Val Asp	
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Gly Val Asn Ile Gln Gly Phe Ala Asn His Asp Val Val Glu Val Leu	
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Val Glu Pro Leu Lys Pro Pro Ala Leu Phe Leu Thr Gly Ala Val Glu	
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Thr Glu Thr Asn Val Asp Gly Glu Asp Glu Glu Ile Lys Glu Arg Ile	
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Asp Thr Leu Lys Asn Asp Asn Ile Gln Ala Leu Glu Lys Leu Glu Lys	
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759	764	769	774	
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Leu Ile Leu Glu Ala Pro Lys Gly Phe Arg Asp Glu Pro Tyr Phe Lys				
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Glu Glu Leu Val Asp Glu Pro Phe Leu Asp Leu Gly Lys Ser Phe His				
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Ser Gln Gln Lys Glu Ile Glu Gln Ser Lys Glu Ala Trp Glu Met His				
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Glu Leu Tyr Pro Leu Ser His Ile Gln Glu Ala Thr Pro Val Pro Ser				
887	892	897	902	
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Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg Thr Val Tyr Ser Gln Glu				
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Val Met Glu Ser Leu Pro Ser Val Pro Ser Thr Glu Gly Asn Ser Gln				
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Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu Asn Ser Leu Ala Lys Thr				
967	972	977	982	

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1191 1196 1201 1206	

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Ile Ile Glu Leu Glu Lys Asp Lys Asn Gly Leu Gly Leu Ser Leu Ala	
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ttg cct ttg agt gat ggt cca gaa ggc tca agc agt cgt cct cag atg	523
Leu Pro Leu Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met	
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Ile Arg Gly Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln	
18 23 28 33	
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Leu Trp Thr Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys	
34 39 44 49	
tac cct cct gaa gaa gta gaa tct cga cgc tgg cag aag ata gca gat	667
Tyr Pro Pro Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp	
50 55 60 65	
gaa ttg ggc aac agg aca gca aaa cag gtt gcc agc cga gta cag aag	715
Glu Leu Gly Asn Arg Thr Ala Lys Gln Val Ala Ser Arg Val Gln Lys	
66 71 76 81	
tat ttc ata aag cta act aaa gct ggc att cca gta cca ggc aga aca	763
Tyr Phe Ile Lys Leu Thr Lys Ala Gly Ile Pro Val Pro Gly Arg Thr	
82 87 92 97	
cca aac tta tat ata tac tcc aaa aag tct tca aca agc aga cga cag	811
Pro Asn Leu Tyr Ile Tyr Ser Lys Lys Ser Ser Thr Ser Arg Arg Gln	
98 103 108 113	
cac cct ctt aat aag cat ctc ttt aag cct tcc act ttc atg act tca	859
His Pro Leu Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser	
114 119 124 129	
cat gaa ccg cca gtg tat atg gat gaa gat gat gac cga tct tgt ttt	907
His Glu Pro Pro Val Tyr Met Asp Glu Asp Asp Asp Arg Ser Cys Phe	
130 135 140 145	
cat agc cac atg aac act gct gtt gaa gat gca tca gat gac gaa agt	955
His Ser His Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser	
146 151 156 161	
att cct atc atg tat agg aat tta cct gaa tat aaa gaa cta tta cag	1003
Ile Pro Ile Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln	
162 167 172 177	
ttt aaa aag tta aag aag cag aaa ctt cag caa atg caa gct gaa agt	1051
Phe Lys Lys Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser	
178 183 188 193	
gga ttt gtg caa cat gtg ggc ttt aag tgt gat aac tgt ggc ata gaa	1099
Gly Phe Val Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu	
194 199 204 209	

ccc atc cag ggt gtt cgg tgg cat tgc cag gat tgt cct cca gaa atg	1147
Pro Ile Gln Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met	
210 215 220 225	
tct ttg gat ttc tgt gat tct tgt tca gac tgt cta cat gaa aca gat	1195
Ser Leu Asp Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp	
226 231 236 241	
att cac aag gaa gat cac caa tta gaa cct att tat agg tca gag aca	1243
Ile His Lys Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr	
242 247 252 257	
ttc tta gac aga gac tac tgt gtg tct cag ggc acc agt tac aat tac	1291
Phe Leu Asp Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr	
258 263 268 273	
ctt gac cca aac tac ttt cca gca aac aga tga catggaag agaacatcat	1342
Leu Asp Pro Asn Tyr Phe Pro Ala Asn Arg *	
274 279 284	
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aagattctct gctttccag aaatgacact cacagcatga gagcttcctg agtggtctcg	1462
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cacatgcatt cttttatact gctggatttt gttgtgcac attttaaaca ttttgtatgt	2362
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2470

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<213> Homo sapiens

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tcagagacta ttacagacga ttgctgtact cgaggetcag cgttctcaag cagtccaaga	180
ccttgaaagt ttaggcaggc accagagaga agcactgaaa aatcccattg gatttgtgga	240
aaaactccag aagaaggctg atattgggct tccatatcca cagagagttg ttcaattgcc	300
tgagatcgta tgggaccaat atacccatag ccttggggaat tttgaaagag aatttaaaaa	360
tcgtaaaaaga catactagaa gagttaagct agtttttgat aaagtagggt tacctgctag	420
accaaaaaagt cctttagatc ctaagaagga tggagagtcc ctttcatatt ct atg	475
	Met
	1
ttg cct ttg agt gat ggt cca gaa ggc tca agc agt cgt cct cag atg	523
Leu Pro Leu Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met	
2 7 12 17	
ata aga gga cgc ttg tgt gat gat acc aaa cct gaa aca ttt aac cag	571
Ile Arg Gly Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln	
18 23 28 33	
ttg tgg act gtt gaa gaa cag aaa aag ctg gaa cag cta ctc atc aaa	619
Leu Trp Thr Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys	
34 39 44 49	
tac cct cct gaa gaa gta gaa tct cga cgc tgg cag aag ata gca gat	667
Tyr Pro Pro Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp	
50 55 60 65	
gaa ttg ggc aac agg aca gca aaa cag tct tca aca agc aga cga cag	715
Glu Leu Gly Asn Arg Thr Ala Lys Gln Ser Ser Thr Ser Arg Arg Gln	
66 71 76 81	
cac cct ctt aat aag cat ctc ttt aag cct tcc act ttc atg act tca	763
His Pro Leu Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser	
82 87 92 97	

cat gaa ccg cca gtg tat atg gat gaa gat gat gac cga tct tgt ttt	811
His Glu Pro Pro Val Tyr Met Asp Glu Asp Asp Asp Arg Ser Cys Phe	
98 103 108 113	
cat agc cac atg aac act gct gtt gaa gat gca tca gat gac gaa agt	859
His Ser His Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser	
114 119 124 129	
att cct atc atg tat agg aat tta cct gaa tat aaa gaa cta tta cag	907
Ile Pro Ile Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln	
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ttt aaa aag tta aag aag cag aaa ctt cag caa atg caa gct gaa agt	955
Phe Lys Lys Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser	
146 151 156 161	
gga ttt gtg caa cat gtg ggc ttt aag tgt gat aac tgt ggc ata gaa	1003
Gly Phe Val Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu	
162 167 172 177	
ccc atc cag ggt gtt cgg tgg cat tgc cag gat tgt cct cca gaa atg	1051
Pro Ile Gln Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met	
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tct ttg gat ttc tgt gat tct tgt tca gac tgt cta cat gaa aca gat	1099
Ser Leu Asp Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp	
194 199 204 209	
att cac aag gaa gat cac caa tta gaa cct att tat agg tca gag aca	1147
Ile His Lys Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr	
210 215 220 225	
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Phe Leu Asp Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr	
226 231 236 241	
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Leu Asp Pro Asn Tyr Phe Pro Ala Asn Arg *	
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 cttctgcctc tgtatttgga gttgtcagta caactcatca aagaaaactg cctaataata 2086
 aaatcatata tatggtaata atttcctct tttgtagtct gcacaagatc cataaaagat 2146
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 cacatgcatt cttttatact gctggatttt gttgtgcac attttaaaca ttttgtatgt 2266
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 tac acg tat cct gaa aac tgg agg gcc ttc aag gct ctc atc gct gct 96
 Tyr Thr Tyr Pro Glu Asn Trp Arg Ala Phe Lys Ala Leu Ile Ala Ala
 13 18 23 28
 cag tac agc ggg gct cat gtc cgc gtg ctc tcc gca cca ccc cac ttc 144
 Gln Tyr Ser Gly Ala His Val Arg Val Leu Ser Ala Pro Pro His Phe
 29 34 39 44
 cat ttt ggc caa acc aac cgc acc cct gaa ttt ctc cgc aaa ttt cct 192
 His Phe Gly Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro
 45 50 55 60
 gcc ggc aag gtc cca gca ttt gag ggt gat gat gga ttc tgt gtg ttt 240
 Ala Gly Lys Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe
 61 66 71 76
 gag agc aac gcc att gcc tac tat gtg agc aat gag gag ctg cgg gga 288
 Glu Ser Asn Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly
 77 82 87 92

agc act cca gag gca gca gcc cag gtg gtg cag tgg gtg agc ttt gct	336
Ser Thr Pro Glu Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala	
93 98 103 108	
gat tcc gat ata gtg ccc cca gcc agt acc tgg gtg ttc ccc acc ttg	384
Asp Ser Asp Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu	
109 114 119 124	
ggc atc atg cac cac aac aaa cag gcc act gag aat gca aag gag gaa	432
Gly Ile Met His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu	
125 130 135 140	
gtg agg cga att ctg ggg ctg ctg gat gct tac ttg aag acg agg act	480
Val Arg Arg Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr	
141 146 151 156	
ttt ctg gtg ggc gaa cga gtg aca ttg gct gac atc aca gtt gtc tgc	528
Phe Leu Val Gly Glu Arg Val Thr Leu Ala Asp Ile Thr Val Val Cys	
157 162 167 172	
acc ctg ttg tgg ctc tat aag cag gtt cta gag cct tct ttc cgc cag	576
Thr Leu Leu Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe Arg Gln	
173 178 183 188	
gcc ttt ccc aat acc aac cgc tgg ttc ctc acc tgc att aac cag ccc	624
Ala Phe Pro Asn Thr Asn Arg Trp Phe Leu Thr Cys Ile Asn Gln Pro	
189 194 199 204	
cag ttc cgg gct gtc ttg ggc gaa gtg aaa ctg tgt gag aag atg gcc	672
Gln Phe Arg Ala Val Leu Gly Glu Val Lys Leu Cys Glu Lys Met Ala	
205 210 215 220	
cag ttt gat gct aaa aag ttt gca gag acc caa cct aaa aag gac aca	720
Gln Phe Asp Ala Lys Lys Phe Ala Glu Thr Gln Pro Lys Lys Asp Thr	
221 226 231 236	
cca cgg aaa gag aag ggt tca cgg gaa gag aag cag aag ccc cag gct	768
Pro Arg Lys Glu Lys Gly Ser Arg Glu Glu Lys Gln Lys Pro Gln Ala	
237 242 247 252	
gag cgg aag gag gag aaa aag gcg gct gcc cct gct cct gag gag gag	816
Glu Arg Lys Glu Glu Lys Lys Ala Ala Ala Pro Ala Pro Glu Glu Glu	
253 258 263 268	
atg gat gaa tgt gag cag gcg ctg gct gct gag ccc aag gcc aag gac	864
Met Asp Glu Cys Glu Gln Ala Leu Ala Ala Glu Pro Lys Ala Lys Asp	
269 274 279 284	
ccc ttc gct cac ctg ccc aag agt acc ttt gtg ttg gat gaa ttt aag	912
Pro Phe Ala His Leu Pro Lys Ser Thr Phe Val Leu Asp Glu Phe Lys	
285 290 295 300	
cgc aag tac tcc aat gag gac aca ctc tct gtg gca ctg cca tat ttc	960
Arg Lys Tyr Ser Asn Glu Asp Thr Leu Ser Val Ala Leu Pro Tyr Phe	
301 306 311 316	

tgg gag cac ttt gat aag gac ggc tgg tcc ctg tgg tac tca gag tat	1008
Trp Glu His Phe Asp Lys Asp Gly Trp Ser Leu Trp Tyr Ser Glu Tyr	
317 322 327 332	
cgc ttc cct gaa gaa ctc act cag acc ttc atg agc tgc aat ctc atc	1056
Arg Phe Pro Glu Glu Leu Thr Gln Thr Phe Met Ser Cys Asn Leu Ile	
333 338 343 348	
act gga atg ttc cag cga ctg gac aag ctg agg aag aat gcc ttc gcc	1104
Thr Gly Met Phe Gln Arg Leu Asp Lys Leu Arg Lys Asn Ala Phe Ala	
349 354 359 364	
agt gtc atc ctt ttt gga acc aac aat agc agc tcc att tct gga gtc	1152
Ser Val Ile Leu Phe Gly Thr Asn Asn Ser Ser Ser Ile Ser Gly Val	
365 370 375 380	
tgg gtc ttc cga ggc cag gag ctt gcc ttt ccg ctg agt cca gat tgg	1200
Trp Val Phe Arg Gly Gln Glu Leu Ala Phe Pro Leu Ser Pro Asp Trp	
381 386 391 396	
cag gtg gac tac gag tca tac aca tgg cgg aaa ctg gat cct ggc agc	1248
Gln Val Asp Tyr Glu Ser Tyr Thr Trp Arg Lys Leu Asp Pro Gly Ser	
397 402 407 412	
gag gag acc cag acg ctg gtt cga gag tac ttt tcc tgg gag ggg gcc	1296
Glu Glu Thr Gln Thr Leu Val Arg Glu Tyr Phe Ser Trp Glu Gly Ala	
413 418 423 428	
ttc cag cat gtg gca aag cct tca atc agg gca aga tct tca agt gaa	1344
Phe Gln His Val Ala Lys Pro Ser Ile Arg Ala Arg Ser Ser Ser Glu	
429 434 439 444	
cat ctc ttg cca tca cct agc tgc ctg cac ctg ccc ttc agg gag atg	1392
His Leu Leu Pro Ser Pro Ser Cys Leu His Leu Pro Phe Arg Glu Met	
445 450 455 460	
ggg gtc att aaa gga aac tga acattgaaaa aaaaaaaaaa	1432
Gly Val Ile Lys Gly Asn *	
461 466	

<210> 124
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (250)..(627)

<220>
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 taggataata tctaggcatt ttgcgaagtt taaccacccg ggtaccgccg ttcttgtcac 180
 caccaactgg ttttgtaaca gttgcgagaa ctttctcctt ctttttcttt ccaacttgga 240
 cgctgcaga atg gct ccc gca aag aag ggt ggc gag aag aaa aag ggc 288
 Met Ala Pro Ala Lys Lys Gly Gly Glu Lys Lys Lys Gly
 1 5 10
 cgt tct gcc atc aac gaa gtg gta acc cga gaa tac acc atc aac att 336
 Arg Ser Ala Ile Asn Glu Val Val Thr Arg Glu Tyr Thr Ile Asn Ile
 14 19 24 29
 cac aag cgc atc cat gga gtg ggc ttc aag aag cgt gca cct cgg gca 384
 His Lys Arg Ile His Gly Val Gly Phe Lys Lys Arg Ala Pro Arg Ala
 30 35 40 45
 ctc aaa gag att cgg aaa ttt gcc atg aag gag atg gga act cca gat 432
 Leu Lys Glu Ile Arg Lys Phe Ala Met Lys Glu Met Gly Thr Pro Asp
 46 51 56 61
 gtg cgc att gac acc agg ctc aac aaa gct gtc tgg gcc aaa gga ata 480
 Val Arg Ile Asp Thr Arg Leu Asn Lys Ala Val Trp Ala Lys Gly Ile
 62 67 72 77
 agg aat gtg cca tac cga atc cgt gtg cgg ctg tcc aga aaa cgt aat 528
 Arg Asn Val Pro Tyr Arg Ile Arg Val Arg Leu Ser Arg Lys Arg Asn
 78 83 88 93
 gag gat gaa gat tca cca aat aag cta tat act ttg gtt acc tat gta 576
 Glu Asp Glu Asp Ser Pro Asn Lys Leu Tyr Thr Leu Val Thr Tyr Val
 94 99 104 109
 cct gtt acc act ttc aaa aat cta cag aca gtc aat gtg gat gag aac 624
 Pro Val Thr Thr Phe Lys Asn Leu Gln Thr Val Asn Val Asp Glu Asn
 110 115 120 125
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 126
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<212> DNA
 <213> Homo sapiens

<220>
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 <222> (31)..(1938)

<400> 125

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Met Asp Leu Lys Gly Glu Pro Gly Pro Pro Gly Lys Pro Gly Pro Trp		
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ggc ccc cct ggc ccc cct ggc ttc cca gga aaa cca ggc cat gga aag	147	
Gly Pro Pro Gly Pro Pro Gly Phe Pro Gly Lys Pro Gly His Gly Lys		
24 29 34 39		
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Pro Gly Leu His Gly Gln Pro Gly Pro Ala Gly Pro Pro Gly Phe Ser		
40 45 50 55		
cgg atg ggc aag gct ggt ccc cca ggg ctc cct ggc aac gtc ggg cca	243	
Arg Met Gly Lys Ala Gly Pro Pro Gly Leu Pro Gly Asn Val Gly Pro		
56 61 66 71		
cca ggg cag ccg ggg ctt cgg ggg gag cca gga ata cga ggg gac cag	291	
Pro Gly Gln Pro Gly Leu Arg Gly Glu Pro Gly Ile Arg Gly Asp Gln		
72 77 82 87		
ggc ctc cgg gga ccc cca gga ccc cct ggc ctc ccg ggc ccc tca ggc	339	
Gly Leu Arg Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Ser Gly		
88 93 98 103		
att act atc cct gga aaa cca ggt gcc caa ggg gtg cca ggg ccc cca	387	
Ile Thr Ile Pro Gly Lys Pro Gly Ala Gln Gly Val Pro Gly Pro Pro		
104 109 114 119		
gga ttc cag ggg gaa cca ggg ccc cag ggg gag cct ggg ccc cca ggt	435	
Gly Phe Gln Gly Glu Pro Gly Pro Gln Gly Glu Pro Gly Pro Pro Gly		
120 125 130 135		
gat cga ggc ctc aag ggg gat aat gga gtg ggc cag ccc ggg ctg cct	483	
Asp Arg Gly Leu Lys Gly Asp Asn Gly Val Gly Gln Pro Gly Leu Pro		
136 141 146 151		
ggg gcc cca ggg cag ggg ggt gcc ccc ggc ccc ccc ggc ctc cct ggt	531	
Gly Ala Pro Gly Gln Gly Gly Ala Pro Gly Pro Pro Gly Leu Pro Gly		
152 157 162 167		
cca gct ggc tta ggc aaa cct ggt ttg gat ggg ctt cct ggg gcc cca	579	
Pro Ala Gly Leu Gly Lys Pro Gly Leu Asp Gly Leu Pro Gly Ala Pro		
168 173 178 183		
gga gac aag ggt gag tct ggg cct cct gga gtt cca ggc ccc agg ggg	627	

Gly 184	Asp	Lys	Gly	Glu	Ser 189	Gly	Pro	Pro	Gly	Val 194	Pro	Gly	Pro	Arg	Gly 199	
gag	cca	gga	gct	gtg	ggc	cca	aaa	gga	cct	cct	gga	gta	gac	ggt	gtg	675
Glu 200	Pro	Gly	Ala	Val	Gly 205	Pro	Lys	Gly	Pro	Pro 210	Gly	Val	Asp	Gly	Val 215	
gga	gtc	cca	ggg	gca	gca	ggg	ttg	cca	gga	cca	cag	ggc	cca	tca	ggg	723
Gly 216	Val	Pro	Gly	Ala	Ala 221	Gly	Leu	Pro	Gly	Pro 226	Gln	Gly	Pro	Ser	Gly 231	
gcc	aaa	ggg	gag	cca	gga	acc	cgg	ggc	ccc	cct	ggg	ctg	ata	ggc	ccc	771
Ala 232	Lys	Gly	Glu	Pro	Gly 237	Thr	Arg	Gly	Pro	Pro 242	Gly	Leu	Ile	Gly	Pro 247	
act	ggc	tat	ggg	atg	cca	gga	ctg	cca	ggc	ccc	aag	ggg	gac	agg	ggc	819
Thr 248	Gly	Tyr	Gly	Met	Pro 253	Gly	Leu	Pro	Gly	Pro 258	Lys	Gly	Asp	Arg	Gly 263	
cca	gct	ggg	gtc	cca	gga	ctc	ttg	ggg	gac	agg	ggt	gag	cca	ggg	gag	867
Pro 264	Ala	Gly	Val	Pro	Gly 269	Leu	Leu	Gly	Asp	Arg 274	Gly	Glu	Pro	Gly	Glu 279	
gat	ggg	gag	cca	ggg	gag	cag	ggc	cca	cag	ggt	ctt	ggg	ggt	ccc	cct	915
Asp 280	Gly	Glu	Pro	Gly	Glu 285	Gln	Gly	Pro	Gln	Gly 290	Leu	Gly	Gly	Pro	Pro 295	
ggg	ctt	cct	ggg	tct	gca	ggg	ctt	cct	ggc	aga	cgt	ggg	ccc	cct	ggg	963
Gly 296	Leu	Pro	Gly	Ser	Ala 301	Gly	Leu	Pro	Gly	Arg 306	Arg	Gly	Pro	Pro	Gly 311	
cct	aag	ggt	gag	gca	ggg	cct	gga	gga	ccc	cca	gga	gtg	cct	ggc	att	1011
Pro 312	Lys	Gly	Glu	Ala	Gly 317	Pro	Gly	Gly	Pro	Pro 322	Gly	Val	Pro	Gly	Ile 327	
cga	ggt	gac	cag	ggg	cct	agt	ggg	ctg	gct	ggg	aaa	cca	ggg	gtc	cca	1059
Arg 328	Gly	Asp	Gln	Gly	Pro 333	Ser	Gly	Leu	Ala	Gly 338	Lys	Pro	Gly	Val	Pro 343	
ggt	gag	agg	gga	ctt	cct	ggg	gcc	cat	gga	ccc	cct	gga	cca	act	ggg	1107
Gly 344	Glu	Arg	Gly	Leu	Pro 349	Gly	Ala	His	Gly	Pro 354	Pro	Gly	Pro	Thr	Gly 359	
ccc	aag	ggt	gag	ccg	ggt	ttc	acg	ggt	cgc	cct	gga	gga	cca	ggg	gtg	1155
Pro 360	Lys	Gly	Glu	Pro	Gly 365	Phe	Thr	Gly	Arg	Pro 370	Gly	Gly	Pro	Gly	Val 375	
gca	gga	gcc	ctg	ggg	cag	aaa	ggt	gac	ttg	ggg	ctc	cct	ggg	cag	cct	1203
Ala 376	Gly	Ala	Leu	Gly	Gln 381	Lys	Gly	Asp	Leu	Gly 386	Leu	Pro	Gly	Gln	Pro 391	
ggc	ctg	agg	ggt	ccc	tca	gga	atc	cca	gga	ctc	cag	ggt	cca	gct	ggc	1251
Gly 392	Leu	Arg	Gly	Pro	Ser 397	Gly	Ile	Pro	Gly	Leu 402	Gln	Gly	Pro	Ala	Gly 407	
cct	att	ggc	ccc	caa	ggc	ctg	ccg	ggc	ctg	aag	ggg	gaa	cca	ggc	ctg	1299
Pro	Ile	Gly	Pro	Gln	Gly	Leu	Pro	Gly	Leu	Lys	Gly	Glu	Pro	Gly	Leu	

408	413	418	423	
cca ggg ccc cct gga gag ggg aga gca ggg gaa cct ggc acg gct ggc				1347
Pro Gly Pro Pro Gly Glu Gly Arg Ala Gly Glu Pro Gly Thr Ala Gly				
424	429	434	439	
cca cgg ggg ccc cca ggg gtc cct ggc tcc cct gga atc acg ggg cct				1395
Pro Arg Gly Pro Pro Gly Val Pro Gly Ser Pro Gly Ile Thr Gly Pro				
440	445	450	455	
ccg ggg ctc ccg gga ccc cct ggt gcc cct ggg gcc ttc gat gag act				1443
Pro Gly Leu Pro Gly Pro Pro Gly Ala Pro Gly Ala Phe Asp Glu Thr				
456	461	466	471	
ggc atc gca ggc ttg cac ctg ccc aac ggc ggt gtg gag ggt gcc gtg				1491
Gly Ile Ala Gly Leu His Leu Pro Asn Gly Gly Val Glu Gly Ala Val				
472	477	482	487	
ctg ggc aag ggg ggc aag cca cag ttt ggg ctg ggc gag ctg tct gcc				1539
Leu Gly Lys Gly Gly Lys Pro Gln Phe Gly Leu Gly Glu Leu Ser Ala				
488	493	498	503	
cat gcc aca ccg gcc ttc act gcg gtg ctc acc tcg ccc tta ccc gcc				1587
His Ala Thr Pro Ala Phe Thr Ala Val Leu Thr Ser Pro Leu Pro Ala				
504	509	514	519	
tcg ggc atg ccc gtg aaa ttt gac cgg act ctc tac aat ggc cac agc				1635
Ser Gly Met Pro Val Lys Phe Asp Arg Thr Leu Tyr Asn Gly His Ser				
520	525	530	535	
ggc tac aac cca gcc act ggc atc ttc acc tgc cct gtg ggc ggc gtc				1683
Gly Tyr Asn Pro Ala Thr Gly Ile Phe Thr Cys Pro Val Gly Gly Val				
536	541	546	551	
tac tac ttt gct tac cat gtg cac gtc aag ggc acc aac gtg tgg gtg				1731
Tyr Tyr Phe Ala Tyr His Val His Val Lys Gly Thr Asn Val Trp Val				
552	557	562	567	
gcc ctg tac aag aac aac gtg ccg gcc acc tat acc tac gat gag tac				1779
Ala Leu Tyr Lys Asn Asn Val Pro Ala Thr Tyr Thr Tyr Asp Glu Tyr				
568	573	578	583	
aag aag ggc tac ctg gac cag gca tct ggt ggg gcc gtg ctc cag ctg				1827
Lys Lys Gly Tyr Leu Asp Gln Ala Ser Gly Gly Ala Val Leu Gln Leu				
584	589	594	599	
cgg ccc aac gac cag gtc tgg gtg cag atg ccg tcg gac cag gcc aac				1875
Arg Pro Asn Asp Gln Val Trp Val Gln Met Pro Ser Asp Gln Ala Asn				
600	605	610	615	
ggc ctc tac tcc acg gag tac atc cac tcc tcc ttt tca gga ttc ttg				1923
Gly Leu Tyr Ser Thr Glu Tyr Ile His Ser Ser Phe Ser Gly Phe Leu				
616	621	626	631	
ctc tgc ccc aca taa cccgcggggg gtgtcctgct gccctggcct cctccccctt				1978
Leu Cys Pro Thr *				
632				

agtggtagag cgaccttttc aattacaaag aacctcctgg aaaaaaaaaac aaaagctgaa 2038
 cagaggcggc cgtggccttg gcccaggag actaacttgc tttctccctg catgcaggct 2098
 gagattgttt ctggaagggg ctggcctgag tttctttccc ccaaagtgtc gtgcagtgtc 2158
 agggctgcac cccataggcc ctgaggcaca cagcccagcc ccttgtgagt cctggcctct 2218
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 ggaggaggga gggcgccccc cgacccttaa ccagagcgag gttgttgctt tgtgtccaca 180
 gggaccagga gcgaaccatg atgccaggta ggaggggctg actgggccct gcgagcgcgt 240
 gcctttcctg ctgggcagag gccctccaca tggggccacg cgggcccggc acaggagggc 300
 agtcagatgg gcagggcctg agagcctccc tcctctcctt aggtccctaa tc atg 355
 Met
 1

gac tcc cca aga gct ggc acc cac cag ggc ccc ctc gat gca gag aca 403
 Asp Ser Pro Arg Ala Gly Thr His Gln Gly Pro Leu Asp Ala Glu Thr
 2 7 12 17

gag gtc ggt gct gac cgc tgc acg tcg act gcc tac cag gag cag agg 451
 Glu Val Gly Ala Asp Arg Cys Thr Ser Thr Ala Tyr Gln Glu Gln Arg
 18 23 28 33

ccc cag gtg gag caa gtt ggc aaa cag gct cct ctc tcc cca ggg ctg 499
 Pro Gln Val Glu Gln Val Gly Lys Gln Ala Pro Leu Ser Pro Gly Leu
 34 39 44 49

ccg gca atg ggg ggg cct ggc ccc ggc ccc tgt gag gac ccc gcg ggt 547
 Pro Ala Met Gly Gly Pro Gly Pro Gly Pro Cys Glu Asp Pro Ala Gly
 50 55 60 65

gct ggg gga gca ggt gca ggg ggc tcc gag ccc ctg gtg act gtc acc 595

Ala	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Ser	Glu	Pro	Leu	Val	Thr	Val	Thr	
66					71					76					81	
gtg	cag	tgc	gcc	ttc	aca	gtg	gcc	ctg	agg	gca	cga	aga	gga	gcc	gac	643
Val	Gln	Cys	Ala	Phe	Thr	Val	Ala	Leu	Arg	Ala	Arg	Arg	Gly	Ala	Asp	
82					87					92					97	
ctg	tcc	agc	ctg	cgg	gca	ctg	ctg	ggc	caa	gcc	ctc	cct	cac	cag	gcc	691
Leu	Ser	Ser	Leu	Arg	Ala	Leu	Leu	Gly	Gln	Ala	Leu	Pro	His	Gln	Ala	
98					103					108					113	
cag	ctt	ggg	caa	ctc	agt	tac	cta	gcc	cca	ggt	gag	gac	ggg	cac	tgg	739
Gln	Leu	Gly	Gln	Leu	Ser	Tyr	Leu	Ala	Pro	Gly	Glu	Asp	Gly	His	Trp	
114					119					124					129	
gtc	ccc	atc	ccc	gag	gag	gag	tcg	ctg	cag	agg	gcc	tgg	cag	gac	gca	787
Val	Pro	Ile	Pro	Glu	Glu	Glu	Ser	Leu	Gln	Arg	Ala	Trp	Gln	Asp	Ala	
130					135					140					145	
gct	gcc	tgc	ccc	agg	ggg	ctg	cag	ctg	cag	tgc	agg	gga	gcc	ggg	ggt	835
Ala	Ala	Cys	Pro	Arg	Gly	Leu	Gln	Leu	Gln	Cys	Arg	Gly	Ala	Gly	Gly	
146					151					156					161	
cgg	ccg	gtc	ctc	tac	cag	gtg	gtg	gcc	cag	cac	agc	tac	tcc	gcc	cag	883
Arg	Pro	Val	Leu	Tyr	Gln	Val	Val	Ala	Gln	His	Ser	Tyr	Ser	Ala	Gln	
162					167					172					177	
ggg	cca	gag	gac	ctg	ggc	ttc	cga	cag	ggg	gac	acg	gtg	gac	gtc	ctg	931
Gly	Pro	Glu	Asp	Leu	Gly	Phe	Arg	Gln	Gly	Asp	Thr	Val	Asp	Val	Leu	
178					183					188					193	
tgt	gaa	gtg	gac	cag	gca	tgg	ctg	gag	ggc	cac	tgt	gac	ggc	cgc	atc	979
Cys	Glu	Val	Asp	Gln	Ala	Trp	Leu	Glu	Gly	His	Cys	Asp	Gly	Arg	Ile	
194					199					204					209	
ggc	atc	ttc	ccc	aag	tgc	ttc	gtg	gtc	ccc	gcc	ggc	cct	cgg	atg	tca	1027
Gly	Ile	Phe	Pro	Lys	Cys	Phe	Val	Val	Pro	Ala	Gly	Pro	Arg	Met	Ser	
210					215					220					225	
gga	gcc	ccc	ggc	cgc	ctg	ccc	cga	tcc	cag	cag	gga	gat	cag	ccc	taa	1075
Gly	Ala	Pro	Gly	Arg	Leu	Pro	Arg	Ser	Gln	Gln	Gly	Asp	Gln	Pro	*	
226					231					236					241	
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 <213> Homo sapiens

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 <222> (694)..(1779)

<400> 127

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gcggatgcac acaaatgaaa ccctcacttc aacctgaaga cattcgcaca tgagttacgt	180
agaggggacct gcaggaagcg gtagagaaaa cataaggctt atgcgtttta tttccacacc	240
aatttcagga tctttgtcac tgacagcagc actaagactt gttaacttta tatagttaag	300
aagaacaagg ctgagcgcg tgactcacgc ctgtaagcct agaacttttg gagggcaaag	360
caggcagact gcttgagccc aggagttcca gaccagcctg ggcaacatgg caacacccca	420
tctctacaaa aaaatacaag aatcagctgg gcgtgggtgat gtgttcctgt aatctcagct	480
actcgggagg cagaggcagg aggattgctt gaacccggga ggagagggtt gtagttagcc	540
gagatctcgc cactgcactc cagtctggac gacagagtga gactcagtct caaataaata	600
aataaataca taaatataag gaaaaaaata aagctgcttt ctctcttcc tctcttttg	660
tctcatctgg ctctgctcca ggcactgccc aca atg tgg gtg ctt aca cct gct	714
Met Trp Val Leu Thr Pro Ala	
1 5	
gct ttt gct ggg aag ctc ttg agt gtg ttc agg caa cct ctg agc tct	762
Ala Phe Ala Gly Lys Leu Leu Ser Val Phe Arg Gln Pro Leu Ser Ser	
8 13 18 23	
ctg tgg agg agc ctg gtc ccg ctg ttc tgc tgg ctg agg gca acc ttc	810
Leu Trp Arg Ser Leu Val Pro Leu Phe Cys Trp Leu Arg Ala Thr Phe	
24 29 34 39	
tgg ctg cta gct acc aag agg aga aag cag cag ctg gtc ctg aga ggg	858
Trp Leu Leu Ala Thr Lys Arg Arg Lys Gln Gln Leu Val Leu Arg Gly	
40 45 50 55	
cca gat gag acc aaa gag gag gaa gag gac cct cct ctg ccc acc acc	906
Pro Asp Glu Thr Lys Glu Glu Glu Glu Asp Pro Pro Leu Pro Thr Thr	
56 61 66 71	
cca acc agc gtc aac tat cac ttc act cgc cag tgc aac tac aaa tgc	954
Pro Thr Ser Val Asn Tyr His Phe Thr Arg Gln Cys Asn Tyr Lys Cys	
72 77 82 87	
ggc ttc tgt ttc cac aca gcc aaa aca tcc ttt gtg ctg ccc ctt gag	1002
Gly Phe Cys Phe His Thr Ala Lys Thr Ser Phe Val Leu Pro Leu Glu	
88 93 98 103	
gaa gca aag aga gga ttg ctt ttg ctt aag gaa gct ggt atg gag aag	1050
Glu Ala Lys Arg Gly Leu Leu Leu Leu Lys Glu Ala Gly Met Glu Lys	
104 109 114 119	
atc aac ttt tca ggt gga gag cca ttt ctt caa gac cgg gga gaa tac	1098
Ile Asn Phe Ser Gly Gly Glu Pro Phe Leu Gln Asp Arg Gly Glu Tyr	

120	125	130	135	
ctg ggc aag ttg gtg agg ttc tgc aaa gta gag ttg cgg ctg ccc agc				1146
Leu Gly Lys Leu Val Arg Phe Cys Lys Val Glu Leu Arg Leu Pro Ser				
136	141	146	151	
gtg acg atc gtg agc aat gga agc ctg atc cgg gag agg tgg ttc cag				1194
Val Thr Ile Val Ser Asn Gly Ser Leu Ile Arg Glu Arg Trp Phe Gln				
152	157	162	167	
aat tat ggt gag tat ttg gac att ctc gct atc tcc tgt gac agc ttt				1242
Asn Tyr Gly Glu Tyr Leu Asp Ile Leu Ala Ile Ser Cys Asp Ser Phe				
168	173	178	183	
gac gag gaa gtc aat gtc ctt att ggc cgt ggc caa gga aag aag aac				1290
Asp Glu Glu Val Asn Val Leu Ile Gly Arg Gly Gln Gly Lys Lys Asn				
184	189	194	199	
cat gtg gaa aac ctt caa aag ctg agg agg tgg tgt agg gat tat aga				1338
His Val Glu Asn Leu Gln Lys Leu Arg Arg Trp Cys Arg Asp Tyr Arg				
200	205	210	215	
gtc gct ttc aag ata aat tct gtc att aat cgt ttc aac gtg gaa gag				1386
Val Ala Phe Lys Ile Asn Ser Val Ile Asn Arg Phe Asn Val Glu Glu				
216	221	226	231	
gac atg acg gaa cag atc aaa gca cta aac cct gtc cgc tgg aaa gtg				1434
Asp Met Thr Glu Gln Ile Lys Ala Leu Asn Pro Val Arg Trp Lys Val				
232	237	242	247	
ttc cag tgc ctc tta att gag ggt gag aat tgt gga gaa gat gct cta				1482
Phe Gln Cys Leu Leu Ile Glu Gly Glu Asn Cys Gly Glu Asp Ala Leu				
248	253	258	263	
aga gaa gca gaa aga ttt gtt att ggt gat gaa gaa ttt gaa aga ttc				1530
Arg Glu Ala Glu Arg Phe Val Ile Gly Asp Glu Glu Phe Glu Arg Phe				
264	269	274	279	
ttg gag cgc cac aaa gaa gtg tcc tgc ttg gtg cct gaa tct aac cag				1578
Leu Glu Arg His Lys Glu Val Ser Cys Leu Val Pro Glu Ser Asn Gln				
280	285	290	295	
aag atg aaa gac tcc tac ctt att ctg gat gaa tat atg cgc ttt ctg				1626
Lys Met Lys Asp Ser Tyr Leu Ile Leu Asp Glu Tyr Met Arg Phe Leu				
296	301	306	311	
aac tgt aga aag gga cgg aag gac cct tcc aag tcc atc ctg gat gtt				1674
Asn Cys Arg Lys Gly Arg Lys Asp Pro Ser Lys Ser Ile Leu Asp Val				
312	317	322	327	
ggt gta gaa gaa gct ata aaa ttc agt gga ttt gat gaa aag atg ttt				1722
Gly Val Glu Glu Ala Ile Lys Phe Ser Gly Phe Asp Glu Lys Met Phe				
328	333	338	343	
ctg aag cga gga gga aaa tac ata tgg agt aag gct gat ctg aag ctg				1770
Leu Lys Arg Gly Gly Lys Tyr Ile Trp Ser Lys Ala Asp Leu Lys Leu				
344	349	354	359	

gat tgg tag agcggaa agtggaaacga gacttcaaca caccagtggg aaaactccta 1826
Asp Trp *
360

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gttattgaaa cagcacttct gtttttgagt ttgttttagc taaaaagaag gaatacacac 2066
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<213> Homo sapiens

<220>

<221> CDS

<222> (480) .. (3572)

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tttgcctcac	ctaggcctgt	ggcttcttgc	ctggcaggtg	ccacttctcc	acttttaagc	300
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ctcacctatg	tcagccaggt	gagcacatac	gttgctcgaca	ggaggcggag	cttgcaagg	479
atg ggc ttt gac ctg cag aac gtc tgg aga gtc tca cac atc aac agc	527					
Met Gly Phe Asp Leu Gln Asn Val Trp Arg Val Ser His Ile Asn Ser						
1 5 10 15						
aac tac aaa ttg tgc ccc agt tac ccc cag aag ctg ctg gtt cct gtg	575					
Asn Tyr Lys Leu Cys Pro Ser Tyr Pro Gln Lys Leu Leu Val Pro Val						
17 22 27 32						
tgg atc act gac aaa gag ctg gag aac gtg gct tcc ttc cgc tcc tgg	623					
Trp Ile Thr Asp Lys Glu Leu Glu Asn Val Ala Ser Phe Arg Ser Trp						
33 38 43 48						
aag cgg att ccc gtg gtt gtg tat aga cac ttg cgc aat ggg gct gcc	671					
Lys Arg Ile Pro Val Val Val Tyr Arg His Leu Arg Asn Gly Ala Ala						
49 54 59 64						
atc gcc cgc tgc agc cag cca gag atc agc tgg tgg ggc tgg cgc aat	719					
Ile Ala Arg Cys Ser Gln Pro Glu Ile Ser Trp Trp Gly Trp Arg Asn						
65 70 75 80						
gct gat gat gag tac ctg gtc acg tcc att gct aaa gcc tgt gcc ctg	767					
Ala Asp Asp Glu Tyr Leu Val Thr Ser Ile Ala Lys Ala Cys Ala Leu						
81 86 91 96						
gac ccg ggg aca agg gcc act ggg ggc tcc ctc agc acc ggg aat aat	815					
Asp Pro Gly Thr Arg Ala Thr Gly Gly Ser Leu Ser Thr Gly Asn Asn						
97 102 107 112						
gat acc agc gag gcg tgt gat gct gac ttt gat tct tct ctg act gcg	863					
Asp Thr Ser Glu Ala Cys Asp Ala Asp Phe Asp Ser Ser Leu Thr Ala						
113 118 123 128						
tgc tct gga gtg gag agc aca gca gct cct caa aag ctg ctg atc ctg	911					
Cys Ser Gly Val Glu Ser Thr Ala Ala Pro Gln Lys Leu Leu Ile Leu						
129 134 139 144						

gat gcg cga tcc tac acg gca gca gtg gcc aac cgg gcc aag ggt gga	959
Asp Ala Arg Ser Tyr Thr Ala Ala Val Ala Asn Arg Ala Lys Gly Gly	
145 150 155 160	
ggc tgt gaa tgt gaa gag tac tat ccc aac tgt gag gtc gtg ttc atg	1007
Gly Cys Glu Cys Glu Glu Tyr Tyr Pro Asn Cys Glu Val Val Phe Met	
161 166 171 176	
gga atg gcc aac atc cat gcc atc cgg aac agc ttt cag tac ctc cgg	1055
Gly Met Ala Asn Ile His Ala Ile Arg Asn Ser Phe Gln Tyr Leu Arg	
177 182 187 192	
gct gtg tgt agc cag atg ccg gat cct agc aac tgg ttg tcg gca ctg	1103
Ala Val Cys Ser Gln Met Pro Asp Pro Ser Asn Trp Leu Ser Ala Leu	
193 198 203 208	
gag agt acc aaa tgg ctg cag cac ttg tcg gtg atg cta aaa gca gct	1151
Glu Ser Thr Lys Trp Leu Gln His Leu Ser Val Met Leu Lys Ala Ala	
209 214 219 224	
gtg ctg gtg gct aat aca gta gac cgg gaa ggc cgg cct gtg ctg gta	1199
Val Leu Val Ala Asn Thr Val Asp Arg Glu Gly Arg Pro Val Leu Val	
225 230 235 240	
cac tgc tca gat ggc tgg gac cgc aca ccg cag atc gta gcc ctg gcc	1247
His Cys Ser Asp Gly Trp Asp Arg Thr Pro Gln Ile Val Ala Leu Ala	
241 246 251 256	
aaa ata tta ctg gac cca tat tac agg acg ttg gag ggc ttc caa gtg	1295
Lys Ile Leu Leu Asp Pro Tyr Tyr Arg Thr Leu Glu Gly Phe Gln Val	
257 262 267 272	
tta gtg gag tct gac tgg ctg gat ttt ggg cac aag ttt gga gat cgc	1343
Leu Val Glu Ser Asp Trp Leu Asp Phe Gly His Lys Phe Gly Asp Arg	
273 278 283 288	
tgt ggc cac caa gag aat gtg gag gac caa aac gaa caa tgc cct gtg	1391
Cys Gly His Gln Glu Asn Val Glu Asp Gln Asn Glu Gln Cys Pro Val	
289 294 299 304	
ttc ctc cag tgg ctt gat tct gtt cat cag ttg ctt aag cag ttc ccc	1439
Phe Leu Gln Trp Leu Asp Ser Val His Gln Leu Leu Lys Gln Phe Pro	
305 310 315 320	
tgc atg ttt gaa ttt aat gaa gca ttc ctg gta aaa ctg gtg caa cac	1487
Cys Met Phe Glu Phe Asn Glu Ala Phe Leu Val Lys Leu Val Gln His	
321 326 331 336	
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Thr Tyr Ser Cys Leu Tyr Gly Thr Phe Leu Ala Asn Asn Pro Cys Glu	
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Val Gln Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr
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127 132 137 142	
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Ser Cys Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro	
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Lys Pro Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys	
159 164 169 174	
cat acc act gtg act gca ttg aaa gat gtc cct ttc tct ctc tgc cag	878
His Thr Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln	
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Ser Val Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys	
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Asn Phe Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser	
207 212 217 222	
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Gly Pro Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro	
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Thr Pro Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val	
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Asp Val Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu	
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Thr Ala *	
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cgggcacctg cgcgggcgccg ggtgaaggcg agagcctcgg cgagccctct gcagcggagc      180
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Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys Thr Leu Ser Ala Cys Asp
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Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu Leu Gly Ser Thr Ser Phe
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atc ccg att ggc cgt cgg act tat gcc agt gcg gcg gag ccg gtt ggc      558
Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser Ala Ala Glu Pro Val Gly
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agc aaa gct gtc ctg gtc aca ggc tgt gac tct gga ttt ggg ttc tca      606
Ser Lys Ala Val Leu Val Thr Gly Cys Asp Ser Gly Phe Gly Phe Ser
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ttg gcc aag cat ctg cat tca aaa ggc ttc ctt gtg ttt gct ggc tgc      654
Leu Ala Lys His Leu His Ser Lys Gly Phe Leu Val Phe Ala Gly Cys
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Leu Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu
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aac agt gac cga ttg aga acc gtc cag ctc aat gtc tgc agc agc gaa      750
Asn Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu
 103                108                113                118

gag gtg gag aaa gtg gtg gag att gtc cgc tcg agc ctg aag gac cct      798
Glu Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro
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Gly Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu	
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Val Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu	
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Ile Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly	
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Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly	
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Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly	
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Val Lys Val Ser Val Val Glu Pro Gly Asn Phe Ile Ala Ala Thr Ser	
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Glu Leu Pro Glu Val Val Arg Lys Asp Tyr Gly Lys Lys Tyr Phe Asp	
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279 284 289 294	
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Thr Ser Pro Val Ile Asp Ala Val Thr His Ala Leu Thr Ala Thr Thr	
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Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr Tyr Trp Trp Leu Arg Met	
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Gln Ile Met Thr His Leu Pro Gly Ala Ile Ser Asp Met Ile Tyr Ile	
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Arg *	
343	

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 cagctcggcg cggagcgtcc tgtcaggcgc gcggccgaggg cgtcgaggac tctccccgcg 240
 atg atg ccg atg ata tta act gtt ttc ttg agc aac aat gaa cag att 288
 Met Met Pro Met Ile Leu Thr Val Phe Leu Ser Asn Asn Glu Gln Ile
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 Leu Thr Glu Val Pro Ile Thr Pro Glu Thr Thr Cys Arg Asp Val Val
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 gaa ttt tgc aag gaa cct gga gaa ggc agc tgc cat tta gct gaa gtg 384
 Glu Phe Cys Lys Glu Pro Gly Glu Gly Ser Cys His Leu Ala Glu Val
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 His Leu Gln Lys Trp Gly Pro Arg Arg Glu Glu Val Lys Phe Phe Leu
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 Arg His Glu Asp Ser Pro Thr Glu Asn Ser Glu Gln Gly Gly Arg Gln
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 acc caa gag caa cga act cag aga aat gta ata aat gta cct gga gaa 576
 Thr Gln Glu Gln Arg Thr Gln Arg Asn Val Ile Asn Val Pro Gly Glu

97	102	107	112	
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Lys Arg Thr Glu Asn Gly Val Gly Asn Pro Arg Val Glu Leu Thr Leu				
113	118	123	128	
tca gag ctc caa gat atg gca gct agg caa cag cag cag att gaa aat				672
Ser Glu Leu Gln Asp Met Ala Ala Arg Gln Gln Gln Gln Ile Glu Asn				
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Gln Gln Gln Met Leu Val Ala Lys Glu Gln Arg Leu His Phe Leu Lys				
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Gln Gln Glu Arg Arg Gln Gln Gln Ser Ile Ser Glu Asn Glu Lys Leu				
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cag aaa ttg aaa gaa cga gtt gaa gcc cag gag aac aag ctg aag aaa				816
Gln Lys Leu Lys Glu Arg Val Glu Ala Gln Glu Asn Lys Leu Lys Lys				
177	182	187	192	
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Ile Arg Ala Met Arg Gly Gln Val Asp Tyr Ser Lys Ile Met Asn Gly				
193	198	203	208	
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Asn Leu Ser Ala Glu Ile Glu Arg Phe Ser Ala Met Phe Gln Glu Lys				
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Lys Gln Glu Val Gln Thr Ala Ile Leu Arg Val Asp Gln Leu Ser Gln				
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353 358 363 368	
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Asp Pro Ile Lys Pro Gln Ser Leu Ser Ile Ala Ser Asn Ala Ala His	
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Glu Ile Gly Lys Val Pro Pro Pro Ile Pro Gly Val Gly Lys Gln Leu	
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gcc cca ctc ccc gct gag cct gcc ccg tca tca gat gcc aat gat aat	2640

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His	Gln	Thr	Ala	Glu	Pro	Ala	Glu	Asp	Asn	Asn	Asn	Asn	Val	Ala	Thr		
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Phe	Leu	Leu	Asp	Phe	Gly	Val	Asn	Val	Asn	Ala	Ala	Asp	Ser	Asp	Gly		
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Met His Val
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Asp Met Asp Cys Phe Phe Val Ser Val Gly Ile Arg Asn Arg Pro Asp
4 9 14 19
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Leu Lys Gly Lys Pro Val Ala Val Thr Ser Asn Arg Gly Thr Gly Arg
20 25 30 35
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Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln Leu Glu Trp Gln Tyr Tyr
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Gln Asn Lys Ile Leu Lys Gly Lys Ala Asp Ile Pro Asp Ser Ser Leu
52 57 62 67
tgg gag aat cca gat tct gcg caa gca aat gga att gat tct gtt ttg 355
Trp Glu Asn Pro Asp Ser Ala Gln Ala Asn Gly Ile Asp Ser Val Leu
68 73 78 83
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Ser Arg Ala Glu Ile Ala Ser Cys Ser Tyr Glu Ala Arg Gln Leu Gly
84 89 94 99
att aag aac gga atg ttt ttt ggg cat gct aaa caa cta tgt cct aat 451

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Leu	Gln	Ala	Val	Pro	Tyr	Asp	Phe	His	Ala	Tyr	Lys	Glu	Val	Ala	Gln		
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Thr	Leu	Tyr	Glu	Thr	Leu	Ala	Ser	Tyr	Thr	His	Asn	Ile	Glu	Ala	Val		
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Ser	Cys	Asp	Glu	Ala	Leu	Val	Asp	Ile	Thr	Glu	Ile	Leu	Ala	Glu	Thr		
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Lys	Leu	Thr	Pro	Asp	Glu	Phe	Ala	Asn	Ala	Val	Arg	Met	Glu	Ile	Lys		
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Leu	Ala	Arg	Met	Ala	Thr	Arg	Lys	Ala	Lys	Pro	Asp	Gly	Gln	Tyr	His		
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212					217					222					227		
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Gln	Lys	Glu	Phe	Gly	Pro	Lys	Thr	Gly	Gln	Met	Leu	Tyr	Arg	Phe	Cys		
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Arg	Gly	Leu	Asp	Asp	Arg	Pro	Val	Arg	Thr	Glu	Lys	Glu	Arg	Lys	Ser		
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Val	Ser	Ala	Glu	Ile	Asn	Tyr	Gly	Ile	Arg	Phe	Thr	Gln	Pro	Lys	Glu		
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gca	gaa	gct	ttt	ctt	ctg	agt	ctt	tca	gaa	gaa	att	caa	aga	aga	cta		1075
Ala	Glu	Ala	Phe	Leu	Leu	Ser	Leu	Ser	Glu	Glu	Ile	Gln	Arg	Arg	Leu		
308					313					318					323		
gaa	gcc	act	ggc	atg	aag	ggg	aaa	cgt	cta	act	ctc	aaa	atc	atg	gta		1123
Glu	Ala	Thr	Gly	Met	Lys	Gly	Lys	Arg	Leu	Thr	Leu	Lys	Ile	Met	Val		

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Arg Lys Pro Gly Ala	Pro Val Glu Thr Ala	Lys Phe Gly Gly His Gly		
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Ile Cys Asp Asn Ile	Ala Arg Thr Val Thr	Leu Asp Gln Ala Thr	Asp	
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aat gca aaa ata att gga aag gcg atg cta aac atg ttt cat aca atg				1267
Asn Ala Lys Ile Ile	Gly Lys Ala Met Leu	Asn Met Phe His Thr	Met	
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Lys Leu Asn Ile Ser	Asp Met Arg Gly Val	Gly Ile His Val Asn	Gln	
388	393	398	403	
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Leu Val Pro Thr Asn	Leu Asn Pro Ser Thr	Cys Pro Ser Arg Pro	Ser	
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Val Gln Ser Ser His	Phe Pro Ser Gly Ser	Tyr Ser Val Arg Asp	Val	
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Phe Gln Val Gln Lys	Ala Lys Lys Ser Thr	Glu Glu Glu His Lys	Glu	
436	441	446	451	
gta ttt cgg gct gct gtg gat ctg gaa ata tca tct gct tct aga act				1507
Val Phe Arg Ala Ala	Val Asp Leu Glu Ile	Ser Ser Ala Ser Arg	Thr	
452	457	462	467	
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Cys Thr Phe Leu Pro	Pro Phe Pro Ala His	Leu Pro Thr Ser Pro	Asp	
468	473	478	483	
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Thr Asn Lys Ala Glu	Ser Ser Gly Lys Trp	Asn Gly Leu His Thr	Pro	
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Val Ser Val Gln Ser	Arg Leu Asn Leu Ser	Ile Glu Val Pro Ser	Pro	
500	505	510	515	
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Ser Gln Leu Asp Gln	Ser Val Leu Glu Ala	Leu Pro Pro Asp Leu	Arg	
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Glu Gln Val Glu Gln	Val Cys Ala Val Gln	Gln Ala Glu Ser His	Gly	
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Val Asp Pro Glu Val Phe Ala Ala Leu Pro Ala Glu Leu Gln Arg Glu	
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Leu Lys Ala Ala Tyr Asp Gln Arg Gln Arg Gln Gly Glu Asn Ser Thr	
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His Gln Gln Ser Ala Ser Ala Ser Val Pro Lys Asn Pro Leu Leu His	
628 633 638 643	
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Leu Lys Ala Ala Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Lys Thr	
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Ile Gly Ser Pro Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu	
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aac agt cct gca aaa act ctg cca ggg gcc tgt ggc agt ccc cag aag	2179
Asn Ser Pro Ala Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys	
676 681 686 691	
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Leu Ile Asp Gly Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro	
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Leu Glu Glu Leu Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser	
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Ala Gly Ala Val Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp	
740 745 750 755	
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Ile Thr Thr Ile Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val	
756 761 766 771	
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Lys Tyr Cys Thr Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp	
772 777 782 787	

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Lys His Asp Glu Trp Leu Ser Cys Ala Pro Lys Thr Arg Pro Gln Asn	
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Gly Ser Ile Ile Leu Tyr Asn Arg Lys Lys Val Lys Tyr Arg Lys Asp	
72 77 82 87	
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88 93 98 103	
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His Met Lys Leu Lys Val Gln Gly Met Glu Cys Leu Tyr Gly Cys Tyr	
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Val His Ser Ser Ile Val Pro Thr Phe His Arg Arg Cys Tyr Trp Leu	
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Leu Gln Asn Pro Asp Ile Val Leu Val His Tyr Leu Asn Val Pro Ala	
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Leu Glu Asp Cys Gly Lys Gly Cys Ser Pro Ile Phe Cys Ser Ile Ser	
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248 253 258 263	
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ccc	act	tct	cga	ggg	ggg	tct	tca	aga	gga	ggc	act	gct	atc	ctc	ctc	1131	
Pro	Thr	Ser	Arg	Gly	Gly	Ser	Ser	Arg	Gly	Gly	Thr	Ala	Ile	Leu	Leu		
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ttg	gct	cca	cag	gct	gat	cct	agg	cct	tcc	atg	agt	ttg	gca	gtg	gtt	1227	
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Val	Gly	Thr	Glu	Pro	Ser	Ala	Pro	Pro	Ala	Pro	Pro	Ser	Pro	Ala	Phe		
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Thr	Pro	Cys	Ser	Ala	Leu	Glu	Pro	Ala	Ala	Ala	Leu	Glu	Pro	Gln	Ala		
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Thr Asp Phe Ser Pro Glu Trp Ser Tyr Pro Glu Gly Gly Val Lys Val				
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Leu Ile Thr Gly Pro Trp Thr Glu Ala Ala Glu His Tyr Ser Cys Val				
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Phe Asp His Ile Ala Val Pro Ala Ser Leu Val Gln Pro Gly Val Leu				
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Arg Cys Tyr Cys Pro Ala His Glu Val Gly Leu Val Ser Leu Gln Val				
584	589	594	599	
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Ala Gly Arg Glu Gly Pro Leu Ser Ala Ser Val Leu Phe Glu Tyr Arg				
600	605	610	615	
gcc cgc cga ttc ctg tct ctg cct agt act caa ctt gac tgg ctg tca				2043
Ala Arg Arg Phe Leu Ser Leu Pro Ser Thr Gln Leu Asp Trp Leu Ser				
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Leu Asp Asp Asn Gln Phe Arg Met Ser Ile Leu Glu Arg Leu Glu Gln				
632	637	642	647	
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Met Glu Lys Arg Met Ala Glu Ile Ala Ala Ala Gly Gln Val Pro Cys				
648	653	658	663	
cag ggt cct gat gct cct cca gtt cag gat gaa ggc cag ggg cct ggg				2187
Gln Gly Pro Asp Ala Pro Pro Val Gln Asp Glu Gly Gln Gly Pro Gly				
664	669	674	679	
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Phe Glu Ala Arg Val Val Val Leu Val Glu Ser Met Ile Pro Arg Ser				
680	685	690	695	
acc tgg aag ggt cct gaa cgt ctg gcc cat gga agc ccc ttc cgg ggc				2283
Thr Trp Lys Gly Pro Glu Arg Leu Ala His Gly Ser Pro Phe Arg Gly				
696	701	706	711	
atg agc ctt ctg cac ctg gct gct gcc cag ggc tat gcc cgc ctc atc				2331
Met Ser Leu Leu His Leu Ala Ala Ala Gln Gly Tyr Ala Arg Leu Ile				
712	717	722	727	
gag acc ctg agc cag tgg cgg agt gtg gag act gga agc ttg gac tta				2379
Glu Thr Leu Ser Gln Trp Arg Ser Val Glu Thr Gly Ser Leu Asp Leu				
728	733	738	743	

gag cag gag gtt gac ccg ctc aac gtg gat cat ttc tct tgc acc cct	2427
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1192

1197

1202

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Trp *				
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His Ser Gln Glu Tyr Lys Ile Pro Glu Gly Phe Gln Gly Lys Arg Val				
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Leu Val Ile Gly Leu Gly Asn Thr Gly Gly Asp Ile Ala Val Glu Leu				
188	193	198	203	
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Cys Lys Ile Pro Pro Ser Gln Lys Leu Met Met Glu Ala Thr Glu Lys	
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Phe Asp Tyr Ile Ala Tyr Met Asp Asp Ile Ala Ala Cys Ile Gly Thr	
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Pro Ala Ser Met Ser His Tyr Leu Lys Ala Trp Gly Ala Pro Val Leu	
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Glu Cys Val Gly Ile Ala Ser Lys Ala Leu Cys Gly Leu Thr Glu Ala	

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cca tca cag gtc ctg tca gcc gcc aca att gtt gcc aag cac acg tca				403
Pro Ser Gln Val Leu Ser Ala Ala Thr Ile Val Ala Lys His Thr Ser				
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gcc ttg tgt aat gcc tgc cgc atc gcc tca tcc aag acg gcc aac cca				451
Ala Leu Cys Asn Ala Cys Arg Ile Ala Ser Ser Lys Thr Ala Asn Pro				
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Ile Pro Ala Gln Ile Ser Ser Glu Gly Ser Gln Ala Gln Glu Pro Ile				
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Ile Thr Ser Ile Arg Asp Lys Ala Pro Gly Gln Arg Glu Cys Asp Tyr				
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Lys Ala Ala Ala Leu Asn Leu Ser Ala Leu His Ser Pro Ala His Arg
7 12 17 22
cct ccg ggt ttc agt gta gct cag aag cca ttt gga gcc acg tat gta 149
Pro Pro Gly Phe Ser Val Ala Gln Lys Pro Phe Gly Ala Thr Tyr Val
23 28 33 38
tgg agc agc atc ata aac act ctt caa aca caa gtg gaa gtg aaa aaa 197
Trp Ser Ser Ile Ile Asn Thr Leu Gln Thr Gln Val Glu Val Lys Lys
39 44 49 54
cga agg cac cgt tta aaa cga cat aat gac tgc ttt gtt ggt tca gaa 245
Arg Arg His Arg Leu Lys Arg His Asn Asp Cys Phe Val Gly Ser Glu
55 60 65 70
gct gtg gat gtc att ttt tct cac cta att cag aat aag tat ttt ggt 293
Ala Val Asp Val Ile Phe Ser His Leu Ile Gln Asn Lys Tyr Phe Gly
71 76 81 86
gat gta gat att cct cga gcc aaa gtg gtg aga gtg tgt caa gcg ctt 341
Asp Val Asp Ile Pro Arg Ala Lys Val Val Arg Val Cys Gln Ala Leu
87 92 97 102
atg gac tac aaa gta ttt gaa gca gtt cca acc aaa gtc ttt gga aaa 389

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Asp	Lys	Lys	Pro	Thr	Phe	Glu	Asp	Ser	Ser	Cys	Ser	Leu	Tyr	Arg	Phe	
119					124					129					134	
acc	aca	ata	cct	aac	caa	gac	agt	cag	tta	ggc	aaa	gag	aac	aaa	cta	485
Thr	Thr	Ile	Pro	Asn	Gln	Asp	Ser	Gln	Leu	Gly	Lys	Glu	Asn	Lys	Leu	
135					140					145					150	
tat	tca	cct	gcc	agg	tat	gca	gat	gca	tta	ttt	aag	tca	tcc	gat	atc	533
Tyr	Ser	Pro	Ala	Arg	Tyr	Ala	Asp	Ala	Leu	Phe	Lys	Ser	Ser	Asp	Ile	
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aga	tca	gcc	agt	tta	gag	gac	ctg	tgg	gaa	aat	ctg	agt	tta	aag	cct	581
Arg	Ser	Ala	Ser	Leu	Glu	Asp	Leu	Trp	Glu	Asn	Leu	Ser	Leu	Lys	Pro	
167					172					177					182	
gcc	aac	tcc	cct	cat	gta	aat	atc	tct	aca	acc	ttg	tct	cca	caa	gtt	629
Ala	Asn	Ser	Pro	His	Val	Asn	Ile	Ser	Thr	Thr	Leu	Ser	Pro	Gln	Val	
183					188					193					198	
att	aat	gaa	gtg	tgg	caa	gaa	gaa	aca	att	ggg	cgt	cta	cta	caa	ctt	677
Ile	Asn	Glu	Val	Trp	Gln	Glu	Glu	Thr	Ile	Gly	Arg	Leu	Leu	Gln	Leu	
199					204					209					214	
gta	gac	ctt	cca	ctt	ctt	gac	tcc	tta	ctg	aaa	cag	caa	gag	gct	gta	725
Val	Asp	Leu	Pro	Leu	Leu	Asp	Ser	Leu	Leu	Lys	Gln	Gln	Glu	Ala	Val	
215					220					225					230	
cct	aaa	att	cct	caa	cct	aag	agg	cag	tcc	acc	atg	gtc	aac	agc	agt	773
Pro	Lys	Ile	Pro	Gln	Pro	Lys	Arg	Gln	Ser	Thr	Met	Val	Asn	Ser	Ser	
231					236					241					246	
aac	tat	ctg	gat	cga	ggg	att	ctc	aag	gct	tat	agt	gac	tct	cag	gaa	821
Asn	Tyr	Leu	Asp	Arg	Gly	Ile	Leu	Lys	Ala	Tyr	Ser	Asp	Ser	Gln	Glu	
247					252					257					262	
gat	gag	tgg	ctc	tcg	gca	gca	att	gac	tgt	tta	gaa	tac	ctt	cca	gac	869
Asp	Glu	Trp	Leu	Ser	Ala	Ala	Ile	Asp	Cys	Leu	Glu	Tyr	Leu	Pro	Asp	
263					268					273					278	
caa	atg	gtg	gtg	gaa	ata	agc	aga	agc	ttt	cct	gag	caa	cca	gac	cga	917
Gln	Met	Val	Val	Glu	Ile	Ser	Arg	Ser	Phe	Pro	Glu	Gln	Pro	Asp	Arg	
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aca	gac	tta	gtg	aaa	gaa	ctt	ctg	ttt	gat	gcc	att	ggc	aga	tat	tac	965
Thr	Asp	Leu	Val	Lys	Glu	Leu	Leu	Phe	Asp	Ala	Ile	Gly	Arg	Tyr	Tyr	
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agt	agt	agg	gaa	cct	ctg	tta	aat	cac	tta	tct	gac	gtt	cat	aat	gga	1013
Ser	Ser	Arg	Glu	Pro	Leu	Leu	Asn	His	Leu	Ser	Asp	Val	His	Asn	Gly	
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att	gca	gaa	ctc	tta	gtg	aat	ggg	aag	acg	gaa	ata	gct	tta	gaa	gct	1061
Ile	Ala	Glu	Leu	Leu	Val	Asn	Gly	Lys	Thr	Glu	Ile	Ala	Leu	Glu	Ala	

327	332	337	342	
acc cag ctc ctt cta aag ctt tta gat ttc caa aat aga gaa gaa ttt				1109
Thr Gln Leu Leu Leu Lys Leu Leu Asp Phe Gln Asn Arg Glu Glu Phe				
343	348	353	358	
aga aga cta ctg tat ttc atg gct gtt gca gca aat cct tct gag ttt				1157
Arg Arg Leu Leu Tyr Phe Met Ala Val Ala Ala Asn Pro Ser Glu Phe				
359	364	369	374	
aaa tta cag aaa gaa agt gac aac cga atg gtt gtg aaa agg ata ttc				1205
Lys Leu Gln Lys Glu Ser Asp Asn Arg Met Val Val Lys Arg Ile Phe				
375	380	385	390	
tca aaa gct att gtt gac aat aaa aat tta tcc aaa ggc aaa aca gat				1253
Ser Lys Ala Ile Val Asp Asn Lys Asn Leu Ser Lys Gly Lys Thr Asp				
391	396	401	406	
ctt ctg gta ctc ttt tta atg gat cat cag aaa gat gtt ttt aag att				1301
Leu Leu Val Leu Phe Leu Met Asp His Gln Lys Asp Val Phe Lys Ile				
407	412	417	422	
cct gga act cta cat aaa att gta agt gtt aag ctt atg gcc ata cag				1349
Pro Gly Thr Leu His Lys Ile Val Ser Val Lys Leu Met Ala Ile Gln				
423	428	433	438	
aac gga aga gat cca aat aga gat gca gga tat att tat tgc cag aga				1397
Asn Gly Arg Asp Pro Asn Arg Asp Ala Gly Tyr Ile Tyr Cys Gln Arg				
439	444	449	454	
att gat caa cgt gac tat tcc aac aat aca gag aag aca acc aaa gat				1445
Ile Asp Gln Arg Asp Tyr Ser Asn Asn Thr Glu Lys Thr Thr Lys Asp				
455	460	465	470	
gag ctg ttg aat tta cta aaa act ctt gat gag gat tca aaa ctt tct				1493
Glu Leu Leu Asn Leu Leu Lys Thr Leu Asp Glu Asp Ser Lys Leu Ser				
471	476	481	486	
gcc aaa gag aag aaa aaa ttg cta ggt caa ttc tat aag tgt cac cca				1541
Ala Lys Glu Lys Lys Lys Leu Leu Gly Gln Phe Tyr Lys Cys His Pro				
487	492	497	502	
gac atc ttt att gag cat ttt gga gac tga g tttttaatat ctgtatataa				1592
Asp Ile Phe Ile Glu His Phe Gly Asp *				
503	508			
gttgtgtatt ttaagaataa attatgtatc ctaaatatcc aatcacattt gtaagtgtgg				1652
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gccagtcac	tatgtagtgg	aggggcagac	accctccgc	aaattctgga	aggttcttag	300
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aacggagctg	ccgtcgcc	atg ttt ggc tgc ttg gtg gcg ggg agg ctg gtg				411
		Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val				
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caa aca gct gca cag	caa gtg gca gag gat	aaa ttt gtt ttt gac tta				459
Gln Thr Ala Ala Gln	Gln Val Ala Glu Asp Lys	Phe Val Phe Asp Leu				
12 17	22	27				
cct gat tat gaa agt atc aac cat gtt gtg gtt ttt atg ctg gga aca						507
Pro Asp Tyr Glu Ser Ile Asn His Val Val Val Phe Met Leu Gly Thr						
28 33	38	43				
atc cca ttt cct gag gga atg gga gga tct gtc tac ttt tct tat cct						555
Ile Pro Phe Pro Glu Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro						
44 49	54	59				
gat tca aat gga atg cca gta tgg caa ctc cta gga ttt gtc acg aat						603
Asp Ser Asn Gly Met Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn						
60 65	70	75				
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Gly Lys Pro Ser Ala Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu						
76 81	86	91				
gga agc caa cat cct ttt gga gcc atg aat att gtc cga act cca tct						699
Gly Ser Gln His Pro Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser						
92 97	102	107				
gtt gct cag att gga att tca gtg gaa tta tta gac agt atg gct cag						747
Val Ala Gln Ile Gly Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln						
108 113	118	123				
cag act cct gta ggt aat gct gct gta tcc tca gtt gac tca ttc act						795
Gln Thr Pro Val Gly Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr						
124 129	134	139				
cag ttc aca caa aag atg ttg gac aat ttc tac aat ttt gct tca tca						843
Gln Phe Thr Gln Lys Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser						
140 145	150	155				

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Phe Ala Val Ser Gln Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe	
156 161 166 171	
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Ile Pro Ala Asn Val Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg	
172 177 182 187	
cta gca cag aac cct ctg ttt tgg aaa aca taa tttgaata aaataatttt	990
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Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val	
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Gly Pro Gly Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg	
14 19 24 29	
cta ctg ttg atc ctg tcc ggc tgc ttg gtc tac ggc aca gct gaa act	206
Leu Leu Leu Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr	
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Asp Val Asn Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg	
46 51 56 61	
gcc agc caa caa ttc tgt tac aca aat gtg ctt atc cca caa tgg cat	302
Ala Ser Gln Gln Phe Cys Tyr Thr Asn Val Leu Ile Pro Gln Trp His	
62 67 72 77	
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Asp Ile Trp Thr Arg Ile Gln Ile Arg Val Asn Ser Ser Arg Leu Val	
78 83 88 93	
cga gtc acc cag gtg gag aat gag gag aaa ctg aag gag cta gag cag	398
Arg Val Thr Gln Val Glu Asn Glu Glu Lys Leu Lys Glu Leu Glu Gln	
94 99 104 109	

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Phe Ser Ile Trp Asn Phe Phe Ser Ser Phe Leu Lys Glu Lys Leu Asn	
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gac acc tat gtt aac gtg ggt cta tac agc aca aaa acc tgc ctc aaa	494
Asp Thr Tyr Val Asn Val Gly Leu Tyr Ser Thr Lys Thr Cys Leu Lys	
126 131 136 141	
gtt gag att ata gag aag gac acc aag tac agt gtc att gtg atc cgg	542
Val Glu Ile Ile Glu Lys Asp Thr Lys Tyr Ser Val Ile Val Ile Arg	
142 147 152 157	
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Arg Phe Asp Pro Lys Leu Phe Leu Val Phe Leu Leu Gly Leu Met Leu	
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Phe Phe Cys Gly Asp Leu Leu Ser Arg Ser Gln Ile Phe Tyr Tyr Ser	
174 179 184 189	
act ggg atg act gtg gga att gtg gcc tct ctg cta atc atc att ttt	686
Thr Gly Met Thr Val Gly Ile Val Ala Ser Leu Leu Ile Ile Ile Phe	
190 195 200 205	
ata cta tct aag ttt atg cct aag aaa agt ccc att tac gtc atc ctg	734
Ile Leu Ser Lys Phe Met Pro Lys Lys Ser Pro Ile Tyr Val Ile Leu	
206 211 216 221	
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Val Gly Gly Trp Ser Phe Ser Leu Tyr Leu Ile Gln Leu Val Phe Lys	
222 227 232 237	
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Asn Leu Gln Glu Ile Trp Arg Cys Tyr Trp Gln Tyr Leu Leu Ser Tyr	
238 243 248 253	
gtc ctc aca gtt gga ttc atg agt ttt gca gta tgt tac aag tat ggg	878
Val Leu Thr Val Gly Phe Met Ser Phe Ala Val Cys Tyr Lys Tyr Gly	
254 259 264 269	
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Pro Leu Glu Asn Glu Arg Ser Ile Asn Leu Leu Thr Trp Thr Leu Gln	
270 275 280 285	
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Leu Met Gly Leu Cys Phe Met Tyr Ser Gly Ile Gln Ile Pro His Ile	
286 291 296 301	
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Ala Leu Ala Ile Ile Ile Ile Ala Leu Cys Thr Lys Asn Leu Glu His	
302 307 312 317	
cct att cag tgg ctg tac atc acc tgc aga aag gtg tgt aag gga gca	1070
Pro Ile Gln Trp Leu Tyr Ile Thr Cys Arg Lys Val Cys Lys Gly Ala	
318 323 328 333	

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Glu Lys Pro Val Pro Pro Arg Leu Leu Thr Glu Glu Glu Tyr Arg Ile	
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Cys Asn Ser Pro Asp Cys Ser Ala Trp Lys Thr Val Ser Arg Ile Gln	
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Ser Pro Lys Arg Phe Ala Asp Phe Val Glu Gly Ser Ser His Leu Thr	
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30             35             40             45

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46             51             56             61

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Ala Asn Tyr Ile Ala Arg Asp Thr Arg Arg Leu Gly Ala Thr Ile Leu
62             67             72             77

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His	Val	Arg	Phe	Leu	Gly	Asn	Leu	Val	Leu	Asn	Leu	Trp	Asp	Cys	Gly	
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Ile	Phe	Arg	Asn	Val	Glu	Val	Leu	Ile	Tyr	Val	Phe	Asp	Val	Glu	Ser	
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Glu	Glu	Asp	Leu	Arg	Arg	Leu	Ser	Arg	Pro	Leu	Glu	Cys	Ser	Cys	Phe	
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Ala	His	Arg	Phe	Glu	Lys	Ile	Ser	Asn	Ile	Ile	Lys	Gln	Phe	Lys	Leu	
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Ser	Cys	Ser	Lys	Leu	Ala	Ala	Ser	Phe	Gln	Ser	Met	Glu	Val	Arg	Asn	
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Met Val Val Met Ser Asp Pro Ser Ile Pro Ser Ala Ala Thr Leu Ile				
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Asn Ile Arg Asn Ala Arg Lys His Phe Glu Lys Leu Glu Arg Val Asp				
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Gly Pro Lys Gln Cys Leu Leu Met Arg *				
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Leu Phe Glu Arg Ala Thr Phe Leu Val Ile Ser His Tyr Gln Cys Lys	
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Glu Gln Arg Asp Ala His Arg Phe Glu Lys Ile Ser Asn Ile Ile Lys	
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Gln Phe Lys Leu Ser Cys Ser Lys Leu Ala Ala Ser Phe Gln Ser Met	
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Oxygen	O	O	16.00	Oxygen	O
Nitrogen	N	N	14.01	Nitrogen	N
Sulfur	S	S	32.07	Sulfur	S
Phosphorus	P	P	30.97	Phosphorus	P
Chlorine	Cl	Cl	35.45	Chlorine	Cl
Bromine	Br	Br	79.90	Bromine	Br
Iodine	I	I	126.90	Iodine	I
Fluorine	F	F	18.99	Fluorine	F
Selenium	Se	Se	78.96	Selenium	Se
Zinc	Zn	Zn	65.38	Zinc	Zn
Copper	Cu	Cu	63.55	Copper	Cu
Iron	Fe	Fe	55.85	Iron	Fe
Aluminum	Al	Al	26.98	Aluminum	Al
Magnesium	Mg	Mg	24.31	Magnesium	Mg
Silver	Ag	Ag	107.87	Silver	Ag
Gold	Au	Au	196.97	Gold	Au
Platinum	Pt	Pt	195.08	Platinum	Pt
Palladium	Pd	Pd	106.38	Palladium	Pd
Rhodium	Rh	Rh	102.91	Rhodium	Rh
Ruthenium	Ru	Ru	101.07	Ruthenium	Ru
Rosetta	Ro	Ro	100.00	Rosetta	Ro

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120

180

240

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840

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936

984

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334 339 344 349	
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Met Ser Asp Pro Ser Ile Pro Ser Ala Ala Thr Leu Ile Asn Ile Arg
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 366 371 376 381

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 Gln Cys Leu Leu Met Arg *
 382 387

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 Thr Val Val Leu Gln Asp Ala Ser Met Glu Ala Gln Pro Ala Glu Thr
 17 22 27 32

ttg cct gaa gga ccc cag cag gat ctg ccc cca gaa gca tct gct gcc 204
 Leu Pro Glu Gly Pro Gln Gln Asp Leu Pro Pro Glu Ala Ser Ala Ala
 33 38 43 48

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 Ser Ser Glu Ala Ala Gln Asn Pro Ser Ser Thr Asp Gly Ser Thr Leu
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Tyr	Cys	Asp	Phe	Arg	Ser	His	Asp	Met	Thr	Gln	Phe	Val	Gly	His	Met	
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Asn	Ser	Glu	His	Thr	Asp	Phe	Asn	Lys	Asp	Pro	Thr	Phe	Val	Cys	Ser	
97					102					107					112	
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Glu Lys Ile Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu	
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Phe Leu Thr Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg	
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Ala Cys Lys Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys	
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Met Pro Gln Thr Pro Val Pro Pro Glu
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Gly Gln Gly Gln Leu Pro Arg Arg Ala Gly Ser Arg Glu Ala Val Pro
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Gly Lys Leu Tyr Ala Met Lys Val Leu Arg Lys Ala Ala Leu Val Gln
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Thr Asp Ala Lys Leu His Leu Ile Leu Asp Tyr Val Ser Gly Gly Glu				
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Met Phe Thr His Leu Tyr Gln Arg Gln Tyr Phe Lys Glu Ala Glu Val				
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Phe	Leu	Asn	Val	Thr	Asn	Tyr	Cys	His	Leu	Ala	His	Glu	Leu	Arg	Leu	
136					141					146					151	
agc	tgc	atg	gag	agg	aaa	aag	gtc	cag	att	cga	agc	atg	gat	ccc	tcc	713
Ser	Cys	Met	Glu	Arg	Lys	Lys	Val	Gln	Ile	Arg	Ser	Met	Asp	Pro	Ser	
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Ala	Leu	Ala	Ser	Asp	Arg	Phe	Asn	Leu	Ile	Leu	Ala	Asp	Thr	Asn	Ser	
168					173					178					183	
gac	cgg	ctc	ttc	aca	gtg	aac	gat	gtt	aca	gtt	gga	ggc	tcc	aag	tat	809
Asp	Arg	Leu	Phe	Thr	Val	Asn	Asp	Val	Thr	Val	Gly	Gly	Ser	Lys	Tyr	
184					189					194					199	
ggt	atc	atc	aac	ctg	caa	agt	ctg	aag	acc	cct	acg	ctc	aag	gtg	ttc	857
Gly	Ile	Ile	Asn	Leu	Gln	Ser	Leu	Lys	Thr	Pro	Thr	Leu	Lys	Val	Phe	
200					205					210					215	
atg	cac	gaa	aac	ctc	tac	ttc	acc	aac	cgg	aag	gtg	aat	tcg	gtg	tgc	905
Met	His	Glu	Asn	Leu	Tyr	Phe	Thr	Asn	Arg	Lys	Val	Asn	Ser	Val	Cys	
216					221					226					231	
tgg	gcc	tcg	ctg	aat	cac	ttg	gat	tcc	cac	att	ctg	cta	tgc	ctc	atg	953
Trp	Ala	Ser	Leu	Asn	His	Leu	Asp	Ser	His	Ile	Leu	Leu	Cys	Leu	Met	
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Gly	Leu	Ala	Glu	Thr	Pro	Gly	Cys	Ala	Thr	Leu	Leu	Pro	Ala	Ser	Leu	

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Phe Val Asn Ser His Pro Gly Ile Asp Arg Pro Gly Met Leu Cys Ser				
264	269	274	279	
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Phe Arg Ile Pro Gly Ala Trp Ser Cys Ala Trp Ser Leu Asn Ile Gln				
280	285	290	295	
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296	301	306	311	
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Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp Val				
312	317	322	327	
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Leu Ala Gln Gln Phe Ala Phe Met Ala Pro Leu Leu Phe Asn Gly Cys				
328	333	338	343	
cgc tct ggg gaa atc ttt gcc att gat ctg cgt tgt gga aat caa ggc				1289
Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln Gly				
344	349	354	359	
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Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr Ser				
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gtg cgg atc ctc caa gat gag caa tac ctg atg gct tca gac atg gct				1385
Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met Ala				
376	381	386	391	
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Gly Lys Ile Lys Leu Trp Asp Leu Arg Thr Thr Lys Cys Val Arg Gln				
392	397	402	407	
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ctc atc tat agc agt gac acc ctg ggg gcc gcg ttg tgc cct acc ttt Leu Ile Tyr Ser Ser Asp Thr Leu Gly Ala Ala Leu Cys Pro Thr Phe 56 61 66 71	243
cgg ata gac aac acc aca tac gga tgt aac ctt caa gat tta caa gca Arg Ile Asp Asn Thr Thr Tyr Gly Cys Asn Leu Gln Asp Leu Gln Ala 72 77 82 87	291
gga acc atc tat aac ttc aag att att tct ctg gat gaa gag aga act Gly Thr Ile Tyr Asn Phe Lys Ile Ile Ser Leu Asp Glu Glu Arg Thr 88 93 98 103	339
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caa aag ata cag ggg gtt caa att caa gaa agt act tca tgg aat gaa Gln Lys Ile Gln Gly Val Gln Ile Gln Glu Ser Thr Ser Trp Asn Glu 152 157 162 167	531
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Tyr Arg Leu Met Leu Met Asp Lys Gly Ile Leu Val His Gly Gly Val				
232	237	242	247	
gtg gac aaa cat gct act tcc tat gct ttt cac ggg ctg tcc cct ggc				819
Val Asp Lys His Ala Thr Ser Tyr Ala Phe His Gly Leu Ser Pro Gly				
248	253	258	263	
tac ctc tac aac ctc act gtt atg act gag gct gca ggg ctg caa aac				867
Tyr Leu Tyr Asn Leu Thr Val Met Thr Glu Ala Ala Gly Leu Gln Asn				
264	269	274	279	
tac agg tgg aaa cta gtc agg aca gcc ccc atg gaa gtc tca aat ctg				915
Tyr Arg Trp Lys Leu Val Arg Thr Ala Pro Met Glu Val Ser Asn Leu				
280	285	290	295	
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Lys Val Thr Asn Asp Gly Ser Leu Thr Ser Leu Lys Val Lys Trp Gln				
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Arg Pro Pro Gly Asn Val Asp Ser Tyr Asn Ile Thr Leu Ser His Lys				
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ggg acc atc aag gaa tcc aga gta tta gca cct tgg att act gaa act				1059
Gly Thr Ile Lys Glu Ser Arg Val Leu Ala Pro Trp Ile Thr Glu Thr				
328	333	338	343	
cac ttt aaa gag tta gtc ccc ggt cga ctt tat caa gtt act gtc agc				1107
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Phe Pro Asp Lys Val Ala Asn Leu Glu Ala Asn Asn Asn Gly Arg Met				
376	381	386	391	
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Arg Ser Leu Val Val Ser Trp Ser Pro Pro Ala Gly Asp Trp Glu Gln				
392	397	402	407	
tat cgg atc cta ctc ttc aat gat tct gtg gtg ctg ctc aac atc act				1299
Tyr Arg Ile Leu Leu Phe Asn Asp Ser Val Val Leu Leu Asn Ile Thr				
408	413	418	423	
gtg gga aag gaa gaa aca cag tat gtc atg gat ggc acg ggg ctc gta				1347
Val Gly Lys Glu Glu Thr Gln Tyr Val Met Asp Gly Thr Gly Leu Val				
424	429	434	439	
ccg gga aga cag tat gag gtg gaa gtc att gtt gag agt gga aat ttg				1395
Pro Gly Arg Gln Tyr Glu Val Glu Val Ile Val Glu Ser Gly Asn Leu				
440	445	450	455	

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Lys Asn Ser Glu Arg Cys Gln Gly Arg Thr Val Pro Leu Ala Val Leu	
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Gln Leu Arg Val Lys His Ala Asn Glu Thr Ser Leu Ser Ile Met Trp	
472 477 482 487	
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Arg Asp Leu Leu Leu Ile His Lys Ser Leu Ser Lys Asp Ala Lys Glu	
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Thr Ser Ile Ser Gly Asp Leu Lys Asn Ser Ser Ser Val Lys Gly Arg	
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Thr Ser Ser Leu Phe Thr Asn Trp Thr Gln Ala Gln Gly Asp Val Glu	
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Phe Tyr Gln Val Leu Leu Ile His Glu Asn Val Val Ile Lys Asn Glu	
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Ser Ile Ser Ser Glu Thr Ser Arg Tyr Ser Phe His Ser Leu Lys Ser	
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Ser Arg Gln Val Val Val Glu Gly Arg Thr Val Pro Ser Ser Val Ser	
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Gly Val Thr Val Asn Asn Ser Gly Arg Asn Asp Tyr Leu Ser Val Ser	
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Trp Leu Leu Ala Pro Gly Asp Val Asp Asn Tyr Glu Val Thr Leu Ser	
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Glu Cys Ser Phe Ser Ser Leu Thr Pro Gly Arg Leu Tyr Thr Val Thr	
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Glu Tyr Arg Phe Thr Ser Leu Thr Pro Gly Arg Gln Tyr Lys Ile Leu	
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Val Leu Thr Ile Ser Gly Asp Val Gln Gln Ser Ala Phe Ile Glu Gly	
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Gln Thr Ile Pro Lys His Val Phe Glu His Thr Phe His Arg Leu Glu	
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Phe Asn Trp Ser Pro Ala Ser Gly Asp Phe Asp Phe Tyr Glu Leu Ile				
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Leu Tyr Asn Pro Asn Gly Thr Lys Lys Glu Asn Trp Lys Asp Lys Asp				
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Leu Trp Val Val Thr His Ser Gly Asp Leu Ser Asn Lys Val Thr Ala				
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1272	1277	1282	1287	
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Thr Asp Tyr Asn Asp Phe Glu Leu Gln Trp Leu Pro Arg Asp Ala Leu				
1288	1293	1298	1303	
act gtc ttc aac ccc tac aac aac aga aaa tca gaa gga cgc att gtg				3987
Thr Val Phe Asn Pro Tyr Asn Asn Arg Lys Ser Glu Gly Arg Ile Val				
1304	1309	1314	1319	
tat ggt ctt cgt cca ggg aga tcc tat caa ttc aac gtc aag act gtc				4035
Tyr Gly Leu Arg Pro Gly Arg Ser Tyr Gln Phe Asn Val Lys Thr Val				
1320	1325	1330	1335	
agt ggt gat tcc tgg aaa act tac agc aaa cca att ttt gga tct gtg				4083
Ser Gly Asp Ser Trp Lys Thr Tyr Ser Lys Pro Ile Phe Gly Ser Val				
1336	1341	1346	1351	
agg aca aag cct gac aag ata caa aac ctg cat tgc cgg cct cag aac				4131
Arg Thr Lys Pro Asp Lys Ile Gln Asn Leu His Cys Arg Pro Gln Asn				
1352	1357	1362	1367	

tcc acg gcc att gcc tgt tct tgg atc cct cct gat tct gac ttt gat	4179
Ser Thr Ala Ile Ala Cys Ser Trp Ile Pro Pro Asp Ser Asp Phe Asp	
1368 1373 1378 1383	
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Gly Tyr Ser Ile Glu Cys Arg Lys Met Asp Thr Gln Glu Val Glu Phe	
1384 1389 1394 1399	
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Ser Arg Lys Leu Glu Lys Glu Lys Ser Leu Leu Asn Ile Met Met Leu	
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gtg ccc cat aag agg tac ctg gtg tcc atc aaa gtg cag tcg gcc ggc	4323
Val Pro His Lys Arg Tyr Leu Val Ser Ile Lys Val Gln Ser Ala Gly	
1416 1421 1426 1431	
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Met Thr Ser Glu Val Val Glu Asp Ser Thr Ile Thr Met Ile Asp Arg	
1432 1437 1442 1447	
ccc cct cct cca ccc cca cac att cgt gtg aat gaa aag gat gtg cta	4419
Pro Pro Pro Pro Pro Pro His Ile Arg Val Asn Glu Lys Asp Val Leu	
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Ile Ser Lys Ser Ser Ile Asn Phe Thr Val Asn Cys Ser Trp Phe Ser	
1464 1469 1474 1479	
gac acc aat gga gct gtg aaa tac ttc aca gtg gtg gtg aga gag gct	4515
Asp Thr Asn Gly Ala Val Lys Tyr Phe Thr Val Val Val Arg Glu Ala	
1480 1485 1490 1495	
gat ggc agt gat gag ctg aag cca gaa cag cag cac cct ctc cct tcc	4563
Asp Gly Ser Asp Glu Leu Lys Pro Glu Gln Gln His Pro Leu Pro Ser	
1496 1501 1506 1511	
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Tyr Leu Glu Tyr Arg His Asn Ala Ser Ile Arg Val Tyr Gln Thr Asn	
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tat ttt gcc agc aaa tgt gcc gaa aat cct aac agc aac tcc aag agt	4659
Tyr Phe Ala Ser Lys Cys Ala Glu Asn Pro Asn Ser Asn Ser Lys Ser	
1528 1533 1538 1543	
ttt aac att aag ctt gga gca gag atg gag agc cta ggt gga aaa tgc	4707
Phe Asn Ile Lys Leu Gly Ala Glu Met Glu Ser Leu Gly Gly Lys Cys	
1544 1549 1554 1559	
gat ccc act cag caa aaa ttc tgt gat gga cca ctg aag cca cac act	4755
Asp Pro Thr Gln Gln Lys Phe Cys Asp Gly Pro Leu Lys Pro His Thr	
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gcc tac aga atc agc att cga gct ttt aca cag ctc ttt gat gag gac	4803
Ala Tyr Arg Ile Ser Ile Arg Ala Phe Thr Gln Leu Phe Asp Glu Asp	
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Leu Lys Glu Phe Thr Lys Pro Leu Tyr Ser Asp Thr Phe Phe Ser Leu	
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Pro Ile Thr Thr Glu Ser Glu Pro Leu Phe Gly Ala Ile Glu Gly Val	
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Ser Ala Gly Leu Phe Leu Ile Gly Met Leu Val Ala Val Val Ala Leu	
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Leu Ile Cys Arg Gln Lys Val Ser His Gly Arg Glu Arg Pro Ser Ala	
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Arg Leu Ser Ile Arg Arg Asp Arg Pro Leu Ser Val His Leu Asn Leu	
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Gly Gln Lys Gly Asn Arg Lys Thr Ser Cys Pro Ile Lys Ile Asn Gln	
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Phe Glu Gly His Phe Met Lys Leu Gln Ala Asp Ser Asn Tyr Leu Leu	
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Ser Lys Glu Tyr Glu Glu Leu Lys Asp Val Gly Arg Asn Gln Ser Cys	
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Asp Ile Ala Leu Leu Pro Glu Asn Arg Gly Lys Asn Arg Tyr Asn Asn	
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ata ttg ccc tat gat gcc acg cga gtg aag ctc tcc aat gta gat gat	5283
Ile Leu Pro Tyr Asp Ala Thr Arg Val Lys Leu Ser Asn Val Asp Asp	
1736 1741 1746 1751	
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Asp Pro Cys Ser Asp Tyr Ile Asn Ala Ser Tyr Ile Pro Gly Asn Asn	
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Met Val Thr Gln Cys Val Glu Lys Gly Arg Val Lys Cys Asp His Tyr	
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Met	Leu	Ser	Glu	Ser	Val	Leu	Pro	Glu	Trp	Thr	Ile	Arg	Glu	Phe	Lys		
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Ile	Cys	Gly	Glu	Glu	Gln	Leu	Asp	Ala	His	Arg	Leu	Ile	Arg	His	Phe		
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cac	tat	acg	gtg	tgg	cca	gac	cat	gga	gtc	cca	gaa	acc	acc	cag	tct	5667	
His	Tyr	Thr	Val	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Thr	Thr	Gln	Ser		
1864					1869					1874					1879		
ctg	atc	cag	ttt	gtg	aga	act	gtc	agg	gac	tac	atc	aac	aga	agc	ccg	5715	
Leu	Ile	Gln	Phe	Val	Arg	Thr	Val	Arg	Asp	Tyr	Ile	Asn	Arg	Ser	Pro		
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ggg	gct	ggg	ccc	act	gtg	gtg	cac	tgc	agt	gct	ggg	gtg	ggg	agg	act	5763	
Gly	Ala	Gly	Pro	Thr	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr		
1896					1901					1906					1911		
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Gly	Thr	Phe	Ile	Ala	Leu	Asp	Arg	Ile	Leu	Gln	Gln	Leu	Asp	Ser	Lys		
1912					1917					1922					1927		
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Asp	Ser	Val	Asp	Ile	Tyr	Gly	Ala	Val	His	Asp	Leu	Arg	Leu	His	Arg		
1928					1933					1938					1943		
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Val	His	Met	Val	Gln	Thr	Glu	Cys	Gln	Tyr	Val	Tyr	Leu	His	Gln	Cys		
1944					1949					1954					1959		
gta	aga	gat	gtc	ctc	aga	gca	aga	aag	cta	cgg	agt	gaa	caa	gaa	aac	5955	
Val	Arg	Asp	Val	Leu	Arg	Ala	Arg	Lys	Leu	Arg	Ser	Glu	Gln	Glu	Asn		
1960					1965					1970					1975		
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Pro	Leu	Phe	Pro	Ile	Tyr	Glu	Asn	Val	Asn	Pro	Glu	Tyr	His	Arg	Asp		
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cca	gtc	tat	tca	agg	cat	tga	ga	atgtacctga	agagctcctg	gataaaaatt						6056	
Pro	Val	Tyr	Ser	Arg	His	*											
1992					1997												
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Val Pro Leu Gly Arg Tyr Thr Glu Glu Glu His Lys Ala Thr Glu Lys				
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atc ctg aaa atg ttt gga gag agg gct aga agt ttc atg att ctc ata				904
Ile Leu Lys Met Phe Gly Glu Arg Ala Arg Ser Phe Met Ile Leu Ile				
137	142	147	152	
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Phe Thr Arg Lys Asp Asp Leu Gly Asp Thr Asn Leu His Asp Tyr Leu				
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Arg Glu Ala Pro Glu Asp Ile Gln Asp Leu Met Asp Ile Phe Gly Asp				
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Arg Tyr Cys Ala Leu Asn Asn Lys Ala Thr Gly Ala Glu Gln Glu Ala				
185	190	195	200	
cag agg gca cag ttg ctg ggc ctg atc cag cgc gtg gtg agg gag aac				1096
Gln Arg Ala Gln Leu Leu Gly Leu Ile Gln Arg Val Val Arg Glu Asn				
201	206	211	216	
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Lys Glu Gly Cys Tyr Thr Asn Arg Met Tyr Gln Arg Ala Glu Glu Glu				
217	222	227	232	
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Ile Gln Lys Gln Thr Gln Ala Met Gln Glu Leu His Arg Val Glu Leu				
233	238	243	248	
gag aga gag aaa gcg cgg ata aga gag gag tat gaa gag aaa atc aga				1240
Glu Arg Glu Lys Ala Arg Ile Arg Glu Glu Tyr Glu Glu Lys Ile Arg				
249	254	259	264	
aag ctg gaa gat aaa gtg gag cag gaa aag aga aag aag caa atg gag				1288
Lys Leu Glu Asp Lys Val Glu Gln Glu Lys Arg Lys Lys Gln Met Glu				
265	270	275	280	
aag aaa cta gca gaa cag gag gct cac tat gct gta agg cag caa agg				1336
Lys Lys Leu Ala Glu Gln Glu Ala His Tyr Ala Val Arg Gln Gln Arg				
281	286	291	296	
gca aga acg gaa gtg gag agt aag gat ggg ata ctt gaa tta atc atg				1384
Ala Arg Thr Glu Val Glu Ser Lys Asp Gly Ile Leu Glu Leu Ile Met				
297	302	307	312	
aca gcg tta cag att gct tcc ttt att ttg tta cgt ctg ttc gcg gaa				1432
Thr Ala Leu Gln Ile Ala Ser Phe Ile Leu Leu Arg Leu Phe Ala Glu				
313	318	323	328	
gat taa acttaatgaa aatctgtttg tattttctgc atattctctg gcaaccttgc				1488
Asp *				
329				

cccataactta cttatttagc atagtcgagt gctctagttt ctgtctctca ggcactcgta 1548
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 tgactgtgga atccttaagg gccattaca tttctgaaga agaaagctaa gatgaaggac 240
 atg cca ctc cga att cat gtg cta ctt ggc cta gct atc act aca cta 288
 Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile Thr Thr Leu
 1 5 10 15
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 Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu Cys Thr Cys
 17 22 27 32
 gaa atc agg cct tgg ttt aca ccc aga tcc att tat atg gaa gca tct 384
 Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met Glu Ala Ser
 33 38 43 48
 aca gtg gat tgt aat gat tta ggt ctt tta act ttc cca gcc aga ttg 432
 Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro Ala Arg Leu
 49 54 59 64
 cca gct aac aca cag att ctt ctc cta cag act aac aat att gca aaa 480
 Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn Ile Ala Lys
 65 70 75 80
 att gaa tac tcc aca gac ttt cca gta aac ctt act ggc ctg gat tta 528

Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly	Leu	Asp	Leu		
81					86					91					96		
tct	caa	aac	aat	tta	tct	tca	gtc	acc	aat	att	aat	gta	aaa	aag	atg	576	
Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	Lys	Lys	Met		
97					102					107					112		
cct	cag	ctc	ctt	tct	gtg	tac	cta	gag	gaa	aac	aaa	ctt	act	gaa	ctg	624	
Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	Thr	Glu	Leu		
113					118					123					128		
cct	gaa	aaa	tgt	ctg	tcc	gaa	ctg	agc	aac	tta	caa	gaa	ctc	tat	att	672	
Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu	Leu	Tyr	Ile		
129					134					139					144		
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Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe	Ile	Gly	Leu		
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cat	aat	ctt	ctt	cga	ctt	cat	ctc	aat	tca	aat	aga	ttg	cag	atg	atc	768	
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aac	agt	aag	tgg	ttt	gat	gct	ctt	cca	aat	cta	gag	att	ctg	atg	att	816	
Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	Ile		
177					182					187					192		
ggg	gaa	aat	cca	att	atc	aga	atc	aaa	gac	atg	aac	ttt	aag	cct	ctt	864	
Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	Lys	Pro	Leu		
193					198					203					208		
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Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	Thr	Glu	Ile		
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Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser	Ile	Ser	Phe		
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Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu	Gln	Lys	Val		
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Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile	Asn	Arg	Ile		
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Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu	Leu	Gly	Ile		
273					278					283					288		
aat	aat	atg	cct	gag	ctg	att	tcc	atc	gat	agt	ctt	gct	gtg	gat	aac	1152	
Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala	Val	Asp	Asn		
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ctg	cca	gat	tta	aga	aaa	ata	gaa	gct	act	aac	aac	cct	aga	ttg	tct	1200	
Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro	Arg	Leu	Ser		

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Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu Glu Ser Leu				
321	326	331	336	
atg ctg aac agc aat gct ctc agt gcc ctg tac cat ggt acc att gag				1296
Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly Thr Ile Glu				
337	342	347	352	
tct ctg cca aac ctc aag gaa atc agc ata cac agt aac ccc atc agg				1344
Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn Pro Ile Arg				
353	358	363	368	
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Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg				
369	374	379	384	
ttc atg gag cca gat tca ctg ttt tgc gtg gac cca cct gaa ttc caa				1440
Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln				
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ggc cag aat gtt cgg caa gtg cat ttc agg gac atg atg gaa att tgt				1488
Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys				
401	406	411	416	
ctc cct ctt ata gct cct gag agc ttt cct tct aat cta aat gta gaa				1536
Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu				
417	422	427	432	
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Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro Gln				
433	438	443	448	
cct gaa atc tac tgg ata aca cct tct ggt caa aaa ctc ttg cct aat				1632
Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu Pro Asn				
449	454	459	464	
acc ctg aca gac aag ttc tat gtc cat tct gag gga aca cta gat ata				1680
Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr Leu Asp Ile				
465	470	475	480	
aat ggc gta act ccc aaa gaa ggg ggt tta tat act tgt ata gca act				1728
Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys Ile Ala Thr				
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aac cta gtt ggc gct gac ttg aag tct gtt atg atc aaa gtg gat gga				1776
Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys Val Asp Gly				
497	502	507	512	
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Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys Ile Arg Asp				
513	518	523	528	
att cag gcc aat tca gtt ttg gtg tcc tgg aaa gca agt tct aaa att				1872
Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser Ser Lys Ile				
529	534	539	544	

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His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys	Val	Tyr	Asn	
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Glu	Glu	Glu	Thr	Lys	Ser	Pro	Pro	Val	Glu	Glu	Ala	Ala	Ser	Pro	Glu	
498					503					508					513	
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Lys	Glu	Ala	Lys	Ser	Pro	Val	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	
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gcc	aag	tcc	cca	gag	aag	gag	gaa	gca	aaa	tcc	cca	gcc	gaa	gtc	aag	5587
Ala	Lys	Ser	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	Val	Lys	
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Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Ala	Lys	Glu	Glu	Ala	Lys	Ser	Pro	
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Pro	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	
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Val	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Ala	Lys	Glu	Glu	Ala	Lys	
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Ser	Pro	Ala	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Val	Lys	
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Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	Ala	Lys	Ser	Pro	Val	Lys	Glu	Glu	
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Ala	Lys	Ser	Pro	Ala	Glu	Val	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	
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Thr	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Glu	Lys	

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Ala Lys Ser Pro Glu Lys Glu Glu Ala Lys Ser Pro Glu Lys Ala Lys				
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Ser Pro Val Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro				
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gtg aag gca gaa gca aag tcc cct gag aag gcc aag tcc cca gtg aag				6067
Val Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys				
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gaa gaa gca aag tcc cct gag aag gcc aag tcc cca gtg aag gaa gaa				6115
Glu Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu				
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Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Ala Lys				
722	727	732	737	
acc ccc gag aag gcc aag tcc cca gtg aag gaa gaa gcc aag tcc cca				6211
Thr Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Ala Lys Ser Pro				
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gag aag gcc aag tcc cca gag aag gcc aag act ctt gat gtg aag tct				6259
Glu Lys Ala Lys Ser Pro Glu Lys Ala Lys Thr Leu Asp Val Lys Ser				
754	759	764	769	
cca gaa gcc aag act cca gcg aag gag gaa gca agg tcc cct gca gac				6307
Pro Glu Ala Lys Thr Pro Ala Lys Glu Glu Ala Arg Ser Pro Ala Asp				
770	775	780	785	
aaa ttc cct gaa aag gcc aaa agc cct gtc aag gag gag gtc aag tcc				6355
Lys Phe Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Val Lys Ser				
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Pro Glu Lys Ala Lys Ser Pro Leu Lys Glu Asp Ala Lys Ala Pro Glu				
802	807	812	817	
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Lys Glu Ile Pro Lys Lys Glu Glu Val Lys Ser Pro Val Lys Glu Glu				
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Glu Lys Pro Gln Glu Val Lys Val Lys Glu Pro Pro Lys Lys Ala Glu				
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gaa gag aaa gcc cct gcc aca cca aaa aca gag gag aag aag gac agc				6547
Glu Glu Lys Ala Pro Ala Thr Pro Lys Thr Glu Glu Lys Lys Asp Ser				
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aag aaa gag gag gca ccc aag aag gag gct cca aag ccc aag gtg gag				6595
Lys Lys Glu Glu Ala Pro Lys Lys Glu Ala Pro Lys Pro Lys Val Glu				
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Ala Lys Lys Glu Glu Ala Glu Asp Lys Lys Lys Val Pro Thr Pro Glu	
898 903 908 913	
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Lys Glu Ala Pro Ala Lys Val Glu Val Lys Glu Asp Ala Lys Pro Lys	
914 919 924 929	
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Glu Lys Thr Glu Val Ala Lys Lys Glu Pro Asp Asp Ala Lys Ala Lys	
930 935 940 945	
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Glu Pro Ser Lys Pro Ala Glu Lys Lys Glu Ala Ala Pro Glu Lys Lys	
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Asp Thr Lys Glu Glu Lys Ala Lys Lys Pro Glu Glu Lys Pro Lys Thr	
962 967 972 977	
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Glu Ala Lys Ala Lys Glu Asp Asp Lys Thr Leu Ser Lys Glu Pro Ser	
978 983 988 993	
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Lys Pro Lys Ala Glu Lys Ala Glu Lys Ser Ser Ser Thr Asp Gln Lys	
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Asp Ser Lys Pro Pro Glu Lys Ala Thr Glu Asp Lys Ala Ala Lys Gly	
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Lys *	
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 Met Ser Ile Ala Gly Val Ala Ala Gln Glu Ile Arg Val
 cca tta aaa act gga ttt cta cat aat ggc cga gcc atg ggg aat atg 277
 Pro Leu Lys Thr Gly Phe Leu His Asn Gly Arg Ala Met Gly Asn Met
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 Arg Lys Thr Tyr Trp Ser Ser Arg Ser Glu Phe Lys Asn Asn Phe Leu
 30 35 40 45
 aat att gac ccg ata acc atg gcc tac agt ctg aac tct tct gct cag 373
 Asn Ile Asp Pro Ile Thr Met Ala Tyr Ser Leu Asn Ser Ser Ala Gln
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 gag cgc cta ata cca ctt ggg cat gct tcc aaa tct gct ccg atg aat 421
 Glu Arg Leu Ile Pro Leu Gly His Ala Ser Lys Ser Ala Pro Met Asn
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 Gly His Cys Phe Ala Glu Asn Gly Pro Ser Gln Lys Ser Ser Leu Pro
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 Pro Leu Leu Ile Pro Pro Ser Glu Asn Leu Gly Pro His Glu Glu Asp
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 caa gtt gta tgt ggt ttt aag aaa ctc aca gtg aat ggg gtt tgt gct 565
 Gln Val Val Cys Gly Phe Lys Lys Leu Thr Val Asn Gly Val Cys Ala
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Ser Thr Pro Pro Leu Thr Pro Ile Lys Asn Ser Pro Ser Leu Phe Pro	
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Cys Ala Pro Leu Cys Glu Arg Gly Ser Arg Pro Leu Pro Pro Leu Pro	
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Ile Ser Glu Ala Leu Ser Leu Asp Asp Thr Asp Cys Glu Val Glu Phe	
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Asp Phe Lys Tyr Asp Val Pro Gly Arg Arg Ser Phe Arg Gly Cys Gly	
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Gln Ile Asn Tyr Ala Tyr Phe Asp Thr Pro Ala Val Ser Ala Ala Asp	
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Leu Ser Tyr Val Ser Asp Gln Asn Gly Gly Val Pro Asp Pro Asn Pro	
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Pro Pro Pro Gln Thr His Arg Arg Leu Arg Arg Ser His Ser Gly Pro	
238 243 248 253	
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Ala Gly Ser Phe Asn Lys Pro Ala Ile Arg Ile Ser Asn Cys Cys Ile	
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Arg Val Pro Ile Pro Pro Arg Pro Val Lys Pro Asp Tyr Arg Arg Trp	
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Ser Ala Glu Val Thr Ser Ser Thr Tyr Ser Asp Glu Asp Arg Pro Pro	
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Lys Val Pro Pro Arg Glu Pro Leu Ser Pro Ser Asn Ser Arg Thr Pro	
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Ser Pro Lys Ser Leu Pro Ser Tyr Leu Asn Gly Val Met Pro Pro Thr	
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Gln Ser Phe Ala Pro Asp Pro Lys Tyr Val Ser Ser Lys Ala Leu Gln	
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Arg Gln Asn Ser Glu Gly Ser Ala Ser Lys Val Pro Cys Ile Leu Pro	
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Ile Ile Glu Asn Gly Lys Lys Val Ser Ser Thr His Tyr Tyr Leu Leu	
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Cys Gly Ile Ser Ser Ala Thr Glu Lys Pro Asp Ser Lys Thr Lys Met	
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Asp Leu Gly Gly His Val Lys Arg Lys His Leu Ser Tyr Val Val Ser	
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Pro *	
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Ser Thr Ala Ser Arg Gln Ser Val Val Ser Lys Gln Ala Thr Ser Ala								
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Leu Gln Gln Glu Glu Thr Ser Glu Lys Lys Ser Arg Lys Val Val Ile								
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Arg Gly Lys Ala Glu Arg Leu Ser Leu Arg Lys Thr Leu Glu Glu Thr								
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Glu Thr Tyr His Ala Lys Leu Asn Glu Asp His Leu Leu His Ala Pro								
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Cys Asp Phe Glu Asp Thr Ala Gln Tyr Arg Ala Ser Ala Met Asn Val								
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Gly Glu Phe Asp Glu Thr Arg Phe His Ala Gly Ala Ser Thr Met Pro	
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Cys Leu Glu Ala Asn Lys Asp Tyr Ile Ile Ile Ser Trp Lys Gln Pro	
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Ala Val Asp Gly Gly Ser Pro Ile Leu Gly Tyr Phe Ile Asp Lys Cys	
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430 435 440 445	

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Phe Arg Val Arg Ala Val Asn Lys Met Gly Ile Gly Phe Pro Ser Arg	
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gtt tcc gag gcc gtg gct gct ctg gat ccg gct gag aaa gct aga cta	2100
Val Ser Glu Ala Val Ala Ala Leu Asp Pro Ala Glu Lys Ala Arg Leu	
462 467 472 477	
aag tcc ccc ctc agc acc ctg gac tgg aca gtc att gtt act gaa gag	2148
Lys Ser Pro Leu Ser Thr Leu Asp Trp Thr Val Ile Val Thr Glu Glu	
478 483 488 493	
gaa cct tca gag ggt att gtg cct ggc ccc ccg aca gac ctc tct gtc	2196
Glu Pro Ser Glu Gly Ile Val Pro Gly Pro Pro Thr Asp Leu Ser Val	
494 499 504 509	
act gag gcc acc cgg agc tat gtg gtg ctc agc tgg aag ccc cct ggc	2244
Thr Glu Ala Thr Arg Ser Tyr Val Val Leu Ser Trp Lys Pro Pro Gly	
510 515 520 525	
cag cgt ggt cat gag ggc att atg tac ttt gtg gaa aag tgt gag gca	2292
Gln Arg Gly His Glu Gly Ile Met Tyr Phe Val Glu Lys Cys Glu Ala	
526 531 536 541	
gga aca gaa aac tgg cag cga gtg aac acg gag ctc cct gtg aag tct	2340
Gly Thr Glu Asn Trp Gln Arg Val Asn Thr Glu Leu Pro Val Lys Ser	
542 547 552 557	
ccc cgc ttt gct ctg ttt gac ttg gcc gag ggg aaa tcc tac tgt ttc	2388
Pro Arg Phe Ala Leu Phe Asp Leu Ala Glu Gly Lys Ser Tyr Cys Phe	
558 563 568 573	
cgt gtc cgc tgt tct aat tct gca gga gtt ggt gag ccc tca gag gca	2436
Arg Val Arg Cys Ser Asn Ser Ala Gly Val Gly Glu Pro Ser Glu Ala	
574 579 584 589	
acg gag gtg act gtg gta ggg gac aaa ctt gat atc ccc aag gct cct	2484
Thr Glu Val Thr Val Val Gly Asp Lys Leu Asp Ile Pro Lys Ala Pro	
590 595 600 605	
ggc aaa atc atc cca agc aga aac aca gac acc tca gtg gta gtt tcc	2532
Gly Lys Ile Ile Pro Ser Arg Asn Thr Asp Thr Ser Val Val Val Ser	
606 611 616 621	
tgg gag gag tcc aaa gat gcc aaa gag ctg gtc ggg tac tac ata gag	2580
Trp Glu Glu Ser Lys Asp Ala Lys Glu Leu Val Gly Tyr Tyr Ile Glu	
622 627 632 637	
gcg agc gtt gct ggc tct ggc aag tgg gag ccc tgt aac aac aac ccc	2628
Ala Ser Val Ala Gly Ser Gly Lys Trp Glu Pro Cys Asn Asn Asn Pro	
638 643 648 653	
gtg aag ggc tca cga ttc act tgt cat gga tta gtg act ggt cag agt	2676
Val Lys Gly Ser Arg Phe Thr Cys His Gly Leu Val Thr Gly Gln Ser	
654 659 664 669	
tat att ttc cgg gtc aga gca gtc aat gca gct gga ctt agt gaa tat	2724

Tyr Ile Phe Arg Val Arg Ala Val Asn Ala Ala Gly Leu Ser Glu Tyr	
670 675 680 685	
tcc cag gat tca gaa gct att gaa gtc aaa gct gct att gca cca cca	2772
Ser Gln Asp Ser Glu Ala Ile Glu Val Lys Ala Ala Ile Ala Pro Pro	
686 691 696 701	
tct cca ccc tgt gat atc acc tgt ctt gaa agt ttt cgt gac tca atg	2820
Ser Pro Pro Cys Asp Ile Thr Cys Leu Glu Ser Phe Arg Asp Ser Met	
702 707 712 717	
gtt ctt gga tgg aag caa cca gat aag att gga ggg gca gaa att act	2868
Val Leu Gly Trp Lys Gln Pro Asp Lys Ile Gly Gly Ala Glu Ile Thr	
718 723 728 733	
ggc tat tat gtg aac tat cgc gag gtc att gat ggg gta cca gga aaa	2916
Gly Tyr Tyr Val Asn Tyr Arg Glu Val Ile Asp Gly Val Pro Gly Lys	
734 739 744 749	
tgg aga gaa gcc aat gtc aag gct gtc agt gag gag gca tac aag att	2964
Trp Arg Glu Ala Asn Val Lys Ala Val Ser Glu Glu Ala Tyr Lys Ile	
750 755 760 765	
agc aac ttg aag gaa aac atg gtg tat cag ttc caa gtg gca gcc atg	3012
Ser Asn Leu Lys Glu Asn Met Val Tyr Gln Phe Gln Val Ala Ala Met	
766 771 776 781	
aac atg gct ggg ctg ggc gcg ccc tcc gca gta agc gaa tgc ttc aaa	3060
Asn Met Ala Gly Leu Gly Ala Pro Ser Ala Val Ser Glu Cys Phe Lys	
782 787 792 797	
tgt gaa gag tgg acc atc gcc gtc cca gga cca ccg cac agt ctc aag	3108
Cys Glu Glu Trp Thr Ile Ala Val Pro Gly Pro Pro His Ser Leu Lys	
798 803 808 813	
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Cys Ser Glu Val Arg Lys Asp Ser Leu Val Leu Gln Trp Lys Pro Pro	
814 819 824 829	
gtc cac tcc ggg cgg act ccg gtc act ggt tac ttc gtg gac ttg aag	3204
Val His Ser Gly Arg Thr Pro Val Thr Gly Tyr Phe Val Asp Leu Lys	
830 835 840 845	
gag gcc aag gcc aaa gaa gac cag tgg cga ggg ctc aat gag gcg gct	3252
Glu Ala Lys Ala Lys Glu Asp Gln Trp Arg Gly Leu Asn Glu Ala Ala	
846 851 856 861	
att aaa aac gta tac ctg aag gtt cga ggc ctc aag gag ggc gtc agc	3300
Ile Lys Asn Val Tyr Leu Lys Val Arg Gly Leu Lys Glu Gly Val Ser	
862 867 872 877	
tac gtg ttc cgt gtt cga gcc ata aac cag gcg gga gtt ggg aag cca	3348
Tyr Val Phe Arg Val Arg Ala Ile Asn Gln Ala Gly Val Gly Lys Pro	
878 883 888 893	
tct gac ctt gct ggc cct gtt gtg gca gag acc cgt cca gga acc aaa	3396
Ser Asp Leu Ala Gly Pro Val Val Ala Glu Thr Arg Pro Gly Thr Lys	

Tyr Ile Phe Arg Val Arg Ala Val Asn Ala Ala Gly Leu Ser Glu Tyr	
670 675 680 685	
tcc cag gat tca gaa gct att gaa gtc aaa gct gct att gca cca cca	2772
Ser Gln Asp Ser Glu Ala Ile Glu Val Lys Ala Ala Ile Ala Pro Pro	
686 691 696 701	
tct cca ccc tgt gat atc acc tgt ctt gaa agt ttt cgt gac tca atg	2820
Ser Pro Pro Cys Asp Ile Thr Cys Leu Glu Ser Phe Arg Asp Ser Met	
702 707 712 717	
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Val Leu Gly Trp Lys Gln Pro Asp Lys Ile Gly Gly Ala Glu Ile Thr	
718 723 728 733	
ggc tat tat gtg aac tat cgc gag gtc att gat ggg gta cca gga aaa	2916
Gly Tyr Tyr Val Asn Tyr Arg Glu Val Ile Asp Gly Val Pro Gly Lys	
734 739 744 749	
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Trp Arg Glu Ala Asn Val Lys Ala Val Ser Glu Glu Ala Tyr Lys Ile	
750 755 760 765	
agc aac ttg aag gaa aac atg gtg tat cag ttc caa gtg gca gcc atg	3012
Ser Asn Leu Lys Glu Asn Met Val Tyr Gln Phe Gln Val Ala Ala Met	
766 771 776 781	
aac atg gct ggg ctg ggc gcg ccc tcc gca gta agc gaa tgc ttc aaa	3060
Asn Met Ala Gly Leu Gly Ala Pro Ser Ala Val Ser Glu Cys Phe Lys	
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tgt gaa gag tgg acc atc gcc gtc cca gga cca ccg cac agt ctc aag	3108
Cys Glu Glu Trp Thr Ile Ala Val Pro Gly Pro Pro His Ser Leu Lys	
798 803 808 813	
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Cys Ser Glu Val Arg Lys Asp Ser Leu Val Leu Gln Trp Lys Pro Pro	
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gtc cac tcc ggg cgg act ccg gtc act ggt tac ttc gtg gac ttg aag	3204
Val His Ser Gly Arg Thr Pro Val Thr Gly Tyr Phe Val Asp Leu Lys	
830 835 840 845	
gag gcc aag gcc aaa gaa gac cag tgg cga ggg ctc aat gag gcg gct	3252
Glu Ala Lys Ala Lys Glu Asp Gln Trp Arg Gly Leu Asn Glu Ala Ala	
846 851 856 861	
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Ile Lys Asn Val Tyr Leu Lys Val Arg Gly Leu Lys Glu Gly Val Ser	
862 867 872 877	
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Tyr Val Phe Arg Val Arg Ala Ile Asn Gln Ala Gly Val Gly Lys Pro	
878 883 888 893	
tct gac ctt gct ggc cct gtt gtg gca gag acc cgt cca gga acc aaa	3396
Ser Asp Leu Ala Gly Pro Val Val Ala Glu Thr Arg Pro Gly Thr Lys	

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Glu Val Val Val Asn	Val Asp Asp Asp Gly	Val Ile Ser Leu Asn Phe		
910	915	920	925	
gag tgt gat aag atg	act cca aag tcc gag	ttc tcc tgg tcc aaa gat		3492
Glu Cys Asp Lys Met	Thr Pro Lys Ser Glu	Phe Ser Trp Ser Lys Asp		
926	931	936	941	
tat gta tcc act gag	gac tct cca cga ttg	gaa gtc gaa agc aag ggc		3540
Tyr Val Ser Thr Glu	Asp Ser Pro Arg Leu	Glu Val Glu Ser Lys Gly		
942	947	952	957	
aac aag acg aaa atg	acc ttc aaa gac ctt	ggg atg gat gac ttg ggt		3588
Asn Lys Thr Lys Met	Thr Phe Lys Asp Leu	Gly Met Asp Asp Leu Gly		
958	963	968	973	
att tac tct tgc gat	gta aca gac act gat	gga ata gca tca agc tac		3636
Ile Tyr Ser Cys Asp	Val Thr Asp Thr Asp	Gly Ile Ala Ser Ser Tyr		
974	979	984	989	
tta ata gat gag gaa	gaa ttg aaa cgt tta	ctt gct ctc agc cat gaa		3684
Leu Ile Asp Glu Glu	Glu Leu Lys Arg Leu	Leu Ala Leu Ser His Glu		
990	995	1000	1005	
cac aag ttc cca act	gtc cca gtt aaa tca	gag ttg gca gtt gaa att		3732
His Lys Phe Pro Thr	Val Pro Val Lys Ser	Glu Leu Ala Val Glu Ile		
1006	1011	1016	1021	
ttg gag aaa ggc cag	gtc cgg ttt tgg atg	cag gct gag aaa ctg tct		3780
Leu Glu Lys Gly Gln	Val Arg Phe Trp Met	Gln Ala Glu Lys Leu Ser		
1022	1027	1032	1037	
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Gly Asn Ala Lys Val	Asn Tyr Ile Phe Asn	Glu Lys Glu Ile Phe Glu		
1038	1043	1048	1053	
ggc ccg aaa tat aaa	atg cat att gac cga	aac act ggc atc atc gaa		3876
Gly Pro Lys Tyr Lys	Met His Ile Asp Arg	Asn Thr Gly Ile Ile Glu		
1054	1059	1064	1069	
atg ttc atg gaa aag	cta cag gat gag gat	gag gga acg tac act ttc		3924
Met Phe Met Glu Lys	Leu Gln Asp Glu Asp	Glu Gly Thr Tyr Thr Phe		
1070	1075	1080	1085	
cag ctt caa gat gga	aaa gca act aac cat	tct act gtt gtt ctc gtt		3972
Gln Leu Gln Asp Gly	Lys Ala Thr Asn His	Ser Thr Val Val Leu Val		
1086	1091	1096	1101	
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Gly Asp Val Phe Lys	Lys Leu Gln Lys Glu	Ala Glu Phe Gln Arg Gln		
1102	1107	1112	1117	
gaa tgg atc agg aaa	caa ggt cct cac ttt	ggt gag tat ttg agc tgg		4068
Glu Trp Ile Arg Lys	Gln Gly Pro His Phe	Val Glu Tyr Leu Ser Trp		
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Glu Val Thr Gly Glu Cys Asn Val Leu Leu Lys Cys Lys Val Ala Asn	
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Ile Lys Lys Glu Thr His Ile Val Trp Tyr Lys Asp Glu Arg Glu Ile	
1150 1155 1160 1165	
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Ser Val Asp Glu Lys His Asp Phe Lys Asp Gly Ile Cys Thr Leu Leu	
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Ile Thr Glu Phe Ser Lys Lys Asp Ala Gly Ile Tyr Glu Val Ile Leu	
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Lys Asp Asp Arg Gly Lys Asp Lys Ser Arg Leu Lys Leu Val Asp Glu	
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Ala Phe Lys Glu Leu Met Met Glu Val Cys Lys Lys Ile Ala Leu Ser	
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Ala Thr Asp Leu Lys Ile Gln Ser Thr Ala Glu Gly Ile Gln Leu Tyr	
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Ser Phe Val Thr Tyr Tyr Val Glu Asp Leu Lys Val Asn Trp Ser His	
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Asn Gly Ser Ala Ile Arg Tyr Ser Asp Arg Val Lys Thr Gly Val Thr	
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Gly Glu Gln Ile Trp Leu Gln Ile Asn Glu Pro Thr Pro Asn Asp Lys	
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Gln Arg Leu Lys Gln Ala Ala Ile Ala Glu Lys Asn Arg Ala Arg Val	
1326 1331 1336 1341	
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1342 1347 1352 1357	

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Ser Asp Lys Glu Lys Glu Asn Gly Lys Met Gly Cys Trp Ser Ile Glu	
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His Val Glu Gln Tyr Leu Gly Thr Asp Glu Leu Pro Lys Asn Asp Leu	
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Ile Thr Tyr Leu Gln Lys Asn Ala Asp Ala Ala Phe Leu Arg His Trp	
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Lys Leu Thr Gly Thr Asn Lys Ser Ile Arg Lys Asn Arg Asn Cys Ser	
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Gln Leu Ile Ala Ala Tyr Lys Asp Phe Cys Glu His Gly Thr Lys Ser	
364 369 374 379	
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Gly Leu Asn Gln Gly Ala Ile Ser Thr Leu Gln Ser Ser Asp Ile Leu	
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Ser Cys Gly Val Glu Asp Val Leu Gln Leu Leu Arg Ile Leu Tyr Ile	
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Val Ala Ser Asp Pro Tyr Ser Arg Ile Ser Gln Glu Asp Gly Asp Glu	
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Val	Glu	Arg	Thr	Arg	Thr	Thr	Ser	Ser	Val	Arg	Arg	Asp	Asp	Pro	Gly	
524					529					534					539	
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Glu	Phe	Arg	Val	Gly	Arg	Leu	Lys	His	Glu	Arg	Val	Lys	Val	Pro	Arg	
540					545					550					555	
ggc	gag	tca	ctg	atg	gaa	tgg	gct	gag	aat	gtc	atg	caa	ata	cat	gca	6411
Gly	Glu	Ser	Leu	Met	Glu	Trp	Ala	Glu	Asn	Val	Met	Gln	Ile	His	Ala	
556					561					566					571	
gat	cgg	aaa	tca	gtt	ctt	gag	gtt	gaa	ttt	tta	gga	gaa	gaa	gga	act	6459
Asp	Arg	Lys	Ser	Val	Leu	Glu	Val	Glu	Phe	Leu	Gly	Glu	Glu	Gly	Thr	
572					577					582					587	
ggc	ttg	gga	ccc	aca	tta	gag	ttt	tat	gct	ctg	gtg	gca	gca	gaa	ttc	6507
Gly	Leu	Gly	Pro	Thr	Leu	Glu	Phe	Tyr	Ala	Leu	Val	Ala	Ala	Glu	Phe	
588					593					598					603	
cag	aga	act	gac	ttg	gga	gct	tgg	ctt	tgt	gat	gat	aat	ttt	cca	gat	6555
Gln	Arg	Thr	Asp	Leu	Gly	Ala	Trp	Leu	Cys	Asp	Asp	Asn	Phe	Pro	Asp	
604					609					614					619	
gat	gaa	tct	cgt	cac	gtt	gat	ctt	gga	ggt	gga	ttg	aaa	cct	cct	gga	6603
Asp	Glu	Ser	Arg	His	Val	Asp	Leu	Gly	Gly	Gly	Leu	Lys	Pro	Pro	Gly	
620					625					630					635	
tat	tat	gtg	cag	agg	tca	tgt	gga	ctg	ttc	aca	gca	cca	ttt	cca	cag	6651
Tyr	Tyr	Val	Gln	Arg	Ser	Cys	Gly	Leu	Phe	Thr	Ala	Pro	Phe	Pro	Gln	
636					641					646					651	
gat	agt	gat	gag	ctt	gaa	agg	atc	acg	aaa	ctg	ttt	cat	ttc	ctt	gga	6699
Asp	Ser	Asp	Glu	Leu	Glu	Arg	Ile	Thr	Lys	Leu	Phe	His	Phe	Leu	Gly	
652					657					662					667	
att	ttc	ttg	gcc	aaa	tgc	att	caa	gac	aat	aga	ctt	gtg	gac	tta	cct	6747
Ile	Phe	Leu	Ala	Lys	Cys	Ile	Gln	Asp	Asn	Arg	Leu	Val	Asp	Leu	Pro	
668					673					678					683	
att	tct	aaa	cct	ttt	ttt	aaa	ctt	atg	tgt	atg	ggt	gac	att	aaa	agc	6795
Ile	Ser	Lys	Pro	Phe	Phe	Lys	Leu	Met	Cys	Met	Gly	Asp	Ile	Lys	Ser	
684					689					694					699	
aat	atg	agt	aaa	ctg	att	tat	gag	tca	cga	ggt	gat	aga	gac	tta	cac	6843
Asn	Met	Ser	Lys	Leu	Ile	Tyr	Glu	Ser	Arg	Gly	Asp	Arg	Asp	Leu	His	
700					705					710					715	
tgt	act	gaa	agt	cag	tct	gaa	gct	tct	aca	gaa	gaa	ggt	cat	gat	tca	6891
Cys	Thr	Glu	Ser	Gln	Ser	Glu	Ala	Ser	Thr	Glu	Glu	Gly	His	Asp	Ser	
716					721					726					731	
ctc	tcg	gta	gga	agc	ttt	gaa	gag	gat	tca	aaa	tca	gaa	ttt	att	ctt	6939
Leu	Ser	Val	Gly	Ser	Phe	Glu	Glu	Asp	Ser	Lys	Ser	Glu	Phe	Ile	Leu	
732					737					742					747	
gat	ccc	cct	aaa	cca	aaa	ccc	cca	gct	tgg	ttt	aat	gga	att	ttg	act	6987
Asp	Pro	Pro	Lys	Pro	Lys	Pro	Pro	Ala	Trp	Phe	Asn	Gly	Ile	Leu	Thr	

748	753	758	763	
tgg gaa gac ttt gaa tta gta aac cca cac aga gcc aga ttt tta aaa				7035
Trp Glu Asp Phe Glu Leu Val Asn Pro His Arg Ala Arg Phe Leu Lys				
764	769	774	779	
gaa att aaa gac ctt gct atc aag agg cgc caa att tta agc aac aaa				7083
Glu Ile Lys Asp Leu Ala Ile Lys Arg Arg Gln Ile Leu Ser Asn Lys				
780	785	790	795	
ggg ctt tct gaa gat gag aag aac aca aaa tta cag gaa cta gtg ctg				7131
Gly Leu Ser Glu Asp Glu Lys Asn Thr Lys Leu Gln Glu Leu Val Leu				
796	801	806	811	
aag aat cca tca ggt tct ggg cct cca ctt agc ata gag gat tta ggt				7179
Lys Asn Pro Ser Gly Ser Gly Pro Pro Leu Ser Ile Glu Asp Leu Gly				
812	817	822	827	
tta aat ttc cag ttt tgc cct tcc tca aga ata tat ggt ttt aca gct				7227
Leu Asn Phe Gln Phe Cys Pro Ser Ser Arg Ile Tyr Gly Phe Thr Ala				
828	833	838	843	
gtg gat ctc aag cca agt ggt gaa gat gag atg ata aca atg gat aat				7275
Val Asp Leu Lys Pro Ser Gly Glu Asp Glu Met Ile Thr Met Asp Asn				
844	849	854	859	
gca gaa gaa tat gtg gat ttg atg ttt gac ttt tgt atg cat acg ggt				7323
Ala Glu Glu Tyr Val Asp Leu Met Phe Asp Phe Cys Met His Thr Gly				
860	865	870	875	
att cag aaa caa atg gaa gcc ttt aga gat ggg ttt aat aaa gtt ttt				7371
Ile Gln Lys Gln Met Glu Ala Phe Arg Asp Gly Phe Asn Lys Val Phe				
876	881	886	891	
cca atg gag aaa tta agt tcc ttc agc cat gaa gaa gtc caa atg att				7419
Pro Met Glu Lys Leu Ser Ser Phe Ser His Glu Glu Val Gln Met Ile				
892	897	902	907	
ctt tgt gga aac cag tca cca tcc tgg gca gca gag gat att atc aat				7467
Leu Cys Gly Asn Gln Ser Pro Ser Trp Ala Ala Glu Asp Ile Ile Asn				
908	913	918	923	
tac act gaa cct aag ctg ggt tat aca cgt gac agc cct ggt ttc ctg				7515
Tyr Thr Glu Pro Lys Leu Gly Tyr Thr Arg Asp Ser Pro Gly Phe Leu				
924	929	934	939	
agg ttt gtg agg gtt tta tgt ggc atg tct tct gat gaa agg aaa gca				7563
Arg Phe Val Arg Val Leu Cys Gly Met Ser Ser Asp Glu Arg Lys Ala				
940	945	950	955	
ttc ttg cag ttt acc act ggt tgt tca act cta ccc cca ggt gga ctg				7611
Phe Leu Gln Phe Thr Thr Gly Cys Ser Thr Leu Pro Pro Gly Gly Leu				
956	961	966	971	
gct aac ctg cat ccc agg ctc acg gtt gta cgc aag gtt gat gct act				7659
Ala Asn Leu His Pro Arg Leu Thr Val Val Arg Lys Val Asp Ala Thr				
972	977	982	987	

gat gca agc tat cca tca gtc aat aca tgt gtg cat tac ctt aag ttg	7707
Asp Ala Ser Tyr Pro Ser Val Asn Thr Cys Val His Tyr Leu Lys Leu	
988 993 998 1003	
cct gaa tat tct tcc gag gag atc atg aga gag cgc ctg cta gct gct	7755
Pro Glu Tyr Ser Ser Glu Glu Ile Met Arg Glu Arg Leu Leu Ala Ala	
1004 1009 1014 1019	
aca atg gag aaa ggc ttt cat ctc aat tga g ctttgaagtg caatgggaga	7806
Thr Met Glu Lys Gly Phe His Leu Asn *	
1020 1025	
catcagagac tttaaaaata ctagtgaagc ctcttgtgtt tgtgtgcaga gaagtatatg	7866
atccaccatg ctaatgacac ttgccttttt ttccaccatt aaggctttaa gaacatgtgg	7926
aataagtttt ttagctgcta atgacaaaac aaatcctgta actaccagc cagcaagtat	7986
atagcacaga aactgtgtt actttacaag ggcttatgtg actggaataa ggtggtccca	8046
cttgactgtt ccaaagagca gcttctcaga tcttcagtgt tcaactggtaa atttctaaca	8106
gtgtatttgt gtaaagtttg tcatttcata ctccatacac tacagttgct gtcactgatc	8166
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attaatgagc atctcaagct ttttcttttc ctttttaatg atgcctgcac tatcaagagt	8286
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tttgcagctc aaaaataaag atgtattaag gggggaaaac ctggtctaag tgcaaggcac	8466
acttacagcg agttttactt toggttgtat tttctttgta tattataaac atttatttaa	8526
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gtttgcagcg taaaaaaaaa aaa	8609

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Met Thr Lys Ile Lys

1

gca gat ccc gac ggg ccc gag gct cag gcg gag gcg tgt tcc ggg gag	163
Ala Asp Pro Asp Gly Pro Glu Ala Gln Ala Glu Ala Cys Ser Gly Glu	
6 11 16 21	
cgc acc tac cag gag ctg ctg gtc aac cag aac ccc atc gcg cag ccc	211
Arg Thr Tyr Gln Glu Leu Leu Val Asn Gln Asn Pro Ile Ala Gln Pro	
22 27 32 37	
ctg gct tct cgc cgc ctc acg cgg aag ctc tac aaa tgc atc aag aaa	259
Leu Ala Ser Arg Arg Leu Thr Arg Lys Leu Tyr Lys Cys Ile Lys Lys	
38 43 48 53	
gcg gtg aag cag aag cag att cgg cgc ggg gtg aaa gag gtt cag aaa	307
Ala Val Lys Gln Lys Gln Ile Arg Arg Gly Val Lys Glu Val Gln Lys	
54 59 64 69	
ttt gtc aac aaa gga gaa aaa ggg atc atg gtt ttg gca gga gac aca	355
Phe Val Asn Lys Gly Glu Lys Gly Ile Met Val Leu Ala Gly Asp Thr	
70 75 80 85	
ctg ccc att gag gta tac tgc cat ctc cca gtc atg tgt gag gac cga	403
Leu Pro Ile Glu Val Tyr Cys His Leu Pro Val Met Cys Glu Asp Arg	
86 91 96 101	
aat ttg ccc tat gtc tat atc ccc tct aag acg gac ctg ggt gca gcc	451
Asn Leu Pro Tyr Val Tyr Ile Pro Ser Lys Thr Asp Leu Gly Ala Ala	
102 107 112 117	
gca ggc tcc aag cgc ccc acc tgt gtg ata atg gtc aag ccc cat gag	499
Ala Gly Ser Lys Arg Pro Thr Cys Val Ile Met Val Lys Pro His Glu	
118 123 128 133	
gag tac cag gag gct tac gat gag tgc ctg gag gag gtg cag tcc ctg	547
Glu Tyr Gln Glu Ala Tyr Asp Glu Cys Leu Glu Glu Val Gln Ser Leu	
134 139 144 149	
ccc cta ccc cta tga ggggctccgg tagcacctgg gcacctgccg ctggaagcta	602
Pro Leu Pro Leu *	
150	
ttgggctggc agcaggacga ctggctgtcc tctgcccac ccacactgac ggcattctcc	662
cagttcccca aggcaagcct tcttccagg cagctctaac agccctttca tgaaggtaat	722
gctagtcttc tgtccatcag tgccatttcc tgtagaacta aaggctgttc caagaatgtg	782
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<211> 2650

<212> DNA

[illegible]

<221> CDS

<400> 157

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167 172 177 182	
gaa gag aaa act tta aag aaa gat gag gaa aat gat agt aaa gct ccc	808
Glu Glu Lys Thr Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro	
183 188 193 198	
cct cat gag ctg act gaa gaa gaa aag caa caa atc ttg cac tct gag	856
Pro His Glu Leu Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu	
199 204 209 214	
gaa ttt tta agt ttc ttt gac cat tct aca aga att gta gaa aga gct	904
Glu Phe Leu Ser Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala	
215 220 225 230	
ctt tct gag cag att aac atc ttc ttt gac tat agt ggg aga gat ttg	952
Leu Ser Glu Gln Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu	
231 236 241 246	
gaa gac aaa gaa gga gag att caa gca ggt gct aaa ctg tca tta aat	1000
Glu Asp Lys Glu Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn	
247 252 257 262	
cga caa ttt ttt gac gaa cgt tgg tca aag cat cgg gtg gtt agt tgt	1048
Arg Gln Phe Phe Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys	
263 268 273 278	
ttg gat tgg tca tct cag tat ccg gag tta ctc gtg gct tcc tat aac	1096
Leu Asp Trp Ser Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn	
279 284 289 294	
aac aat gaa gat gcc cct cat gag cct gat ggt gtg gcc ctt gta tgg	1144
Asn Asn Glu Asp Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp	
295 300 305 310	
aat atg aaa tac aaa aaa act acc cca gag tat gtg ttt cac tgc cag	1192
Asn Met Lys Tyr Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln	
311 316 321 326	
tca gct gtg atg tct gcc aca ttt gca aaa ttt cat cca aat ctt gtt	1240
Ser Ala Val Met Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val	
327 332 337 342	
gtt ggt ggt aca tat tca ggc caa att gtg ctt tgg gat aac cgt agc	1288
Val Gly Gly Thr Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser	
343 348 353 358	
aat aaa aga act cca gtg caa aga act cca ctg tca gca gct gca cac	1336
Asn Lys Arg Thr Pro Val Gln Arg Thr Pro Leu Ser Ala Ala Ala His	
359 364 369 374	
aca cac cct gta tat tgt gta aat gtt gtt gga aca caa aat gct cac	1384
Thr His Pro Val Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His	
375 380 385 390	
aat ctg att agc atc tct act gat gga aaa att tgt tca tgg agt ctg	1432

Asn	Leu	Ile	Ser	Ile	Ser	Thr	Asp	Gly	Lys	Ile	Cys	Ser	Trp	Ser	Leu	
391					396					401					406	
gac	atg	ctt	tcc	cat	cca	cag	gat	agc	atg	gag	ttg	gtt	cat	aaa	cag	1480
Asp	Met	Leu	Ser	His	Pro	Gln	Asp	Ser	Met	Glu	Leu	Val	His	Lys	Gln	
407					412					417					422	
tca	aaa	gca	gta	gct	gtg	aca	tct	atg	tcc	ttc	cct	gtt	gga	gat	gtc	1528
Ser	Lys	Ala	Val	Ala	Val	Thr	Ser	Met	Ser	Phe	Pro	Val	Gly	Asp	Val	
423					428					433					438	
aac	aac	ttt	gtt	gtt	ggg	agt	gaa	gaa	ggg	tct	gtg	tac	aca	gca	tgc	1576
Asn	Asn	Phe	Val	Val	Gly	Ser	Glu	Glu	Gly	Ser	Val	Tyr	Thr	Ala	Cys	
439					444					449					454	
cgc	cat	ggc	agc	aaa	gct	gga	atc	agt	gag	atg	ttt	gag	ggg	cat	caa	1624
Arg	His	Gly	Ser	Lys	Ala	Gly	Ile	Ser	Glu	Met	Phe	Glu	Gly	His	Gln	
455					460					465					470	
gga	cca	atc	act	ggc	atc	cat	tgt	cat	gca	gct	gtt	gga	gca	gta	gac	1672
Gly	Pro	Ile	Thr	Gly	Ile	His	Cys	His	Ala	Ala	Val	Gly	Ala	Val	Asp	
471					476					481					486	
ttc	tca	cat	ctt	tat	gtc	act	tca	tcg	ttt	gac	tgg	aca	gta	aag	ctt	1720
Phe	Ser	His	Leu	Tyr	Val	Thr	Ser	Ser	Phe	Asp	Trp	Thr	Val	Lys	Leu	
487					492					497					502	
tgg	aca	act	aag	aat	aac	aag	cct	ttg	tat	tca	ttt	gaa	gat	aac	gca	1768
Trp	Thr	Thr	Lys	Asn	Asn	Lys	Pro	Leu	Tyr	Ser	Phe	Glu	Asp	Asn	Ala	
503					508					513					518	
gac	tat	gtt	tat	gat	gtt	atg	tgg	tca	cct	acc	cac	cca	gcc	ctg	ttt	1816
Asp	Tyr	Val	Tyr	Asp	Val	Met	Trp	Ser	Pro	Thr	His	Pro	Ala	Leu	Phe	
519					524					529					534	
gcc	tgt	gtg	gat	ggc	atg	ggg	aga	ttg	gat	ttg	tgg	aat	ctc	aat	aat	1864
Ala	Cys	Val	Asp	Gly	Met	Gly	Arg	Leu	Asp	Leu	Trp	Asn	Leu	Asn	Asn	
535					540					545					550	
gac	aca	gag	gta	cca	act	gcc	agc	att	tct	gtg	gag	ggg	aat	cct	gct	1912
Asp	Thr	Glu	Val	Pro	Thr	Ala	Ser	Ile	Ser	Val	Glu	Gly	Asn	Pro	Ala	
551					556					561					566	
ctt	aat	cgt	gtg	aga	tgg	acc	cat	tct	ggc	aga	gag	att	gct	gtg	ggg	1960
Leu	Asn	Arg	Val	Arg	Trp	Thr	His	Ser	Gly	Arg	Glu	Ile	Ala	Val	Gly	
567					572					577					582	
gat	tct	gaa	gga	cag	att	gtt	ata	tac	gat	gtg	gga	gag	cag	att	gct	2008
Asp	Ser	Glu	Gly	Gln	Ile	Val	Ile	Tyr	Asp	Val	Gly	Glu	Gln	Ile	Ala	
583					588					593					598	
gtt	ccc	cgc	aat	gat	gaa	tgg	gca	cgg	ttt	ggc	cga	aca	ctt	gca	gaa	2056
Val	Pro	Arg	Asn	Asp	Glu	Trp	Ala	Arg	Phe	Gly	Arg	Thr	Leu	Ala	Glu	
599					604					609					614	
att	aat	gca	aac	cga	gct	gat	gca	gag	gag	gaa	gca	gct	acc	cga	ata	2104
Ile	Asn	Ala	Asn	Arg	Ala	Asp	Ala	Glu	Glu	Glu	Ala	Ala	Thr	Arg	Ile	

615	620	625	630	
cct gct tag ttctga aaaggggagt gtaactagt gatttgggaa aggttcttaa				2160
Pro Ala *				
631				
gtagatcctg agactatttg catgcttctg tctaaatgat aattaaaagg aaatttcatg				2220
gattaaacca tgggtttaat gcagcaagga aacttacaat gtccctttat atataacatg				2280
catcttggtt tggatttggt tcatttttta atatactga ttgacttcac agaaagcagc				2340
ttttttgaat tctaatacat aggtgtatat ttggtattag ttattttgag ttcttttcaa				2400
cttataacac tgtatacagt tatttctaaa gcacagatga aataagttct gcatattttt				2460
aaataatcac agttccctgt tatacagata atgttctcac taccataat atgtaggaac				2520
attgtttctc cttagccgta gtatgcatac acctatccat gttcattctg acatcctttg				2580
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aaaaaaaa				2650

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tacagttggt gttgggggct taggcgaggg acgttaccgg gaagttgcag gcgggaggac	180
tcttcccat ccagtcacct gacaggtcac aaac atg tca gac aaa agt gaa	232
	Met Ser Asp Lys Ser Glu
	1
tta aag gct gag ttg gaa cgt aag aag cag cga ctg gcc caa atc aga	280
Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln Arg Leu Ala Gln Ile Arg	
7 12 17 22	
gag gaa aag aag aga aaa gaa gaa gaa agg aaa aaa aaa gaa aca gac	328
Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg Lys Lys Lys Glu Thr Asp	
23 28 33 38	
cag aag aag gaa gct gtt gct cct gtg caa gaa gaa tca gat ctt gaa	376
Gln Lys Lys Glu Ala Val Ala Pro Val Gln Glu Glu Ser Asp Leu Glu	

39	44	49	54	
aaa aaa agg aga gaa gct gaa gca ttg ctt caa agc atg ggg cta act				424
Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu Gln Ser Met Gly Leu Thr				
55	60	65	70	
cca gaa tcc ccc att gtc cct cct cct atg tct cca tcc tcc aaa tct				472
Pro Glu Ser Pro Ile Val Pro Pro Pro Met Ser Pro Ser Ser Lys Ser				
71	76	81	86	
gtg agc act cca agt gaa gct gga agc caa gac tct gga gat ggc gcc				520
Val Ser Thr Pro Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala				
87	92	97	102	
gtg gga tct aga cga gga cct att aaa ctt gga atg gct aaa atc acg				568
Val Gly Ser Arg Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr				
103	108	113	118	
caa gtc gac ttt cct cct cga gaa att gtc acg tat aca aag gaa act				616
Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr				
119	124	129	134	
cag act cca gtt atg gct caa ccc aaa gaa gat gaa gag gaa gat gat				664
Gln Thr Pro Val Met Ala Gln Pro Lys Glu Asp Glu Glu Glu Asp Asp				
135	140	145	150	
gat gta gtg gct cct aaa cca cct att gaa cct gaa gaa gag aaa act				712
Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Glu Lys Thr				
151	156	161	166	
tta aag aaa gat gag gaa aat gat agt aaa gct ccc cct cat gag ctg				760
Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu				
167	172	177	182	
act gaa gaa gaa aag caa caa atc ttg cac tct gag gaa ttt tta agt				808
Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser				
183	188	193	198	
ttc ttt gac cat tct aca aga att gta gaa aga gct ctt tct gag cag				856
Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln				
199	204	209	214	
att aac atc ttc ttt gac tat agt ggg aga gat ttg gaa gac aaa gaa				904
Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu				
215	220	225	230	
gga gag att caa gca ggt gct aaa ctg tca tta aat cga caa ttt ttt				952
Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe				
231	236	241	246	
gac gaa cgt tgg tca aag cat cgg gtg gtt agt tgt ttg gat tgg tca				1000
Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys Leu Asp Trp Ser				
247	252	257	262	
tct cag tat ccg gag tta ctc gtg gct tcc tat aac aac aat gaa gat				1048
Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp				
263	268	273	278	

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Gln Glu Ile Ala Ala Leu Lys Gly His Pro Asn Asn Val Val Ser Ile	585	590	595	600	
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Lys Tyr Cys Ser His Ser Gly Leu Val Phe Ser Val Ser Thr Ser Tyr	601	606	611	616	
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acc cgt gcc atc acc agt gct cag ggc gag cat cag atc aac cag atc	2619				
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Gln His Asp Leu Val Val Thr Gly Ser Lys Asp His Tyr Val Lys Met	713	718	723	728	
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Cys Ser Asp Leu His Thr Gly Arg Gly Gly Pro Cys Thr Gln Trp Leu	
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aac gtc aga gac tta gac cgc ctg cag cgc gag tcc cag cgg gaa gtg	2544
Asn Val Arg Asp Leu Asp Arg Leu Gln Arg Glu Ser Gln Arg Glu Val	
833 838 843 848	
ctg cgc ctg cag agg cag ttg atg ctt cag cag ggc aac ggt ggc gct	2592
Leu Arg Leu Gln Arg Gln Leu Met Leu Gln Gln Gly Asn Gly Gly Ala	
849 854 859 864	
tgg ccc gag gcg ggc ggc cag agc gca acc tgc gag gag gtg cga cgg	2640
Trp Pro Glu Ala Gly Gly Gln Ser Ala Thr Cys Glu Glu Val Arg Arg	
865 870 875 880	
cag atg ctg gcg ctg gag cgc gag ctg gac cag cgg cgg cgc gag tgc	2688
Gln Met Leu Ala Leu Glu Arg Glu Leu Asp Gln Arg Arg Arg Glu Cys	
881 886 891 896	
cag gag ctg ggc gcg cag gcg gcc ccg gcg cgg cga cgt ggc gag gag	2736
Gln Glu Leu Gly Ala Gln Ala Ala Pro Ala Arg Arg Arg Gly Glu Glu	
897 902 907 912	
gcc gag aca cag ctg cag gcg gcg ctg ctc aaa aac gcc tgg ctg gcg	2784
Ala Glu Thr Gln Leu Gln Ala Ala Leu Leu Lys Asn Ala Trp Leu Ala	

913	918	923	928	
gag gag aat ggg cgg ctg cag gcc aag acc gac tgg gtg cgg aag gtg				2832
Glu Glu Asn Gly Arg Leu Gln Ala Lys Thr Asp Trp Val Arg Lys Val				
929	934	939	944	
gag gct gag aat agc gaa gtg cgc ggc cac ctg ggc cgc gcg tgt caa				2880
Glu Ala Glu Asn Ser Glu Val Arg Gly His Leu Gly Arg Ala Cys Gln				
945	950	955	960	
gag cgc gat gcc tcc ggc ttg atc gcc gaa cag ctg ctg cag cag gcg				2928
Glu Arg Asp Ala Ser Gly Leu Ile Ala Glu Gln Leu Leu Gln Gln Ala				
961	966	971	976	
gcg cgc ggg cag gac agg cag cag cag ctg caa cgc gac ccg cag aag				2976
Ala Arg Gly Gln Asp Arg Gln Gln Gln Leu Gln Arg Asp Pro Gln Lys				
977	982	987	992	
gcc ctg tgt gac ctc cat cct tcc tgg aag gag ata cag gcg ctc cag				3024
Ala Leu Cys Asp Leu His Pro Ser Trp Lys Glu Ile Gln Ala Leu Gln				
993	998	1003	1008	
tgt cgg cct ggt cac cct cct gaa cag ccc tgg gag acc agt caa atg				3072
Cys Arg Pro Gly His Pro Pro Glu Gln Pro Trp Glu Thr Ser Gln Met				
1009	1014	1019	1024	
ccg gag tcc caa gtt aaa ggt agc aga agg ccc aag ttc cac gca cgg				3120
Pro Glu Ser Gln Val Lys Gly Ser Arg Arg Pro Lys Phe His Ala Arg				
1025	1030	1035	1040	
cct gaa gac tac gca gtg tca cag ccc aac aga gac ata cag gag aaa				3168
Pro Glu Asp Tyr Ala Val Ser Gln Pro Asn Arg Asp Ile Gln Glu Lys				
1041	1046	1051	1056	
agg gaa gcc tcc ctc gag gag agc cca gtt gcc ctt ggg gag tca gcc				3216
Arg Glu Ala Ser Leu Glu Glu Ser Pro Val Ala Leu Gly Glu Ser Ala				
1057	1062	1067	1072	
agt gtc ccc caa gtt tca gag aca gtc cct gcc agc caa cct ctg tcc				3264
Ser Val Pro Gln Val Ser Glu Thr Val Pro Ala Ser Gln Pro Leu Ser				
1073	1078	1083	1088	
aag aaa acc agc tcc cag tca aac tcc tcc tct gag ggg tcg atg tgg				3312
Lys Lys Thr Ser Ser Gln Ser Asn Ser Ser Ser Glu Gly Ser Met Trp				
1089	1094	1099	1104	
gcc acc gtg ccg tcc tcc cct act ctg gac agg gac aca gcc agt gag				3360
Ala Thr Val Pro Ser Ser Pro Thr Leu Asp Arg Asp Thr Ala Ser Glu				
1105	1110	1115	1120	
gtg gat gac ctg gag cct gac agc gtg tcc ctg gcc ctg gaa atg ggg				3408
Val Asp Asp Leu Glu Pro Asp Ser Val Ser Leu Ala Leu Glu Met Gly				
1121	1126	1131	1136	
ggc tcg gcg gct cct gct gcc ccc aag ctc aag atc ttc atg gct cag				3456
Gly Ser Ala Ala Pro Ala Ala Pro Lys Leu Lys Ile Phe Met Ala Gln				
1137	1142	1147	1152	

tat aac tac aac cca ttt gag ggg ccc aat gat cac cct gag ggt gag	3504
Tyr Asn Tyr Asn Pro Phe Glu Gly Pro Asn Asp His Pro Glu Gly Glu	
1153 1158 1163 1168	
ctg ccc ctc aca gct ggg gac tac ata tat atc ttc ggg gac atg gat	3552
Leu Pro Leu Thr Ala Gly Asp Tyr Ile Tyr Ile Phe Gly Asp Met Asp	
1169 1174 1179 1184	
gag gat ggc ttc tat gag ggg gag ctt gag gat ggc cgg cgg ggg ctg	3600
Glu Asp Gly Phe Tyr Glu Gly Glu Leu Glu Asp Gly Arg Arg Gly Leu	
1185 1190 1195 1200	
gtg ccc tcc aac ttc gtg gag cag att ccg gac agc tac atc cca ggc	3648
Val Pro Ser Asn Phe Val Glu Gln Ile Pro Asp Ser Tyr Ile Pro Gly	
1201 1206 1211 1216	
tgc ctg cct gcc aaa tcc cct gat ctt ggc ccc agt caa ctc cca gcg	3696
Cys Leu Pro Ala Lys Ser Pro Asp Leu Gly Pro Ser Gln Leu Pro Ala	
1217 1222 1227 1232	
ggg cag gat gaa gct ctg gag gaa gac agc tta tta tct ggg aaa gcc	3744
Gly Gln Asp Glu Ala Leu Glu Glu Asp Ser Leu Leu Ser Gly Lys Ala	
1233 1238 1243 1248	
cag gga gtg gtg gac aga ggg ctg tgc cag atg gtc agg gtg ggc tcc	3792
Gln Gly Val Val Asp Arg Gly Leu Cys Gln Met Val Arg Val Gly Ser	
1249 1254 1259 1264	
aag aca gaa gta gca aca gag atc ctg gat acc aag acg gaa gcc tgc	3840
Lys Thr Glu Val Ala Thr Glu Ile Leu Asp Thr Lys Thr Glu Ala Cys	
1265 1270 1275 1280	
cag ctg ggc ttg ctg cag agc atg ggg aag cag ggc ctc tcc aga ccc	3888
Gln Leu Gly Leu Leu Gln Ser Met Gly Lys Gln Gly Leu Ser Arg Pro	
1281 1286 1291 1296	
ctt ctg ggg acc aaa ggg gtg ctc cgt atg gct ccc atg cag cta cac	3936
Leu Leu Gly Thr Lys Gly Val Leu Arg Met Ala Pro Met Gln Leu His	
1297 1302 1307 1312	
ctg cag aat gtc aca gcc aca tca gcc aac atc acc tgg gtc tac agc	3984
Leu Gln Asn Val Thr Ala Thr Ser Ala Asn Ile Thr Trp Val Tyr Ser	
1313 1318 1323 1328	
agc cac cgc cac ccc cat gtg gta tat ctt gat gac cga gag cat gcc	4032
Ser His Arg His Pro His Val Val Tyr Leu Asp Asp Arg Glu His Ala	
1329 1334 1339 1344	
ctg acc cca gcg ggc gtg agc tgc tac acc ttc cag ggc ctg tgc ccc	4080
Leu Thr Pro Ala Gly Val Ser Cys Tyr Thr Phe Gln Gly Leu Cys Pro	
1345 1350 1355 1360	
ggc acg cac tac cgg gcg cgg gtg gag gtg cgg ctg cca cgg gac ttg	4128
Gly Thr His Tyr Arg Ala Arg Val Glu Val Arg Leu Pro Arg Asp Leu	
1361 1366 1371 1376	

ctg cag gtg tat tgg gga act atg tcc tcc acc gtc acc ttc gac aca	4176
Leu Gln Val Tyr Trp Gly Thr Met Ser Ser Thr Val Thr Phe Asp Thr	
1377 1382 1387 1392	
ctc ttg gca gga cct ccc tac cca ccg ctg gat gtg ctg gtg gag cgc	4224
Leu Leu Ala Gly Pro Pro Tyr Pro Pro Leu Asp Val Leu Val Glu Arg	
1393 1398 1403 1408	
cat gcc tcg cca ggt gtc ctg gtg gtc agc tgg ctc cct gtg acc att	4272
His Ala Ser Pro Gly Val Leu Val Val Ser Trp Leu Pro Val Thr Ile	
1409 1414 1419 1424	
gac tca gct ggg tcc tcc aat gga gtc cag gtc acc ggt tat gct gtg	4320
Asp Ser Ala Gly Ser Ser Asn Gly Val Gln Val Thr Gly Tyr Ala Val	
1425 1430 1435 1440	
tat gca gat ggg ctt aag gtt tgt gag gtc gcc gat gcc act gct ggg	4368
Tyr Ala Asp Gly Leu Lys Val Cys Glu Val Ala Asp Ala Thr Ala Gly	
1441 1446 1451 1456	
agc acc cta ttg gaa ttc tcc cag cta cag gtg ccc ctc acg tgg cag	4416
Ser Thr Leu Leu Glu Phe Ser Gln Leu Gln Val Pro Leu Thr Trp Gln	
1457 1462 1467 1472	
aag gtc tca gtg aga acc atg tca ctc tgt ggt gag tcc ctg gat tca	4464
Lys Val Ser Val Arg Thr Met Ser Leu Cys Gly Glu Ser Leu Asp Ser	
1473 1478 1483 1488	
gtg cct gct cag atc ccc gag gac ttc ttc atg tgt cac cga tgg cca	4512
Val Pro Ala Gln Ile Pro Glu Asp Phe Phe Met Cys His Arg Trp Pro	
1489 1494 1499 1504	
gag act cca ccc ttt agc tac act tgt ggc gac cca tcc acc tac aga	4560
Glu Thr Pro Pro Phe Ser Tyr Thr Cys Gly Asp Pro Ser Thr Tyr Arg	
1505 1510 1515 1520	
gtc acc ttc ccc gtc tgc ccc cag aag ctg tca ctg gct cct ccg agt	4608
Val Thr Phe Pro Val Cys Pro Gln Lys Leu Ser Leu Ala Pro Pro Ser	
1521 1526 1531 1536	
gcc aag gcc agc ccc cac aac cct gga agc tgc ggg gag ccc cag gcc	4656
Ala Lys Ala Ser Pro His Asn Pro Gly Ser Cys Gly Glu Pro Gln Ala	
1537 1542 1547 1552	
aag ttc cta gaa gca ttc ttt gaa gaa ccc cca agg agg caa tcc cca	4704
Lys Phe Leu Glu Ala Phe Phe Glu Glu Pro Pro Arg Arg Gln Ser Pro	
1553 1558 1563 1568	
gtg tcc aac ctg ggc tca gaa gga gaa tgt ccg agt tca ggg gct ggc	4752
Val Ser Asn Leu Gly Ser Glu Gly Glu Cys Pro Ser Ser Gly Ala Gly	
1569 1574 1579 1584	
agc caa gcc cag gag ctt gca gag gcc tgg gag ggc tgt aga aag gac	4800
Ser Gln Ala Gln Glu Leu Ala Glu Ala Trp Glu Gly Cys Arg Lys Asp	
1585 1590 1595 1600	
ctg ctc ttt cag aag agt ccc cag aac cac agg cca cct tca gtc agt	4848

Leu	Leu	Phe	Gln	Lys	Ser	Pro	Gln	Asn	His	Arg	Pro	Pro	Ser	Val	Ser		
1601					1606					1611					1616		
gac	cag	cct	ggg	gag	aag	gaa	aat	tgc	tcc	cag	cac	atg	ggc	acc	agc		4896
Asp	Gln	Pro	Gly	Glu	Lys	Glu	Asn	Cys	Ser	Gln	His	Met	Gly	Thr	Ser		
1617					1622					1627					1632		
aaa	agc	cct	gct	cca	gga	ttc	atc	cat	cta	cgc	acc	gag	tgt	ggg	ccc		4944
Lys	Ser	Pro	Ala	Pro	Gly	Phe	Ile	His	Leu	Arg	Thr	Glu	Cys	Gly	Pro		
1633					1638					1643					1648		
agg	aaa	gaa	ccg	tgt	cag	gaa	aag	gct	gcc	ctt	gag	agg	gta	ctt	cgg		4992
Arg	Lys	Glu	Pro	Cys	Gln	Glu	Lys	Ala	Ala	Leu	Glu	Arg	Val	Leu	Arg		
1649					1654					1659					1664		
caa	aag	caa	gat	gcc	caa	ggg	ttc	aca	cct	ccc	cag	ctg	ggc	gcc	agc		5040
Gln	Lys	Gln	Asp	Ala	Gln	Gly	Phe	Thr	Pro	Pro	Gln	Leu	Gly	Ala	Ser		
1665					1670					1675					1680		
caa	cag	tat	gca	tct	gac	ttc	cat	aac	gtt	ttg	aag	gag	gag	cag	gag		5088
Gln	Gln	Tyr	Ala	Ser	Asp	Phe	His	Asn	Val	Leu	Lys	Glu	Glu	Gln	Glu		
1681					1686					1691					1696		
gca	ctg	tgc	ttg	gat	ctg	tgg	ggc	aca	gag	agg	cga	gag	gag	agg	agg		5136
Ala	Leu	Cys	Leu	Asp	Leu	Trp	Gly	Thr	Glu	Arg	Arg	Glu	Glu	Arg	Arg		
1697					1702					1707					1712		
gag	cct	gag	ccc	cac	agc	agg	caa	gga	caa	gct	ctg	ggg	gtg	aag	aga		5184
Glu	Pro	Glu	Pro	His	Ser	Arg	Gln	Gly	Gln	Ala	Leu	Gly	Val	Lys	Arg		
1713					1718					1723					1728		
ggg	tgc	cag	ctc	cat	gag	ccc	agc	tcg	gca	ctg	tgt	cca	gct	cca	tcc		5232
Gly	Cys	Gln	Leu	His	Glu	Pro	Ser	Ser	Ala	Leu	Cys	Pro	Ala	Pro	Ser		
1729					1734					1739					1744		
gcc	aaa	gtc	atc	aag	atg	ccc	agg	ggt	ggc	ccc	caa	cag	ctg	ggg	acg		5280
Ala	Lys	Val	Ile	Lys	Met	Pro	Arg	Gly	Gly	Pro	Gln	Gln	Leu	Gly	Thr		
1745					1750					1755					1760		
ggg	gcc	aac	act	cca	gcc	agg	gtc	ttt	gtg	gcc	ctc	tct	gat	tac	aac		5328
Gly	Ala	Asn	Thr	Pro	Ala	Arg	Val	Phe	Val	Ala	Leu	Ser	Asp	Tyr	Asn		
1761					1766					1771					1776		
ccc	ctg	gtg	atg	tct	gcc	aac	ctc	aag	gct	gca	gag	gag	gag	ctg	gtc		5376
Pro	Leu	Val	Met	Ser	Ala	Asn	Leu	Lys	Ala	Ala	Glu	Glu	Glu	Leu	Val		
1777					1782					1787					1792		
ttc	cag	aaa	agg	cag	ttg	cta	aga	gtg	tgg	ggc	tct	cag	gac	acc	cat		5424
Phe	Gln	Lys	Arg	Gln	Leu	Leu	Arg	Val	Trp	Gly	Ser	Gln	Asp	Thr	His		
1793					1798					1803					1808		
gat	ttc	tac	ctc	agc	gag	tgc	aac	agg	caa	gtg	ggc	aat	atc	ccc	ggg		5472
Asp	Phe	Tyr	Leu	Ser	Glu	Cys	Asn	Arg	Gln	Val	Gly	Asn	Ile	Pro	Gly		
1809					1814					1819					1824		
cgc	cta	gtg	gct	gag	atg	gag	gtg	ggg	aca	gag	cag	act	gat	agg	agg		5520
Arg	Leu	Val	Ala	Glu	Met	Glu	Val	Gly	Thr	Glu	Gln	Thr	Asp	Arg	Arg		

1825	1830	1835	1840	
tgg cgt tct ccg gcc caa ggg cac ctg cct tct	gtg gcc cac ctc gag	5568		
Trp Arg Ser Pro Ala Gln Gly His Leu Pro Ser	Val Ala His Leu Glu			
1841	1846	1851	1856	
gac ttt cag ggg ctc acc atc ccc cag ggt tcc tcc	ctg gtg ctc cag	5616		
Asp Phe Gln Gly Leu Thr Ile Pro Gln Gly Ser	Ser Leu Val Leu Gln			
1857	1862	1867	1872	
ggg aac tcc aag aga ctc cca ctg tgg act cca aag	atc atg ata gca	5664		
Gly Asn Ser Lys Arg Leu Pro Leu Trp Thr Pro	Lys Ile Met Ile Ala			
1873	1878	1883	1888	
gct ctg gac tat gat cct ggg gat ggg caa atg	ggg ggc cag ggg aag	5712		
Ala Leu Asp Tyr Asp Pro Gly Asp Gly Gln Met	Gly Gly Gln Gly Lys			
1889	1894	1899	1904	
ggc agg ctg gcg ctg agg gca gga gac gtg gtc	atg gtt tac ggg ccc	5760		
Gly Arg Leu Ala Leu Arg Ala Gly Asp Val Val	Met Val Tyr Gly Pro			
1905	1910	1915	1920	
atg gat gac caa gga ttc tat tat gga gag ttg	ggc ggc cac agg ggc	5808		
Met Asp Asp Gln Gly Phe Tyr Tyr Gly Glu Leu	Gly Gly His Arg Gly			
1921	1926	1931	1936	
ctg gtt cct gcc cac ctg ctg gat cac atg tcc	ctc cat gga cac tga	5856		
Leu Val Pro Ala His Leu Leu Asp His Met Ser	Leu His Gly His *			
1937	1942	1947	1952	
gcaagcatcc ttgcccaggt agtggcctct ggctgctcac	accctgccag aggagaagca	5916		
agcgttcaga ccctcacacc agcaccctc ctcaccacca	taagtagcat gtgctccaag	5976		
tgccactgtg ttaaactgat ggtagtcctt aagtgtcccc	taggctctga aagtagcagg	6036		
acttaagcct gagttatttg caaaagcaaa cacaacaagc	caaccctga gagtctgaga	6096		
agccatttca aagttgctga taactatggc aggtatacgg	agaagcgcct ttttctgtgg	6156		
ccaatgtgtg ttttctctgg gaggttaagg ttatctgtcc	attgccttgt acgaaagtct	6216		
caagaaaagt ctacatctta aaaaaaaaaa aa		6248		

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 <213> Homo sapiens

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Arg Asn Leu Thr Asn Val Leu Gly Thr Gln Ser Arg Tyr Val Leu Asn	
202 207 212 217	
ggc gcg ttc ctg gcc ttc gag cgc cgg cac gag ttc atg gcg ctg tgc	902
Gly Ala Phe Leu Ala Phe Glu Arg Arg His Glu Phe Met Ala Leu Cys	
218 223 228 233	
atg cgg gac ttc gtg gac cac tac aac ggc tgg atc tgg ggt cac cag	950
Met Arg Asp Phe Val Asp His Tyr Asn Gly Trp Ile Trp Gly His Gln	
234 239 244 249	
ggc ccg cag ctg ctc acg cgg gtc ttc aag aag tgg tgt tcc atc cgc	998
Gly Pro Gln Leu Leu Thr Arg Val Phe Lys Lys Trp Cys Ser Ile Arg	
250 255 260 265	
agc ctg gcc gag agc cgc gcc tgc cgc ggc gtc acc acc ctg ccc cct	1046
Ser Leu Ala Glu Ser Arg Ala Cys Arg Gly Val Thr Thr Leu Pro Pro	
266 271 276 281	
gag gcc ttc tac ccc atc ccc tgg cag gac tgg aag aag tac ttt gag	1094
Glu Ala Phe Tyr Pro Ile Pro Trp Gln Asp Trp Lys Lys Tyr Phe Glu	
282 287 292 297	
gac atc aac ccg gag gag ctg ccg cgg ctg ctc agt gcc acc tat gct	1142
Asp Ile Asn Pro Glu Glu Leu Pro Arg Leu Leu Ser Ala Thr Tyr Ala	
298 303 308 313	
gtc cac gtg tgg aac aag aag agc cag ggc acg cgg ttc gag gcc acg	1190
Val His Val Trp Asn Lys Lys Ser Gln Gly Thr Arg Phe Glu Ala Thr	
314 319 324 329	
tcc agg gca ctg ctg gcc cag ctg cat gcc cgc tac tgc ccc acg acg	1238
Ser Arg Ala Leu Leu Ala Gln Leu His Ala Arg Tyr Cys Pro Thr Thr	
330 335 340 345	
cac gag gcc atg aaa atg tac ttg tga	1265
His Glu Ala Met Lys Met Tyr Leu *	
346 351	

<210> 164
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Met Ala Lys Val Ile Leu Lys Gln Ser Lys Gln Cys Lys Asn Leu Leu	

1	5	10	
acc tgc aaa gtg gcc cag gtc tgc ccc gta tgt ggc tgt ctt cat tgt			96
Thr Cys Lys Val Ala Gln Val Cys Pro Val Cys Gly Cys Leu His Cys			
17	22	27	32
tat ttc tgg tgg ctc tca ggt ctt gag tca aga cgt ccc agc tct cca			144
Tyr Phe Trp Trp Leu Ser Gly Leu Glu Ser Arg Arg Pro Ser Ser Pro			
33	38	43	48
ctc atc gat att aaa ccc atc gag ttt ggc gtt ctc agc gcc aag aag			192
Leu Ile Asp Ile Lys Pro Ile Glu Phe Gly Val Leu Ser Ala Lys Lys			
49	54	59	64
gag ccc atc caa cct tcg gtg ctc aga cgg acc tat aac ccc gac gac			240
Glu Pro Ile Gln Pro Ser Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp			
65	70	75	80
tat ttc agg aag ttc gaa ccc cac ctg tac tcc ctc gac tcc aac agc			288
Tyr Phe Arg Lys Phe Glu Pro His Leu Tyr Ser Leu Asp Ser Asn Ser			
81	86	91	96
gac gat gtg gac tct ctg aca gac gag gag atc ctg tcc aag tac cag			336
Asp Asp Val Asp Ser Leu Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln			
97	102	107	112
ctg ggc atg ctg cac ttc agc act cag tac gac ctg ctg cac aac cac			384
Leu Gly Met Leu His Phe Ser Thr Gln Tyr Asp Leu Leu His Asn His			
113	118	123	128
ctc acc gtg cgc gtg atc gag gcc agg gac ctg cca cct ccc atc tcc			432
Leu Thr Val Arg Val Ile Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser			
129	134	139	144
cac gat ggc tcg cgc cag gac atg gcg cac tcc aac ccc tac gtc aag			480
His Asp Gly Ser Arg Gln Asp Met Ala His Ser Asn Pro Tyr Val Lys			
145	150	155	160
atc tgt ctc ctg cca gac cag aag aac tca aag cag acc ggg gtc aaa			528
Ile Cys Leu Leu Pro Asp Gln Lys Asn Ser Lys Gln Thr Gly Val Lys			
161	166	171	176
cgc aag acc cag aag ccc gtg ttt gag gag cgc tac acc ttc gag atc			576
Arg Lys Thr Gln Lys Pro Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile			
177	182	187	192
ccc ttc ctg gag gcc cag agg agg acc ctg ctc ctg acc gtg gtg gat			624
Pro Phe Leu Glu Ala Gln Arg Arg Thr Leu Leu Leu Thr Val Val Asp			
193	198	203	208
ttt gat aag ttc tcc cgc cac tgt gtc att ggg aaa gtt tct gtg cct			672
Phe Asp Lys Phe Ser Arg His Cys Val Ile Gly Lys Val Ser Val Pro			
209	214	219	224
ttg tgt gaa gtt gac ctg gtc aag ggc ggg cac tgg tgg aag gcg cat			720
Leu Cys Glu Val Asp Leu Val Lys Gly Gly His Trp Trp Lys Ala His			
225	230	235	240

gat tcc cag ttc tca gca cca ggc ttg ccc gcc gat caa caa ttt ttc	768
Asp Ser Gln Phe Ser Ala Pro Gly Leu Pro Ala Asp Gln Gln Phe Phe	
241 246 251 256	
gcc gat ctg ttc agc ggc ctg gtg ctt aac ccg caa cta ctg ggg cgc	816
Ala Asp Leu Phe Ser Gly Leu Val Leu Asn Pro Gln Leu Leu Gly Arg	
257 262 267 272	
gtc tgg ttt gcc agc cag cct gcc tcg ttg ccg gtg ggc agt tta tgt	864
Val Trp Phe Ala Ser Gln Pro Ala Ser Leu Pro Val Gly Ser Leu Cys	
273 278 283 288	
att gat ttt ccc cgt ctg gat atc gtg ctg cgc ggc gaa tac ggc aat	912
Ile Asp Phe Pro Arg Leu Asp Ile Val Leu Arg Gly Glu Tyr Gly Asn	
289 294 299 304	
ctg ctg gaa gca aag cag caa cgt ttg gtg gaa gga gaa atg ctg ttt	960
Leu Leu Glu Ala Lys Gln Gln Arg Leu Val Glu Gly Glu Met Leu Phe	
305 310 315 320	
att ccg gcg cgc gcg gct aat tta ccg gtc aac aac aaa ccg gtg atg	1008
Ile Pro Ala Arg Ala Ala Asn Leu Pro Val Asn Asn Lys Pro Val Met	
321 326 331 336	
ctg tta agc ctg gtg ttc gct ccg acc tgg ctt ggg tta tcg ttt tac	1056
Leu Leu Ser Leu Val Phe Ala Pro Thr Trp Leu Gly Leu Ser Phe Tyr	
337 342 347 352	
gat agc cgc acc acg tcg ttg ttg cat cct gct cgc cag atc cag ctt	1104
Asp Ser Arg Thr Thr Ser Leu Leu His Pro Ala Arg Gln Ile Gln Leu	
353 358 363 368	
ccc agc ctg caa cgc ggt gaa ggt gaa gcg atg ctt acc gcc ctc acc	1152
Pro Ser Leu Gln Arg Gly Glu Gly Glu Ala Met Leu Thr Ala Leu Thr	
369 374 379 384	
cat ctt agc cgt tcg ccg ctg gag caa aat atc att cag ccg ctg gtg	1200
His Leu Ser Arg Ser Pro Leu Glu Gln Asn Ile Ile Gln Pro Leu Val	
385 390 395 400	
tta agt ttg ctg cat ctt tgc cgt agc gtg gtg aat atg ccg ccg ggc	1248
Leu Ser Leu Leu His Leu Cys Arg Ser Val Val Asn Met Pro Pro Gly	
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aat tcg cag ccg cgc ggc gat ttt ctc tat cac agc att tgt aac tgg	1296
Asn Ser Gln Pro Arg Gly Asp Phe Leu Tyr His Ser Ile Cys Asn Trp	
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gtt cag gat aat tat gcc cag ccg ctc acc cgc gag agc gtg gcg cag	1344
Val Gln Asp Asn Tyr Ala Gln Pro Leu Thr Arg Glu Ser Val Ala Gln	
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Phe Phe Asn Ile Thr Pro Asn His Leu Ser Lys Leu Phe Ala Gln His	
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Gly Thr Met Arg Phe Ile Glu Tyr Val Arg Trp Val Arg Met Ala Lys	
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gcg agg atg att ttg cag aaa tat cat ctg tca att cat gaa gtg gca	1488
Ala Arg Met Ile Leu Gln Lys Tyr His Leu Ser Ile His Glu Val Ala	
481 486 491 496	

cag cgt tgc ggt ttt ccg gat agc gac tat ttt tgt cgc gtt ttc cgg	1536
Gln Arg Cys Gly Phe Pro Asp Ser Asp Tyr Phe Cys Arg Val Phe Arg	
497 502 507 512	

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Arg Gln Phe Gly Leu Thr Pro Gly Glu Tyr Ser Ala Arg Phe Gln Gly	
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ccaagtgagc gttgcccctc cctctcccaa ctctctaccc ggga atg tct cgg cga	236
Met Ser Arg Arg	
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Lys Gln Arg Lys Pro Gln Gln Leu Ile Ser Asp Cys Glu Gly Pro Ser	
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gcg tct gag aac ggt gat gct agc gag gag gat cac ccc caa gtc tgt	332
Ala Ser Glu Asn Gly Asp Ala Ser Glu Glu Asp His Pro Gln Val Cys	

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Ala Lys Cys Cys Ala Gln Phe Thr Asp Pro Thr Glu Phe Leu Ala His				
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Gln Asn Ala Cys Ser Thr Asp Pro Pro Val Met Val Ile Ile Gly Gly				
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cag gag aac ccc aac aac tct tcg gcc tcc tct gaa ccc cgg cct gag				476
Gln Glu Asn Pro Asn Asn Ser Ser Ala Ser Ser Glu Pro Arg Pro Glu				
69	74	79	84	
ggc cac aat aat cct cag gtc atg gac aca gag cat agc aac ccc cca				524
Gly His Asn Asn Pro Gln Val Met Asp Thr Glu His Ser Asn Pro Pro				
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gat tct ggg tcc tcc gtg ccc acg gat ccc acc tgg ggc cca gag agg				572
Asp Ser Gly Ser Ser Val Pro Thr Asp Pro Thr Trp Gly Pro Glu Arg				
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aga gga gag gag tct tca ggg cat ttc ctg gtc gct gcc aca ggt aca				620
Arg Gly Glu Glu Ser Ser Gly His Phe Leu Val Ala Ala Thr Gly Thr				
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Ala Ala Gly Gly Gly Gly Gly Leu Ile Leu Ala Ser Pro Lys Leu Gly				
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gca acc cca tta cct cca gaa tcg acc cct gca ccc cct cct cct cca				716
Ala Thr Pro Leu Pro Pro Glu Ser Thr Pro Ala Pro Pro Pro Pro Pro				
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Pro Pro Pro Pro Pro Pro Gly Val Gly Ser Gly His Leu Asn Ile Pro				
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ctg atc ttg gaa gag cta cgg gtg ctg cag cag cgg cag atc cat cag				812
Leu Ile Leu Glu Glu Leu Arg Val Leu Gln Arg Gln Ile His Gln				
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Met Gln Met Thr Glu Gln Ile Cys Arg Gln Val Leu Leu Leu Gly Ser				
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Leu Gly Gln Thr Val Gly Ala Pro Ala Ser Pro Ser Glu Leu Pro Gly				
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Thr Gly Thr Ala Ser Ser Thr Lys Pro Leu Leu Pro Leu Phe Ser Pro				
229	234	239	244	
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Ile Lys Pro Val Gln Thr Ser Lys Thr Leu Ala Ser Ser Ser Ser Ser				
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Thr Gly Leu Leu Ala Ala Gln Cys Leu Gly Ala Ala Arg Gly Leu Glu	
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gcc act gcc tcc cca ggg ctc ctg aag cca aag aat gga agt ggt gag	1292
Ala Thr Ala Ser Pro Gly Leu Leu Lys Pro Lys Asn Gly Ser Gly Glu	
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Leu Ser Tyr Gly Glu Val Met Gly Pro Leu Glu Lys Pro Gly Gly Arg	
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His Lys Cys Arg Phe Cys Ala Lys Val Phe Gly Ser Asp Ser Ala Leu	
373 378 383 388	
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Gln Ile His Leu Arg Ser His Thr Gly Glu Arg Pro Tyr Lys Cys Asn	
389 394 399 404	
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Val Cys Gly Asn Arg Phe Thr Thr Arg Gly Asn Leu Lys Val His Phe	
405 410 415 420	
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His Arg His Arg Glu Lys Tyr Pro His Val Gln Met Asn Pro His Pro	
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Val Pro Glu His Leu Asp Tyr Val Ile Thr Ser Ser Gly Leu Pro Tyr	
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Gly Met Ser Val Pro Pro Glu Lys Ala Glu Glu Glu Ala Ala Thr Pro	
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Val Glu Pro Lys Asn Lys Ala Asp Glu Asn Thr Pro Pro Gly Ser Glu	
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Gln Leu Ser Lys Leu Met Thr Ser Leu Pro Ser Trp Ala Leu Leu Thr	
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Asn His Phe Lys Ser Thr Gly Ser Phe Pro Leu Pro Leu Cys Ala Arg	
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Ala Leu Gly Ala Ser Pro Ser Glu Thr Ser Lys Leu Gln Gln Leu Val	
581 586 591 596	
gaa aag att gac cgg caa gga gct gtg gcg gtg acc tca gct gcc tca	2060
Glu Lys Ile Asp Arg Gln Gly Ala Val Ala Val Thr Ser Ala Ala Ser	
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Gly Ala Pro Thr Thr Ser Ala Pro Ala Pro Ser Ser Ser Ala Ser Ser	
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Gly Pro Asn Gln Cys Val Ile Cys Leu Arg Val Leu Ser Cys Pro Arg	
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Cys Lys Val Cys Gly Arg Ala Phe Ser Thr Arg Gly Asn Leu Arg Ala	
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His Phe Val Gly His Lys Ala Ser Pro Ala Ala Arg Ala Gln Asn Ser	
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Cys Pro Ile Cys Gln Lys Lys Phe Thr Asn Ala Val Thr Leu Gln Gln	
693 698 703 708	
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His Val Arg Met His Leu Gly Gly Gln Ile Pro Asn Gly Gly Thr Ala	
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Leu Pro Glu Gly Gly Gly Ala Ala Gln Glu Asn Gly Ser Glu Gln Ser	
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757 762 767 772	
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Glu Glu Glu Asp Val Thr Asp Glu Asp Ser Leu Ala Gly Arg Gly Ser	
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Glu Ser Gly Gly Glu Lys Ala Ile Ser Val Arg Gly Asp Ser Glu Glu	
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Ser Leu Val Pro Gly	Cys Ser Pro Ser Ile	Thr Ser Thr Gly Leu Ser		
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Pro Phe Pro Arg Lys	Asp Asp Pro Thr Ile	Pro *		
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Met Ala Asn Leu Glu Glu Ser Phe Pro Arg Gly Gly Thr Arg Lys Ile
15 20 25 30

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Asp	Gly	Thr	Arg	Ala	Phe	Leu	Pro	Leu	Leu	Lys	Ala	Gln	Glu	Tyr	Ile		
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Arg	Gln	Lys	Asn	Lys	Gly	Ala	Lys	Leu	Lys	Val	Gly	Gln	Tyr	Leu	Asn		
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tgc	att	gtt	gaa	aag	gtg	aaa	ggc	aac	gga	gga	gtt	gtt	agt	ctg	tct	815	
Cys	Ile	Val	Glu	Lys	Val	Lys	Gly	Asn	Gly	Gly	Val	Val	Ser	Leu	Ser		
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Val	Gly	His	Ser	Glu	Val	Ser	Thr	Ala	Ile	Ala	Thr	Glu	Gln	Gln	Ser		
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Trp	Asn	Leu	Asn	Asn	Leu	Leu	Pro	Gly	Leu	Val	Val	Lys	Ala	Gln	Val		
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Gln	Lys	Val	Thr	Pro	Phe	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Thr	Phe	Phe		
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319					324					329					334		
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Arg Thr Arg Val Val	His Leu Ser Leu Arg	Pro Ile Phe Leu Gln Pro		
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gga cgc cca ctc acc	cga ctc tct tgc cag	aac ctt gga gca gtg ctg		1151
Gly Arg Pro Leu Thr	Arg Leu Ser Cys Gln	Asn Leu Gly Ala Val Leu		
367	372	377	382	
gat gat gtt cct gtc	cag ggt ttt ttc aaa	aag gct ggg gcc acc ttt		1199
Asp Asp Val Pro Val	Gln Gly Phe Phe Lys	Lys Ala Gly Ala Thr Phe		
383	388	393	398	
agg ctg aag gat ggg	gtt ctg gcc tat gcc	cgg ctc agc cat ctc tct		1247
Arg Leu Lys Asp Gly	Val Leu Ala Tyr Ala	Arg Leu Ser His Leu Ser		
399	404	409	414	
gat tct aag aac gtc	ttc aat cct gag gcc	ttc aag cca ggg aac act		1295
Asp Ser Lys Asn Val	Phe Asn Pro Glu Ala	Phe Lys Pro Gly Asn Thr		
415	420	425	430	
cac aag tgt aga att	att gac tac agc caa	atg gat gaa ctg gcc ttg		1343
His Lys Cys Arg Ile	Ile Asp Tyr Ser Gln	Met Asp Glu Leu Ala Leu		
431	436	441	446	
ctc tct cta cga acg	tct att att gaa gct	cag tac ctt aga tat cat		1391
Leu Ser Leu Arg Thr	Ser Ile Ile Glu Ala	Gln Tyr Leu Arg Tyr His		
447	452	457	462	
gac atc gaa cct ggg	gca gtg gta aag ggc	aca gtg cta acc ata aag		1439
Asp Ile Glu Pro Gly	Ala Val Val Lys Gly	Thr Val Leu Thr Ile Lys		
463	468	473	478	
tca tat ggg atg ctg	gtg aag gtg ggc gag	cag atg agg ggc ctg gta		1487
Ser Tyr Gly Met Leu	Val Lys Val Gly Glu	Gln Met Arg Gly Leu Val		
479	484	489	494	
cct ccc atg cac ctg	gct gac atc ctg atg	aag aat ccg gag aag aag		1535
Pro Pro Met His Leu	Ala Asp Ile Leu Met	Lys Asn Pro Glu Lys Lys		
495	500	505	510	
tac cac atc ggg gat	gag gtc aag tgc cgg	gtt ttg ctt tgt gac cct		1583
Tyr His Ile Gly Asp	Glu Val Lys Cys Arg	Val Leu Leu Cys Asp Pro		
511	516	521	526	
gaa gcc aag aag ctg	atg atg acc ctg aaa	aaa acc ctg att gag tcc		1631
Glu Ala Lys Lys Leu	Met Met Thr Leu Lys	Lys Thr Leu Ile Glu Ser		
527	532	537	542	
aaa cta cct gtc att	acc tgc tat gcc gat	gcc aag cct ggt ctg cag		1679
Lys Leu Pro Val Ile	Thr Cys Tyr Ala Asp	Ala Lys Pro Gly Leu Gln		
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aca cat ggc ttc atc	atc agg gtc aag gac	tat ggc tgc att gtg aag		1727
Thr His Gly Phe Ile	Ile Arg Val Lys Asp	Tyr Gly Cys Ile Val Lys		
559	564	569	574	

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Phe Tyr Asn Asn Val Gln Gly Leu Val Pro Lys His Glu Leu Ser Thr	
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Glu Tyr Ile Pro Asp Pro Glu Arg Val Phe Tyr Thr Gly Gln Val Val	
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His Ser Gln Lys Lys Gly Lys Ala Ile Asn Ile Gly Gln Leu Val Asp	
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Val Lys Val Leu Glu Lys Thr Lys Asp Gly Leu Glu Val Ala Val Leu	
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Pro His Asn Ile Arg Ala Phe Leu Pro Thr Ser His Leu Ser Asp His	
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Cys Arg Lys Pro Ala Leu Val Ser Thr Val Glu Gly Gly Gln Asp Pro	
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Arg Pro Asp His Lys Leu Gly Ala Lys Thr Gln His Arg Leu Leu Val	
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Val Pro Glu Asn Glu Asn Arg Met Glu Asp Arg Leu Ala Glu Thr Ser	
326 331 336 341	
agg gcc aaa gac cat cac atc tcc gga gct gag gtg ggg aaa gca agc	2191
Arg Ala Lys Asp His His Ile Ser Gly Ala Glu Val Gly Lys Ala Ser	
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acc tag catgacaatg gccccgttgt gtgtggtggg ggtcgggggtt ggggggcatg	2247
Thr *	
358	
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cctgtgagga gcccgaagcc aacaaggcca cactggtgtg tctcatgaat aactttatcc 420
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Met Val Thr Trp Lys Ala Asp Gly Thr Leu Ile Thr Gln
1 5 10

agc gtg gag aag acc acg ccc tcc aaa cag agc aac aac aag tac gtg	517
Ser Val Glu Lys Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Val	
14 19 24 29	
gcc agc agc tac ctg agc ctg acg ccc gag cag tgg agg tcc cgc aga	565
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Arg Ser Arg Arg	
30 35 40 45	
agc tac agc tgc cag gtt atg caa gaa ggg agc acc gtg gag aag tca	613
Ser Tyr Ser Cys Gln Val Met Gln Glu Gly Ser Thr Val Glu Lys Ser	
46 51 56 61	
gtg gcc cct gca gaa tgt tca tag gttccagccc ccacccacac ccacaggggc	667
Val Ala Pro Ala Glu Cys Ser *	
62 67	
ctggagctgc aggatcccag gggaggcgtc tctctctgca tcccaagcca ttcagccctt	727
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gatccccacg tagtgctgtt aacatcagac aacgtaatca gaatttactc actacgtgag	660
ccgcagacac ccactaacgt gataatactt tcagaagccg aagaggaaag tctagtactc	720

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cacagccctg gaaatatttg gaaagctggt ggggtccattg ccc atg cat cct gcg 955
Met His Pro Ala
1
gct gaa gat aac tat ggt tat gat gcg tgt gct gta ctc tgc tta ccc 1003
Ala Glu Asp Asn Tyr Gly Tyr Asp Ala Cys Ala Val Leu Cys Leu Pro
5 10 15 20
tgt gtc ccc aat atc tta gtg atc gct act gaa tca gga atg ctg tat 1051
Cys Val Pro Asn Ile Leu Val Ile Ala Thr Glu Ser Gly Met Leu Tyr
21 26 31 36
cac tgt gtc gtg cta gaa ggg gaa gaa gaa gat gac cac acg tca gaa 1099
His Cys Val Val Leu Glu Gly Glu Glu Glu Asp Asp His Thr Ser Glu
37 42 47 52
aag tcc tgg gat tcc agg att gac ctc att cct tct ctg tat gtg ttt 1147
Lys Ser Trp Asp Ser Arg Ile Asp Leu Ile Pro Ser Leu Tyr Val Phe
53 58 63 68
gaa tgt gtt gag ttg gag ctt gct ttg aaa ctg gca tct gga gag gat 1195
Glu Cys Val Glu Leu Glu Leu Ala Leu Lys Leu Ala Ser Gly Glu Asp
69 74 79 84
gac cct ttt gat tct gac ttt tct tgt cca gtc aaa ctt cat aga gat 1243
Asp Pro Phe Asp Ser Asp Phe Ser Cys Pro Val Lys Leu His Arg Asp
85 90 95 100
ccc aag tgt cct tca aga tat cac tgt act cat gaa gct ggt gta cat 1291
Pro Lys Cys Pro Ser Arg Tyr His Cys Thr His Glu Ala Gly Val His
101 106 111 116
agt gtt ggg cta act tgg att cat aaa ctt cac aaa ttt ctt gga tca 1339
Ser Val Gly Leu Thr Trp Ile His Lys Leu His Lys Phe Leu Gly Ser
117 122 127 132
gat gaa gaa gat aag gat agt tta cag gaa ctc tct aca gaa cag aaa 1387
Asp Glu Glu Asp Lys Asp Ser Leu Gln Glu Leu Ser Thr Glu Gln Lys
133 138 143 148
tgc ttt gtt gaa cac atc ctt tgt acg agg cca ttg ccc tgc agg cag 1435
Cys Phe Val Glu His Ile Leu Cys Thr Arg Pro Leu Pro Cys Arg Gln
149 154 159 164
cca gct cca att cga gga ttt tgg att gta cct gac att ctg gga ccc 1483
Pro Ala Pro Ile Arg Gly Phe Trp Ile Val Pro Asp Ile Leu Gly Pro
165 170 175 180
acg atg atc tgc atc acc agt acc tat gaa tgc ctc ata tgg ccg tta 1531
Thr Met Ile Cys Ile Thr Ser Thr Tyr Glu Cys Leu Ile Trp Pro Leu

181		186		191		196	
tta agt aca gtc cat cca gcg tct cct ccc ctg ctt tgt act cga gaa	1579						
Leu Ser Thr Val His Pro Ala Ser Pro Pro Leu Leu Cys Thr Arg Glu							
197		202		207		212	
gat gtt gaa gtg gca gag tct ccc ctc cgt gtt ctg gct gaa acc cca	1627						
Asp Val Glu Val Ala Glu Ser Pro Leu Arg Val Leu Ala Glu Thr Pro							
213		218		223		228	
gat tcc ttt gaa aag cat att aga agc att ttg caa cgt agt gtt gcc	1675						
Asp Ser Phe Glu Lys His Ile Arg Ser Ile Leu Gln Arg Ser Val Ala							
229		234		239		244	
aat cca gca ttt ttg aaa gct tct gaa aag gac ata gcc cct cct cct	1723						
Asn Pro Ala Phe Leu Lys Ala Ser Glu Lys Asp Ile Ala Pro Pro Pro							
245		250		255		260	
gaa gaa tgc ctt cag ctc ctc agc aga gcc acc cag gtg ttc aga gag	1771						
Glu Glu Cys Leu Gln Leu Leu Ser Arg Ala Thr Gln Val Phe Arg Glu							
261		266		271		276	
cag tac att ctc aaa cag gac ttg gca aag gag gag att cag cgg agg	1819						
Gln Tyr Ile Leu Lys Gln Asp Leu Ala Lys Glu Glu Ile Gln Arg Arg							
277		282		287		292	
gtc aaa tta tta tgt gac caa aaa aag aaa caa cta gaa gat ctc agt	1867						
Val Lys Leu Leu Cys Asp Gln Lys Lys Lys Gln Leu Glu Asp Leu Ser							
293		298		303		308	
tat tgt cga gaa gag agg aaa agt ctg cgg gaa atg gct gag cgt tta	1915						
Tyr Cys Arg Glu Glu Arg Lys Ser Leu Arg Glu Met Ala Glu Arg Leu							
309		314		319		324	
gct gac aaa tat gag gaa gct aaa gaa aaa caa gag gat atc atg aac	1963						
Ala Asp Lys Tyr Glu Glu Ala Lys Glu Lys Gln Glu Asp Ile Met Asn							
325		330		335		340	
agg atg aaa aaa cta ctt cac agt ttt cac tct gag ctc cca gtt ctc	2011						
Arg Met Lys Lys Leu Leu His Ser Phe His Ser Glu Leu Pro Val Leu							
341		346		351		356	
tct gat agt gag cga gac atg aag aaa gaa tta cag ctg ata cct gat	2059						
Ser Asp Ser Glu Arg Asp Met Lys Lys Glu Leu Gln Leu Ile Pro Asp							
357		362		367		372	
caa ctt cga cat ttg ggc aat gcc atc aaa cag gtt act atg aaa aag	2107						
Gln Leu Arg His Leu Gly Asn Ala Ile Lys Gln Val Thr Met Lys Lys							
373		378		383		388	
gat tat caa cag caa aag atg gag aag gtg ttg agt ctt cca aaa ccc	2155						
Asp Tyr Gln Gln Gln Lys Met Glu Lys Val Leu Ser Leu Pro Lys Pro							
389		394		399		404	
acc att att ctc agt gcc tac cag cga aag tgc att cag tcc atc ctg	2203						
Thr Ile Ile Leu Ser Ala Tyr Gln Arg Lys Cys Ile Gln Ser Ile Leu							
405		410		415		420	

tta agc cca aca caa cat cat gta gca ctt ata gga ata aaa gga ctt	441
Leu Ser Pro Thr Gln His His Val Ala Leu Ile Gly Ile Lys Gly Leu	
116 121 126 131	
atg gta tta gaa tta cct aaa aga tgg ggg aag aat tct gaa ttt gaa	489
Met Val Leu Glu Leu Pro Lys Arg Trp Gly Lys Asn Ser Glu Phe Glu	
132 137 142 147	
ggg gga aaa tca aca gtg aat tgt agt acc act cca gtt gcg gag aga	537
Gly Gly Lys Ser Thr Val Asn Cys Ser Thr Thr Pro Val Ala Glu Arg	
148 153 158 163	
ttt ttc acc agt tcc acc tct ctg act cta aag cat gct gca tgg tat	585
Phe Phe Thr Ser Ser Thr Ser Leu Thr Leu Lys His Ala Ala Trp Tyr	
164 169 174 179	
cca agt gaa atc ctg gat ccc cac gta gtg ctg tta aca tca gac aac	633
Pro Ser Glu Ile Leu Asp Pro His Val Val Leu Leu Thr Ser Asp Asn	
180 185 190 195	
gta atc aga att tac tca cta cgt gag ccg cag aca ccc act aac gtg	681
Val Ile Arg Ile Tyr Ser Leu Arg Glu Pro Gln Thr Pro Thr Asn Val	
196 201 206 211	
ata ata ctt tca gaa gcc gaa gag gaa agt cta gta ctc aat aaa gga	729
Ile Ile Leu Ser Glu Ala Glu Glu Glu Ser Leu Val Leu Asn Lys Gly	
212 217 222 227	
agg gcg tat acc gca tct cta gga gag aca gca gtt gca ttt gac ttt	777
Arg Ala Tyr Thr Ala Ser Leu Gly Glu Thr Ala Val Ala Phe Asp Phe	
228 233 238 243	
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Gly Pro Leu Ala Ala Val Pro Lys Thr Leu Phe Gly Gln Asn Gly Lys	
244 249 254 259	
gat gaa gta gtg gca tac cca ctg tac atc tta tat gaa aat gga gag	873
Asp Glu Val Val Ala Tyr Pro Leu Tyr Ile Leu Tyr Glu Asn Gly Glu	
260 265 270 275	
act ttc ctg aca tac atc agt ctg tta cac agc cct gga aat att tgg	921
Thr Phe Leu Thr Tyr Ile Ser Leu Leu His Ser Pro Gly Asn Ile Trp	
276 281 286 291	
aaa gct gtt ggg tcc att gcc cat gca tcc tgc ggc tga agataactat	970
Lys Ala Val Gly Ser Ile Ala His Ala Ser Cys Gly *	
292 297 302	
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actgaatcag gaatgctgta tcaactgtgtc gtgctagaag gggaagaaga agatgaccac	1090
acgtcagaaa agtcctggga ttccaggatt gacctcattc cttctctgta tgtgtttgaa	1150
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<211> 4453

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<213> Homo sapiens

<220>

<221> CDS

<222> (173)..(1909)

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cta agg agg ttg gac aaa atc agg ttc aga ggt cac aag aga gat gac Leu Arg Arg Leu Asp Lys Ile Arg Phe Arg Gly His Lys Arg Asp Asp 2 7 12 17		223
ttc ctc gat cta gcg gag tct cca aat gcc tcg gac acc gaa tgc agc Phe Leu Asp Leu Ala Glu Ser Pro Asn Ala Ser Asp Thr Glu Cys Ser 18 23 28 33		271
gac gaa atc ccc ctg aag gta ccg cgg acc tcg ccc cgg gac agc gag Asp Glu Ile Pro Leu Lys Val Pro Arg Thr Ser Pro Arg Asp Ser Glu 34 39 44 49		319
gag ctg agg gac cct gct ggt cca ggg acc ctc atc atg gcc aca gga Glu Leu Arg Asp Pro Ala Gly Pro Gly Thr Leu Ile Met Ala Thr Gly 50 55 60 65		367
gtc cag gac ttt aac cgg aca gag ttt gat cga ctg aat gag atc aaa Val Gln Asp Phe Asn Arg Thr Glu Phe Asp Arg Leu Asn Glu Ile Lys 66 71 76 81		415
ggc cac ctg gaa att gcc tta ttg gaa aaa cat ttc tta cag gag gag Gly His Leu Glu Ile Ala Leu Leu Glu Lys His Phe Leu Gln Glu Glu 82 87 92 97		463
ctc cgg aag ctg cga gaa gaa acc aac gcg gag atg ctg cgg cag gag Leu Arg Lys Leu Arg Glu Glu Thr Asn Ala Glu Met Leu Arg Gln Glu 98 103 108 113		511
ctg gac cgc gag cgg cag cgg cgg atg gag ctg gag cag aag gtg cag Leu Asp Arg Glu Arg Gln Arg Arg Met Glu Leu Glu Gln Lys Val Gln 114 119 124 129		559
gag gtg ctg aag gcc aga acc gag gag cag atg gct cag cag ccc cca Glu Val Leu Lys Ala Arg Thr Glu Glu Gln Met Ala Gln Gln Pro Pro 130 135 140 145		607
aaa ggg cag gcc cag gcc agc aat gga gca gag cgc cgg agc cag ggg Lys Gly Gln Ala Gln Ala Ser Asn Gly Ala Glu Arg Arg Ser Gln Gly 146 151 156 161		655
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gtg gag gac ttc cgg ttc cag ccc gag gag aac act gtg gag aca gag Val Glu Asp Phe Arg Phe Gln Pro Glu Glu Asn Thr Val Glu Thr Glu 178 183 188 193		751
gaa ccc ctg agc gcc cgc agg tta act gaa aat atg aga cgg ctc aag Glu Pro Leu Ser Ala Arg Arg Leu Thr Glu Asn Met Arg Arg Leu Lys 194 199 204 209		799
cgc ggt gcc aag ccg gtc act aac ttt gtg aag aac ctc tct gcc tta		847

Arg Gly Ala Lys Pro Val Thr Asn Phe Val Lys Asn Leu Ser Ala Leu	
210 215 220 225	
tcc gac tgg tac tcc gtc tac acg tct gcc att gcc ttc acc gtg tac	895
Ser Asp Trp Tyr Ser Val Tyr Thr Ser Ala Ile Ala Phe Thr Val Tyr	
226 231 236 241	
atg aat gcc gtg tgg cat ggc tgg gcc atc cca ttg ttc tta ttt cta	943
Met Asn Ala Val Trp His Gly Trp Ala Ile Pro Leu Phe Leu Phe Leu	
242 247 252 257	
gca att ctg agg tta tcc ctc aat tac ctc atc gcc agg ggg tgg cgg	991
Ala Ile Leu Arg Leu Ser Leu Asn Tyr Leu Ile Ala Arg Gly Trp Arg	
258 263 268 273	
ata cag tgg agc atc gtg ccc gaa gtg tct gag ccc gtg gaa cct cca	1039
Ile Gln Trp Ser Ile Val Pro Glu Val Ser Glu Pro Val Glu Pro Pro	
274 279 284 289	
aag gaa gac ctg act gtg tct gag aag ttc cag ctg gtg ctg gac gtc	1087
Lys Glu Asp Leu Thr Val Ser Glu Lys Phe Gln Leu Val Leu Asp Val	
290 295 300 305	
gcc cag aaa gcc cag aac ctt ttc ggg aag atg gct gac atc ctg gag	1135
Ala Gln Lys Ala Gln Asn Leu Phe Gly Lys Met Ala Asp Ile Leu Glu	
306 311 316 321	
aag atc aag aac ttg ttc atg tgg gtc cag ccg gag atc aca cag aag	1183
Lys Ile Lys Asn Leu Phe Met Trp Val Gln Pro Glu Ile Thr Gln Lys	
322 327 332 337	
ctg tat gtg gcg ctc tgg gct gcc ttc ctg gcc tcc tgc ttc ttc ccc	1231
Leu Tyr Val Ala Leu Trp Ala Ala Phe Leu Ala Ser Cys Phe Phe Pro	
338 343 348 353	
tac cgc ctg gtg ggg ctt gcc gtg gga ctc tat gct ggt atc aag ttc	1279
Tyr Arg Leu Val Gly Leu Ala Val Gly Leu Tyr Ala Gly Ile Lys Phe	
354 359 364 369	
ttc ctc att gat ttc atc ttt aaa cgc tgc ccg agg ctg cgc gcc aag	1327
Phe Leu Ile Asp Phe Ile Phe Lys Arg Cys Pro Arg Leu Arg Ala Lys	
370 375 380 385	
tac gac acg ccc tat atc atc tgg agg agt ctc ccc acc gac ccg cag	1375
Tyr Asp Thr Pro Tyr Ile Ile Trp Arg Ser Leu Pro Thr Asp Pro Gln	
386 391 396 401	
ctc aag gag cgc tcc agc gcc gca gtc tca cgc agg ctg cag acg acc	1423
Leu Lys Glu Arg Ser Ser Ala Ala Val Ser Arg Arg Leu Gln Thr Thr	
402 407 412 417	
tcg tca cgg agc tac gta ccc agc gca ccg gcc ggc ctg ggt aaa gag	1471
Ser Ser Arg Ser Tyr Val Pro Ser Ala Pro Ala Gly Leu Gly Lys Glu	
418 423 428 433	
gag gac gcc ggt cgc ttc cac agc acc aag aag ggc aat ttc cac gag	1519
Glu Asp Ala Gly Arg Phe His Ser Thr Lys Lys Gly Asn Phe His Glu	

434	439	444	449	
atc ttc aat ctg aca gaa aac gag cgt ccg ctg gcg gtg tgc gag aat				1567
Ile Phe Asn Leu Thr Glu Asn Glu Arg Pro Leu Ala Val Cys Glu Asn				
450	455	460	465	
ggc tgg cgc tgc tgc ctc atc aac agg gac cgg aag atg ccc acg gac				1615
Gly Trp Arg Cys Cys Leu Ile Asn Arg Asp Arg Lys Met Pro Thr Asp				
466	471	476	481	
tac atc agg aac ggg gtg ctc tac gtc acg gag aat tac ttg tgc ttc				1663
Tyr Ile Arg Asn Gly Val Leu Tyr Val Thr Glu Asn Tyr Leu Cys Phe				
482	487	492	497	
gaa agc tcc aaa tct ggg tcc tca aag agg aac aaa gtc atc aag cta				1711
Glu Ser Ser Lys Ser Gly Ser Ser Lys Arg Asn Lys Val Ile Lys Leu				
498	503	508	513	
gtg gac atc acg gac atc cag aag tac aag gtc ctg tct gtc ctc cca				1759
Val Asp Ile Thr Asp Ile Gln Lys Tyr Lys Val Leu Ser Val Leu Pro				
514	519	524	529	
ggc tca ggc atg ggg att gcc gtg tcg acg cca tcc acc cag aaa ccg				1807
Gly Ser Gly Met Gly Ile Ala Val Ser Thr Pro Ser Thr Gln Lys Pro				
530	535	540	545	
ctc gtg ttt ggt gcc atg gtg cac agg gat gag gcc ttc gag acc att				1855
Leu Val Phe Gly Ala Met Val His Arg Asp Glu Ala Phe Glu Thr Ile				
546	551	556	561	
ctc agc cag tac atc aag atc acc tca gcg gca gcg tct ggc ggg gac				1903
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Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met Lys Pro
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Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr Gly Glu
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acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac caa aca gcc 319
Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln Thr Ala
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Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His Pro Leu
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gca act tcc cat caa caa tat ttt tat aaa att cca atc ctg gtc atc 511
Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu Val Ile
99 104 109 114

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Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu Leu Asn	
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Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp Ile Glu	
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His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile Val Gly	
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Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro Pro Thr	
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Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe Lys Ser	
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Glu Val Ile Gln Leu Ile Lys Thr Asn Lys Lys His Ile His Ser Arg
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Ser Thr Leu Glu Cys Ala Tyr Arg Thr His Leu Val Ala Gly Ile Gly
39 44 49 54

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Phe Tyr Gln His Leu Leu Leu Tyr Ile Gln Ser His Tyr Gln Leu Glu
55 60 65 70

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Leu Gln Cys Cys Ile Asp Trp Thr His Val Thr Asp Pro Leu Ile Gly
71 76 81 86

tgc aag aag cca gtg tct gcc tca ggg aag gag atg gat tgg gca cag 643
Cys Lys Lys Pro Val Ser Ala Ser Gly Lys Glu Met Asp Trp Ala Gln
87 92 97 102

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Gln	Asn	Glu	Leu	Ala	Gly	Val	Asp	Thr	Glu	Leu	Leu	Ala	Glu	Arg	Phe	
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Tyr	Tyr	Gln	Ala	Leu	Ser	Val	Ala	Pro	Gln	Ile	Gly	Met	Pro	Phe	Asn	
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Tyr	Cys	Tyr	Leu	Arg	Cys	Ile	Gln	Ser	Glu	Val	Ser	Phe	Glu	Gly	Ala	
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Tyr	Gly	Asn	Leu	Lys	Arg	Leu	Tyr	Asp	Lys	Ala	Ala	Lys	Met	Tyr	His	
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Gln	Leu	Lys	Lys	Cys	Glu	Thr	Arg	Lys	Leu	Ser	Pro	Gly	Lys	Lys	Arg	
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Cys	Lys	Asp	Ile	Lys	Arg	Leu	Leu	Val	Asn	Phe	Met	Tyr	Leu	Gln	Ser	
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Tyr	Ser	Ala	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Leu	Phe	Ser	His	Leu	Val	
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Asn	His	Val	Asn	Ile	Arg	Leu	Gln	Ala	Glu	Leu	Glu	Glu	Gly	Glu	Asn	

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Pro Val Pro Ala Phe Gln Ser Asp Gly Thr Asp Glu Pro Glu Ser Lys				
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Glu Pro Val Glu Lys Glu Glu Glu Pro Asp Pro Glu Pro Pro Pro Val				
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Thr Pro Gln Val Gly Glu Gly Arg Lys Ser Arg Lys Phe Ser Arg Leu				
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Ser Cys Leu Arg Arg Arg Arg His Pro Pro Lys Val Gly Asp Asp Ser				
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Ala Ser Glu Gly Ser Asp Ser Gly Ser Asp Lys Ser Leu Glu Gly Gly				
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Ser Arg Ser Asp Leu Glu Asp Met Glu Glu Glu Glu Gly Thr Arg Ser				
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Asn Gly Pro Leu Gly Pro Ser Glu Ala Ser Ile Ala Ser Asn Leu Gln				
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Ala Met Ser Thr Gln Met Phe Gln Thr Lys Arg Cys Phe Arg Leu Ala				
503	508	513	518	
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Pro Thr Phe Ser Asn Leu Leu Leu Gln Pro Thr Thr Asn Pro His Thr				
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tcg gcc agc cac agg cct tgc gtc aat ggg gat gta gac aag cct tca				1987
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 gacaata atg gtt ttt ggt acc aaa ttc cca gag agt aaa ata gtt ctg 229
 Met Val Phe Gly Thr Lys Phe Pro Glu Ser Lys Ile Val Leu
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 gcc tta aga act aaa cgg gaa ggc cct ggg gaa gtt agg att caa gtt 277

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Tyr	Ala	Leu	Arg	Ile	Gly	Glu	Asn	Glu	Asn	Thr	Asp	Arg	Glu	Arg	Asp		
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cca	act	ccc	acc	ccc	tgt	ccc	cag	gga	cac	cgg	atg	atg	acg	gag	cct	373	
Pro	Thr	Pro	Thr	Pro	Cys	Pro	Gln	Gly	His	Arg	Met	Met	Thr	Glu	Pro		
47					52					57					62		
agg	gag	agg	aga	ggg	tac	agt	gta	cca	cct	aga	cca	gag	gtc	cgg	acc	421	
Arg	Glu	Arg	Arg	Gly	Tyr	Ser	Val	Pro	Pro	Arg	Pro	Glu	Val	Arg	Thr		
63					68					73					78		
cag	gcc	acg	gag	tgg	aga	gta	gaa	gaa	tct	aac	ttc	aac	aag	atc	ttc	469	
Gln	Ala	Thr	Glu	Trp	Arg	Val	Glu	Glu	Ser	Asn	Phe	Asn	Lys	Ile	Phe		
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ctg	aaa	aaa	gac	gct	gag	ctt	gga	cgg	tcc	aac	cac	ctc	cct	acc	tgg	517	
Leu	Lys	Lys	Asp	Ala	Glu	Leu	Gly	Arg	Ser	Asn	His	Leu	Pro	Thr	Trp		
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gat	aag	ccg	gag	gat	gct	tct	tgg	ctt	ccc	caa	agc	tgt	ctt	ggg	ggg	565	
Asp	Lys	Pro	Glu	Asp	Ala	Ser	Trp	Leu	Pro	Gln	Ser	Cys	Leu	Gly	Gly		
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Asp	Ala	Val	Ala	Thr	Thr	Gly	Glu	Ile	His	Glu	Glu	Lys	Ala	Trp	Lys		
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Gly	Glu	Leu	Trp	Gly	Lys	Glu	His	Gly	Ala	Asp	Gln	Ala	Ile	Gln	Glu		
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Thr	Leu	Glu	Asp	Leu	Ser	Ser	Leu	Glu	Arg	Thr	Leu	Val	Val	Ser	Glu		
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Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	Ile	Gly	Lys		
207					212					217					222		
ctg	tcc	cag	gaa	ctg	ggc	cgg	gag	gag	agg	cgg	agg	caa	gct	ggg	gct	901	
Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	Gln	Ala	Gly	Ala		
223					228					233					238		
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ctg tgc cga cag tgg gat ccc tgc ctg gtt tcc ttt gat gtg ctt gcc				1045
Leu Cys Arg Gln Trp Asp Pro Cys Leu Val Ser Phe Asp Val Leu Ala				
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aca ggg gat ttg gct ctg atc cat gtg gag atc caa gtg ctg gac atc				1093
Thr Gly Asp Leu Ala Leu Ile His Val Glu Ile Gln Val Leu Asp Ile				
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aat gac cac cag cca cgg ttt ccc aaa ggc gag cag gag ctg gaa atc				1141
Asn Asp His Gln Pro Arg Phe Pro Lys Gly Glu Gln Glu Leu Glu Ile				
303	308	313	318	
tct gag agc gcc tct ctg cga acc cgg atc ccc ctg gac aga gct ctt				1189
Ser Glu Ser Ala Ser Leu Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu				
319	324	329	334	
gac cca gac aca ggc cct aac acc ctg cac acc tac act ctg tct ccc				1237
Asp Pro Asp Thr Gly Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro				
335	340	345	350	
agt gag cac ttt gcc ttg gat gtc att gtg ggc cct gat gag acc aaa				1285
Ser Glu His Phe Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys				
351	356	361	366	
cat gca gaa ctc ata gtg gtg aag gag ctg gac agg gaa atc cat tca				1333
His Ala Glu Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser				
367	372	377	382	
ttt ttt gat ctg gtg tta act gcc tat gac aat ggg aac ccc ccc aag				1381
Phe Phe Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys				
383	388	393	398	
tca ggt acc agc ttg gtc aag gtc aac gtc ttg gac tcc aat gac aat				1429
Ser Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn				
399	404	409	414	
agc cct gcg ttt gct gag agt tca ctg gca ctg gaa atc caa gaa gat				1477
Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu Asp				
415	420	425	430	
gct gca cct ggt acg ctt ctc ata aaa ctg acc gcc aca gac cct gac				1525
Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp Pro Asp				
431	436	441	446	
caa ggc ccc aat ggg gag gtg gag ttc ttc ctc agt aag cac atg cct				1573
Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys His Met Pro				
447	452	457	462	
cca gag gtg ctg gac acc ttc agt att gat gcc aag aca ggc cag gtc				1621
Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys Thr Gly Gln Val				
463	468	473	478	

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Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn Pro Ala Tyr Glu Val	
479 484 489 494	
gat gtt cag gca agg gac ctg ggt ccc aat cct atc cca gcc cat tgc	1717
Asp Val Gln Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys	
495 500 505 510	
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Lys Val Leu Ile Lys Val Leu Asp Val Asn Asp Asn Ile Pro Ser Ile	
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His Val Thr Trp Ala Ser Gln Pro Ser Leu Val Ser Glu Ala Leu Pro	
527 532 537 542	
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Lys Asp Ser Phe Ile Ala Leu Val Met Ala Asp Asp Leu Asp Ser Gly	
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His Asn Gly Leu Val His Cys Trp Leu Ser Gln Glu Leu Gly His Phe	
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Arg Leu Lys Arg Thr Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala	
575 580 585 590	
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Thr Leu Asp Arg Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala	
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Gln Asp Gln Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile	
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Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val Ser	
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Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile Asp Ser	
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Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr Glu Glu Met	
687 692 697 702	

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ctc tcc gtg ctt gtg aat gcc tcc aca ggc cac ctg ctg gtg ccc atc Leu Ser Val Leu Val Asn Ala Ser Thr Gly His Leu Leu Val Pro Ile 751 756 761 766	2485
gag act ccc aat ggc ttg ggc cca gcg ggc act gac aca cct cca ctg Glu Thr Pro Asn Gly Leu Gly Pro Ala Gly Thr Asp Thr Pro Pro Leu 767 772 777 782	2533
gcc act cac agc tcc cgg cca ttc ctt ttg aca acc att gtg gca aga Ala Thr His Ser Ser Arg Pro Phe Leu Leu Thr Thr Ile Val Ala Arg 783 788 793 798	2581
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Gln	Arg	His	Leu	Asn	Gly	Lys	Val	Ser	Pro	Glu	Lys	Glu	Ser	Gly	Pro	
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Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp Pro Glu Glu Asp				
1183	1188	1193	1198	
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Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu Ser Ser Leu Leu Asp				
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Trp Met Ala Arg Leu Ser Leu Pro Leu Thr Thr Asn Tyr Arg Asp Asn				
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Val Ile Ser Pro Asp Ala Ala Ala Thr Glu Glu Pro Arg Thr Phe Gln				
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Thr Phe Gly Lys Ala Glu Ala Pro Glu Leu Ser Pro Thr Gly Thr Arg				
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Leu Ala Ser Thr Phe Val Ser Glu Met Ser Ser Leu Leu Glu Met Leu				
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Ser Ala Ala Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr				
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 Arg Lys Leu Arg Leu Ala Gly Asp Gln Arg Asn Ala Ser Tyr Pro His
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 Cys Leu Gln Phe Tyr Leu Gln Pro Pro Ser Glu Asn Ile Ser Leu Thr
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 Glu Phe Glu Asn Leu Ala Ile Asp Arg Val Lys Leu Leu Lys Ser Val
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 57 62 67 72
 aag ttg gag agt gag ctt cgg aag ctc aag ttt tcc tac aga gag aag 351
 Lys Leu Glu Ser Glu Leu Arg Lys Leu Lys Phe Ser Tyr Arg Glu Lys
 73 78 83 88
 cta gaa gat gaa tat gaa cca cga aga aga gat cat att tct cat ttt 399
 Leu Glu Asp Glu Tyr Glu Pro Arg Arg Arg Asp His Ile Ser His Phe
 89 94 99 104
 att ttg cgg ctt gct tat tgc cag tct gaa gaa ctt aga cgc tgg ttc 447
 Ile Leu Arg Leu Ala Tyr Cys Gln Ser Glu Glu Leu Arg Arg Trp Phe
 105 110 115 120
 att caa caa gaa atg gat ctc ctt cga ttt aga ttt agt att tta ccc 495
 Ile Gln Gln Glu Met Asp Leu Leu Arg Phe Arg Phe Ser Ile Leu Pro
 121 126 131 136
 aag gat aaa att cag gat ttc tta aag gat agc caa ttg cag ttt gag 543
 Lys Asp Lys Ile Gln Asp Phe Leu Lys Asp Ser Gln Leu Gln Phe Glu
 137 142 147 152
 gct ata agt gat gaa gag aag act ctt cga gaa cag gag att gtt gcc 591
 Ala Ile Ser Asp Glu Glu Lys Thr Leu Arg Glu Gln Glu Ile Val Ala
 153 158 163 168

tca tca cca agt tta agt gga ctt aag ttg ggg ttc gag tcc att tat	639
Ser Ser Pro Ser Leu Ser Gly Leu Lys Leu Gly Phe Glu Ser Ile Tyr	
169 174 179 184	
aag atc cct ttt gct gat gct ctg gat ttg ttt cga gga agg aaa gtc	687
Lys Ile Pro Phe Ala Asp Ala Leu Asp Leu Phe Arg Gly Arg Lys Val	
185 190 195 200	
tat ttg gaa gat ggc ttt gct tac gta cca ctt aag gac att gtg gca	735
Tyr Leu Glu Asp Gly Phe Ala Tyr Val Pro Leu Lys Asp Ile Val Ala	
201 206 211 216	
atc atc ctg aat gaa ttt aga gcc aaa ctg tcc aag gct ttg gca tta	783
Ile Ile Leu Asn Glu Phe Arg Ala Lys Leu Ser Lys Ala Leu Ala Leu	
217 222 227 232	
aca gcc agg tcc ttg cct gct gtg cag tct gat gaa aga ctt cag cct	831
Thr Ala Arg Ser Leu Pro Ala Val Gln Ser Asp Glu Arg Leu Gln Pro	
233 238 243 248	
ctg ctc aat cac ctc agt cat tcc tac act ggc caa gat tac agt acc	879
Leu Leu Asn His Leu Ser His Ser Tyr Thr Gly Gln Asp Tyr Ser Thr	
249 254 259 264	
cag gga aat gtt ggg aag att tct tta gat cag att gat ttg ctt tct	927
Gln Gly Asn Val Gly Lys Ile Ser Leu Asp Gln Ile Asp Leu Leu Ser	
265 270 275 280	
acc aaa tcc ttc cca cct tgc atg cgt cag tta cat aaa gcc ttg cgg	975
Thr Lys Ser Phe Pro Pro Cys Met Arg Gln Leu His Lys Ala Leu Arg	
281 286 291 296	
gaa aat cac cat ctt cgt cat gga ggc cga atg cag tat ggc cta ttt	1023
Glu Asn His His Leu Arg His Gly Gly Arg Met Gln Tyr Gly Leu Phe	
297 302 307 312	
ctg aag ggc att ggt tta act ttg gaa cag gca ttg cag ttc tgg aag	1071
Leu Lys Gly Ile Gly Leu Thr Leu Glu Gln Ala Leu Gln Phe Trp Lys	
313 318 323 328	
caa gaa ttt atc aaa gga aag atg ggt tcc aga caa gtt tga taaaggt	1120
Gln Glu Phe Ile Lys Gly Lys Met Gly Ser Arg Gln Val *	
329 334 339	
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cctggaggga taagccagat tttggattta gtaaagggga cacattacca ggtagcctgt	1360
caaaaataact ttgagatgat acacaatgtg gatgattgtg gcttttcttt tgagtcatcc	1420
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acctatccaa ccagaaactc ctcaacccaa accaagtgtc cagaaaacca aggatgcac	1540

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 tgagtgatgt catttaagtc ctatttttagg agataaaaac agctttgggg actgggttaa 2200
 gtccccaga aactacaata aagaacaact tttgttttaa ctcttaatca ctttgtaatt 2260
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 aagggtgacg cgagctctgc cctttaaccg gaaacgtctc cctgctcacc ccacccccgc 180
 gcagacgcag tgctgagcac acagctaccg gacaaagagt gacgcccgga gctggagtt 239
 atg gcg gct acg gag ccg atc ttg gcg gcc act ggg agt ccc gcg gcg 287
 Met Ala Ala Thr Glu Pro Ile Leu Ala Ala Thr Gly Ser Pro Ala Ala
 1 5 10 15

gtg cac cgg aga aac tgg aag gag ccg gtt cga gct cag ccc ctg agc	335
Val His Arg Arg Asn Trp Lys Glu Pro Val Arg Ala Gln Pro Leu Ser	
17 22 27 32	
gta act gtg tgg gct cct cgc tgc cag agg cct cac cgc ctg ccc ctg	383
Val Thr Val Trp Ala Pro Arg Cys Gln Arg Pro His Arg Leu Pro Leu	
33 38 43 48	
agc ctt cca gtc cca acg ccg cgg tcc ctg aag cca tcc cta cgc ccc	431
Ser Leu Pro Val Pro Thr Pro Arg Ser Leu Lys Pro Ser Leu Arg Pro	
49 54 59 64	
gag ctg cgg cct ccg cgg ccc tgg agc tgc ctc tcg ggc ccg cac ccg	479
Glu Leu Arg Pro Pro Arg Pro Trp Ser Cys Leu Ser Gly Pro His Pro	
65 70 75 80	
tga gcgt agcgccctcag gccgaagctg aagcgcgctc cacaccaggc cccgccggct	536
*	
81	
ctagactcgg tcccgagacg ttccgccagc gtttccggca gttccgctac caggatgcgg	596
cggttccccg ggaggctttc cggcagctgc gggagctgtc ccgccagtgg ctgcggcctg	656
acatccgcac caaggagcag atcgtggaga tgctgggtgca agagcagctg ctgccatcc	716
tgcccgaggc ggctcggggc cggcggatcc gccgccgcac ggatgtgcgc atcactggct	776
gagcgggtgga gctgcggggc gccagggccg ggcgctctgt gcggactggg gccatgatcg	836
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aaaaaaaaaa aa	908

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gcgggtctcg gtcgcggggc ccgtttgcag agcccccggc gccgggagga ctttgttctt	180
cttcagaaga gaaaactgaa gaaggagga atg gct gtg ggg ctt tgt aaa gcc	233
Met Ala Val Gly Leu Cys Lys Ala	
1 5	

atg tcc cag ggg ttg gtg acc ttc aga gat gtg gcg cta gac ttt tcc	281
Met Ser Gln Gly Leu Val Thr Phe Arg Asp Val Ala Leu Asp Phe Ser	
9 14 19 24	
caa gaa gag tgg gaa tgg ctg aag cca tct cag aag gat tta tac aga	329
Gln Glu Glu Trp Glu Trp Leu Lys Pro Ser Gln Lys Asp Leu Tyr Arg	
25 30 35 40	
gat gtc atg ttg gag aac tac agg aac ttg gta tgg ctt gga ctc tcc	377
Asp Val Met Leu Glu Asn Tyr Arg Asn Leu Val Trp Leu Gly Leu Ser	
41 46 51 56	
att tct aag ccc aac atg atc tcc tta ctg gag caa ggg aag gaa ccg	425
Ile Ser Lys Pro Asn Met Ile Ser Leu Leu Glu Gln Gly Lys Glu Pro	
57 62 67 72	
tgg atg gtg gag aga aag atg tca cag ggt cac tgt gca gac tgg gag	473
Trp Met Val Glu Arg Lys Met Ser Gln Gly His Cys Ala Asp Trp Glu	
73 78 83 88	
tct tgg tgt gaa att gag gaa tta tct cca aaa tgg ttc att gat gaa	521
Ser Trp Cys Glu Ile Glu Glu Leu Ser Pro Lys Trp Phe Ile Asp Glu	
89 94 99 104	
gat gaa ata tcc cag gag atg gta atg gaa agg cta gca agt cat ggc	569
Asp Glu Ile Ser Gln Glu Met Val Met Glu Arg Leu Ala Ser His Gly	
105 110 115 120	
ctt gaa tgc tcc agt ttc aga gaa gcc tgg aaa tat aag ggt gaa ttt	617
Leu Glu Cys Ser Ser Phe Arg Glu Ala Trp Lys Tyr Lys Gly Glu Phe	
121 126 131 136	
gag cta cat cag gga aat gcg gag agg cat ttc atg caa gtg aca gct	665
Glu Leu His Gln Gly Asn Ala Glu Arg His Phe Met Gln Val Thr Ala	
137 142 147 152	
gtt aag gaa atc tct act ggg aaa aga gac aat gaa ttt agt aat tct	713
Val Lys Glu Ile Ser Thr Gly Lys Arg Asp Asn Glu Phe Ser Asn Ser	
153 158 163 168	
ggg aga agc ata ccc ctg aaa tca gta ttt tta aca caa cag aaa gtt	761
Gly Arg Ser Ile Pro Leu Lys Ser Val Phe Leu Thr Gln Gln Lys Val	
169 174 179 184	
cct acc ata cag caa gta cat aaa ttt gat att tat gat aaa ctc ttc	809
Pro Thr Ile Gln Gln Val His Lys Phe Asp Ile Tyr Asp Lys Leu Phe	
185 190 195 200	
ccc caa aat tca gtc ata att gaa tat aaa aga ctc cat gct gag aag	857
Pro Gln Asn Ser Val Ile Ile Glu Tyr Lys Arg Leu His Ala Glu Lys	
201 206 211 216	
gaa tct ttg ata ggt aat gaa tgt gaa gaa ttc aac cag agt acg tac	905
Glu Ser Leu Ile Gly Asn Glu Cys Glu Glu Phe Asn Gln Ser Thr Tyr	
217 222 227 232	

ctt agt aaa gat ata gga att cct cct ggg gag aaa cct tat gaa agt	953
Leu Ser Lys Asp Ile Gly Ile Pro Pro Gly Glu Lys Pro Tyr Glu Ser	
233 238 243 248	
cat gat ttt tca aag ctc tta agt ttc cac tca tta ttt act caa cat	1001
His Asp Phe Ser Lys Leu Leu Ser Phe His Ser Leu Phe Thr Gln His	
249 254 259 264	
cag acc act cat ttt gga aaa tta ccc cat gga tac gat gaa tgt ggt	1049
Gln Thr Thr His Phe Gly Lys Leu Pro His Gly Tyr Asp Glu Cys Gly	
265 270 275 280	
gat gcc ttt agc tgt tac tca ttc ttt act caa cct cag aga att cac	1097
Asp Ala Phe Ser Cys Tyr Ser Phe Phe Thr Gln Pro Gln Arg Ile His	
281 286 291 296	
agt gga gaa aaa cca tat gca tgc aat gac tgt gga aaa gcc ttt agc	1145
Ser Gly Glu Lys Pro Tyr Ala Cys Asn Asp Cys Gly Lys Ala Phe Ser	
297 302 307 312	
cac gac ttc ttt ctc agt gaa cat caa aga act cat att ggg gag aaa	1193
His Asp Phe Phe Leu Ser Glu His Gln Arg Thr His Ile Gly Glu Lys	
313 318 323 328	
cct tat gaa tgt aag gaa tgt aac aaa gct ttc aga cag agt gct cac	1241
Pro Tyr Glu Cys Lys Glu Cys Asn Lys Ala Phe Arg Gln Ser Ala His	
329 334 339 344	
ctt gct caa cat cag agg atc cac act gga gag aaa ccg ttt gcg tgc	1289
Leu Ala Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Ala Cys	
345 350 355 360	
aat gaa tgt ggg aag gcc ttt agc cgt tat gcc ttc ctt gtt gaa cat	1337
Asn Glu Cys Gly Lys Ala Phe Ser Arg Tyr Ala Phe Leu Val Glu His	
361 366 371 376	
cag aga att cac aca ggt gag aaa cca tat gaa tgt aaa gaa tgt aat	1385
Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Asn	
377 382 387 392	
aaa gcc ttc aga cag agt gct cac ctt aat caa cat cag agg att cac	1433
Lys Ala Phe Arg Gln Ser Ala His Leu Asn Gln His Gln Arg Ile His	
393 398 403 408	
act gga gag aaa ccc tat gaa tgt aat cag tgt gga aaa gcc ttc agc	1481
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ser	
409 414 419 424	
aga cgc ata gcc ctt act cta cat caa aga att cac aca gga gag aaa	1529
Arg Arg Ile Ala Leu Thr Leu His Gln Arg Ile His Thr Gly Glu Lys	
425 430 435 440	
ccc ttc aaa tgt agt gaa tgt ggg aag acc ttt ggc tat cgc tca cac	1577
Pro Phe Lys Cys Ser Glu Cys Gly Lys Thr Phe Gly Tyr Arg Ser His	
441 446 451 456	
ctg aat caa cat cag aga att cat acc gga gaa aag ccc tat gaa tgc	1625

Leu Asn Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys	
457 462 467 472	
atc aaa tgt ggg aag ttt ttt agg act gac tca caa ctt aat cga cat	1673
Ile Lys Cys Gly Lys Phe Phe Arg Thr Asp Ser Gln Leu Asn Arg His	
473 478 483 488	
cat aga att cac act gga gag aga cca ttt gaa tgc agt aaa tgt ggg	1721
His Arg Ile His Thr Gly Glu Arg Pro Phe Glu Cys Ser Lys Cys Gly	
489 494 499 504	
aaa gcc ttc agt gat gct tta gtt cta att cac cat aag aga agt cat	1769
Lys Ala Phe Ser Asp Ala Leu Val Leu Ile His His Lys Arg Ser His	
505 510 515 520	
gca gga gag aaa ccc tat gaa tgt aac aaa tgt gga aag gcc ttc agt	1817
Ala Gly Glu Lys Pro Tyr Glu Cys Asn Lys Cys Gly Lys Ala Phe Ser	
521 526 531 536	
tgt ggc tca tat ctt aat caa cat caa aga att cat act gga gag aaa	1865
Cys Gly Ser Tyr Leu Asn Gln His Gln Arg Ile His Thr Gly Glu Lys	
537 542 547 552	
ccc tat gaa tgt agt gaa tgt ggg aag gct ttt cat cag atc ttg tcc	1913
Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe His Gln Ile Leu Ser	
553 558 563 568	
cta aga cta cac cag aga att cac gct gga gaa aaa cct tat aaa tgt	1961
Leu Arg Leu His Gln Arg Ile His Ala Gly Glu Lys Pro Tyr Lys Cys	
569 574 579 584	
aac gaa tca caa aga gtc cgg cgc tca gag cta gcg gtt tcc cga gga	2009
Asn Glu Ser Gln Arg Val Arg Arg Ser Glu Leu Ala Val Ser Arg Gly	
585 590 595 600	
ctc acc acc aag ccc gcg gac aca ggc ccc gat tcc aca ctt aac gct	2057
Leu Thr Thr Lys Pro Ala Asp Thr Gly Pro Asp Ser Thr Leu Asn Ala	
601 606 611 616	
gcc aaa gtg gca gag ccg gcg cgg gct ggg aca gag gcg gca ctg agg	2105
Ala Lys Val Ala Glu Pro Ala Arg Ala Gly Thr Glu Ala Ala Leu Arg	
617 622 627 632	
ccg gcg ctg tcg gtg gct gag agc gcc aca agt ctc ggt ccg tta cac	2153
Pro Ala Leu Ser Val Ala Glu Ser Ala Thr Ser Leu Gly Pro Leu His	
633 638 643 648	
cag ggg cga cgc ttc cca gag gcc ccc gcg gct cac ccg ggc ggg act	2201
Gln Gly Arg Arg Phe Pro Glu Ala Pro Ala Ala His Pro Gly Gly Thr	
649 654 659 664	
ggc ttc act gtt tgc gcg tcc tga gaagcagacc acggtgttcc agggctcaca	2255
Gly Phe Thr Val Cys Ala Ser *	
665 670	
gctccgcgca ggggagctca gcctagggtt tgcacgagcg gcctcccgcg agcccagctc	2315

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Ala Leu Gly Pro Pro Leu Ala Pro Gly Val Arg Gly Ser Glu Ala Glu
12 17 22 27

ggc cga ctc cgg gag aaa ctt ttc tct ggc tat gat agc tcc gtg cgg 145
Gly Arg Leu Arg Glu Lys Leu Phe Ser Gly Tyr Asp Ser Ser Val Arg
28 33 38 43

cca gcg cgg gag gtg gga gac cgt gtc agg gtc agc gtt ggt ctc atc 193
Pro Ala Arg Glu Val Gly Asp Arg Val Arg Val Ser Val Gly Leu Ile
44 49 54 59

ctg gcg caa ctc atc agc ctg aac gag aag gat gaa gag atg agc aca 241
Leu Ala Gln Leu Ile Ser Leu Asn Glu Lys Asp Glu Glu Met Ser Thr
60 65 70 75

aag gtg tac tta gac ctg gag tgg act gac tac agg ctg agc tgg gac 289
Lys Val Tyr Leu Asp Leu Glu Trp Thr Asp Tyr Arg Leu Ser Trp Asp
76 81 86 91

cct gcg gag cac gac ggc atc gat tcg ctc cgc atc acg gcg gaa tcc 337
Pro Ala Glu His Asp Gly Ile Asp Ser Leu Arg Ile Thr Ala Glu Ser
92 97 102 107

gtg tgg ctc cct gac gtg gtg cta ctg aac aac aat gat ggg aat ttt 385
Val Trp Leu Pro Asp Val Val Leu Leu Asn Asn Asn Asp Gly Asn Phe
108 113 118 123

gac gtg gct ctg gac att agc gtc gtg gtg tcc tcc gac ggc tcc gtg 433
Asp Val Ala Leu Asp Ile Ser Val Val Val Ser Ser Asp Gly Ser Val
124 129 134 139

cgt tgg caa ccc ccg ggc atc tat cgc agc agc tgc agc atc cag gtc 481
Arg Trp Gln Pro Pro Gly Ile Tyr Arg Ser Ser Cys Ser Ile Gln Val
140 145 150 155

acc tac ttc ccc ttc gac tgg cag aat tgc act atg gtg ttc agc tcc	529
Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys Thr Met Val Phe Ser Ser	
156 161 166 171	
tac agc tac gac agc tgc gag gtc agc ctg cag aca ggc ctg ggt cct	577
Tyr Ser Tyr Asp Ser Ser Glu Val Ser Leu Gln Thr Gly Leu Gly Pro	
172 177 182 187	
gac ggg caa ggg cat cag gaa atc cac att cat gaa ggc act ttc att	625
Asp Gly Gln Gly His Gln Glu Ile His Ile His Glu Gly Thr Phe Ile	
188 193 198 203	
gag aat ggc cag tgg gag aat atc cac aag ccc tct cgg cta atc cag	673
Glu Asn Gly Gln Trp Glu Asn Ile His Lys Pro Ser Arg Leu Ile Gln	
204 209 214 219	
cct cca ggc gat cct agg gga ggg agg gaa gga cag cgc cag gaa gtc	721
Pro Pro Gly Asp Pro Arg Gly Gly Arg Glu Gly Gln Arg Gln Glu Val	
220 225 230 235	
atc ttc tac ctc atc atc cgc cgc aag cct ctc ttc tac ctg gtc aac	769
Ile Phe Tyr Leu Ile Ile Arg Arg Lys Pro Leu Phe Tyr Leu Val Asn	
236 241 246 251	
gtc att gcc cca tgc atc ctc atc act ctt ctg gcc atc ttc gtc ttc	817
Val Ile Ala Pro Cys Ile Leu Ile Thr Leu Leu Ala Ile Phe Val Phe	
252 257 262 267	
tac ctg cca cca gat gca gga gag aag atg ggg ctc tca atc ttt gcc	865
Tyr Leu Pro Pro Asp Ala Gly Glu Lys Met Gly Leu Ser Ile Phe Ala	
268 273 278 283	
ctg ctg acc ctt act gtg ttc ctg ctg ctg ctg gct gac aaa gta cct	913
Leu Leu Thr Leu Thr Val Phe Leu Leu Leu Leu Ala Asp Lys Val Pro	
284 289 294 299	
gag acc tca cta tca gta ccc att att atc aag tac ctc atg ttt acc	961
Glu Thr Ser Leu Ser Val Pro Ile Ile Ile Lys Tyr Leu Met Phe Thr	
300 305 310 315	
atg gtc ctc gtc acc ttc tca gtc atc ctt agt gtc gtg gtt ctc aac	1009
Met Val Leu Val Thr Phe Ser Val Ile Leu Ser Val Val Val Leu Asn	
316 321 326 331	
ctg cac cac cgc tca ccc cac acc cac caa atg ccc ctt tgg gtc cgt	1057
Leu His His Arg Ser Pro His Thr His Gln Met Pro Leu Trp Val Arg	
332 337 342 347	
cag atc ttc att cac aaa ctt ccg ctg tac ctg cgt cta aaa agg ccc	1105
Gln Ile Phe Ile His Lys Leu Pro Leu Tyr Leu Arg Leu Lys Arg Pro	
348 353 358 363	
aaa ccc gag aga gac ctg atg ccg gag ccc cct cac tgt tct tct cca	1153
Lys Pro Glu Arg Asp Leu Met Pro Glu Pro Pro His Cys Ser Ser Pro	
364 369 374 379	
gga agt ggc tgg ggt cgg gga aca gat gaa tat ttc atc cgg aag ccg	1201

Gly	Ser	Gly	Trp	Gly	Arg	Gly	Thr	Asp	Glu	Tyr	Phe	Ile	Arg	Lys	Pro	
380					385					390					395	
cca	agt	gat	ttt	ctc	ttc	ccc	aaa	ccc	aat	agg	ttc	cag	cct	gaa	ctg	1249
Pro	Ser	Asp	Phe	Leu	Phe	Pro	Lys	Pro	Asn	Arg	Phe	Gln	Pro	Glu	Leu	
396					401					406					411	
tct	gcc	cct	gat	ctg	cgg	cga	ttt	atc	gat	ggc	cca	aac	cgg	gct	gtg	1297
Ser	Ala	Pro	Asp	Leu	Arg	Arg	Phe	Ile	Asp	Gly	Pro	Asn	Arg	Ala	Val	
412					417					422					427	
gcc	ctg	ctt	cgc	gag	cta	cgg	gag	gtc	gtc	tcc	tct	atc	agc	tac	atc	1345
Ala	Leu	Leu	Pro	Glu	Leu	Arg	Glu	Val	Val	Ser	Ser	Ile	Ser	Tyr	Ile	
428					433					438					443	
gct	cga	cag	ctg	cag	gaa	cag	gag	gac	cac	gat	gcg	ctg	aag	gag	gac	1393
Ala	Arg	Gln	Leu	Gln	Glu	Gln	Glu	Asp	His	Asp	Ala	Leu	Lys	Glu	Asp	
444					449					454					459	
tgg	cag	ttt	gtg	gcc	atg	gta	gtg	gac	cgc	ctc	ttc	ctg	tgg	act	ttc	1441
Trp	Gln	Phe	Val	Ala	Met	Val	Val	Asp	Arg	Leu	Phe	Leu	Trp	Thr	Phe	
460					465					470					475	
atc	atc	ttc	acc	agc	gtt	ggg	acc	cta	gtc	atc	ttc	ctg	gac	gcc	acg	1489
Ile	Ile	Phe	Thr	Ser	Val	Gly	Thr	Leu	Val	Ile	Phe	Leu	Asp	Ala	Thr	
476					481					486					491	
tac	cac	ttg	ccc	cct	cca	gac	ccc	ttt	cct	tga	agactgga	gggttgagac				1540
Tyr	His	Leu	Pro	Pro	Pro	Asp	Pro	Phe	Pro	*						
492					497					502						
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Val Pro Ser Asp Lys Ser Gly Phe Glu Pro Ala Ser Leu Lys Glu Glu	
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ccc	aac	cac	gag	aag	aag	gcc	ggc	aag	ctg	gac	ccg	cat	ctc	gtg	ctg	2301
Pro	Asn	His	Glu	Lys	Lys	Ala	Gly	Lys	Leu	Asp	Pro	His	Leu	Val	Leu	
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Gln	Gly	Phe	Pro	Asn	Arg	Val	Val	Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	
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Glu	Ile	Leu	Thr	Pro	Asn	Ser	Ile	Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	
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Gln	Ala	Cys	Val	Leu	Met	Ile	Lys	Ala	Leu	Glu	Leu	Asp	Ser	Asn	Leu	
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Phe	Gln	Ala	Cys	Cys	Arg	Gly	Tyr	Leu	Ala	Arg	Lys	Ala	Phe	Ala	Lys	
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cgg	cag	cag	cag	ctt	acc	gcc	atg	aag	gtc	ctc	cag	cgg	aac	tgc	gct	2685
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Gln Arg Gln Glu Leu Glu Lys Thr Arg Arg Lys Leu Glu Gly Asp Ser				
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Thr Asp Leu Ser Asp Gln Ile Ala Glu Leu Gln Ala Gln Ile Ala Glu				
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Leu Lys Met Gln Leu Ala Lys Lys Glu Glu Glu Leu Gln Ala Ala Leu				
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Glu Leu Ile Asn Asp Arg Leu Lys Lys Ala Asn Leu Gln Ile Asp Gln	
1746 1751 1756 1761	
atc aac acc gac ctg aac ctg gag cgc agc cac gcc cag aag aac gag	5565
Ile Asn Thr Asp Leu Asn Leu Glu Arg Ser His Ala Gln Lys Asn Glu	
1762 1767 1772 1777	
aat gct cgg cag cag ctg gaa cgc cag aac aag gag ctt aag gtc aag	5613
Asn Ala Arg Gln Gln Leu Glu Arg Gln Asn Lys Glu Leu Lys Val Lys	

1778	1783	1788	1793	
ctg cag gag atg gag ggc act gtc aag tcc aag tac aag gcc tcc atc				5661
Leu Gln Glu Met Glu Gly Thr Val Lys Ser Lys Tyr Lys Ala Ser Ile				
1794	1799	1804	1809	
acc gcc ctc gag gcc aag att gca cag ctg gag gag cag ctg gac aac				5709
Thr Ala Leu Glu Ala Lys Ile Ala Gln Leu Glu Glu Gln Leu Asp Asn				
1810	1815	1820	1825	
gag acc aag gag cgc cag gca gcc tgc aaa cag gtg cgt cgg acc gag				5757
Glu Thr Lys Glu Arg Gln Ala Ala Cys Lys Gln Val Arg Arg Thr Glu				
1826	1831	1836	1841	
aag aag ctg aag gat gtg ctg ctg cag gtg gat gac gag cgg agg aac				5805
Lys Lys Leu Lys Asp Val Leu Leu Gln Val Asp Asp Glu Arg Arg Asn				
1842	1847	1852	1857	
gcc gag cag tac aag gac cag gcc gac aag gca tct acc cgc ctg aag				5853
Ala Glu Gln Tyr Lys Asp Gln Ala Asp Lys Ala Ser Thr Arg Leu Lys				
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cag ctc aag cgg cag ctg gag gag gcc gaa gag gag gcc cag cgg gcc				5901
Gln Leu Lys Arg Gln Leu Glu Glu Ala Glu Glu Glu Ala Gln Arg Ala				
1874	1879	1884	1889	
aac gcc tcc cgc cgg aaa ctg cag cgc gag ctg gag gac gcc act gag				5949
Asn Ala Ser Arg Arg Lys Leu Gln Arg Glu Leu Glu Asp Ala Thr Glu				
1890	1895	1900	1905	
acg gcc gat gcc atg aac cgc gaa gtc agc tcc cta aag aac aag ctc				5997
Thr Ala Asp Ala Met Asn Arg Glu Val Ser Ser Leu Lys Asn Lys Leu				
1906	1911	1916	1921	
agg cgc ggg gac ctg ccg ttt gtc gtg ccc cgc cga atg gcc cgg aaa				6045
Arg Arg Gly Asp Leu Pro Phe Val Val Pro Arg Arg Met Ala Arg Lys				
1922	1927	1932	1937	
ggc gcc ggg gat ggc tcc gac gaa gag gta gat ggc aaa gcg gat ggg				6093
Gly Ala Gly Asp Gly Ser Asp Glu Glu Val Asp Gly Lys Ala Asp Gly				
1938	1943	1948	1953	
gct gag gcc aaa cct gcc gaa taa gcctcttctc ctgcagcctg agatggatgg				6147
Ala Glu Ala Lys Pro Ala Glu *				
1954	1959			
acagacagac accacagcct ccccttccca gaccccgag cacgcctctc cccaccttct				6207
tgaggactgct gtgaacatgc ctctctctgc cctccgcccc gtccccccat cccgtttccc				6267
tccaggtgtt gttgagggca tttggcttcc tctgctgcat ccccttccag ctccctcccc				6327
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ctctcagcc ctctcttgcc aaaaagcaca agatgttgag gcgagcaggg caggcccccg				6447
gggagggggc agagttttct atgaatctat ttttcttcag actgaggcct tttggtagtc				6507

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 gggcatgggg caggagtcaa ttctgtctca ggttcactgg tgggaggctg agccggtgga 180
 aaagacaccg ggaagagact cagaggcgac cata atg tcg tta cgt gta cac 232
 Met Ser Leu Arg Val His

act ctg ccc acc ctg ctt gga gcc gtc gtc aga ccg ggc tgc agg gag	280
Thr Leu Pro Thr Leu Leu Gly Ala Val Val Arg Pro Gly Cys Arg Glu	
7 12 17 22	
ctg ctg tgt ttg ctg atg atc aca gtg act gtg ggc cct ggt gcc tct	328
Leu Leu Cys Leu Leu Met Ile Thr Val Thr Val Gly Pro Gly Ala Ser	
23 28 33 38	
ggg gtg tgc ccc acc gct tgc atc tgt gcc act gac atc gtc agc tgc	376
Gly Val Cys Pro Thr Ala Cys Ile Cys Ala Thr Asp Ile Val Ser Cys	
39 44 49 54	
acc aac aaa aac ctg tcc aag gtg cct ggg aac ctt ttc aga ctg att	424
Thr Asn Lys Asn Leu Ser Lys Val Pro Gly Asn Leu Phe Arg Leu Ile	
55 60 65 70	
aag aga ctg gac ctg agt tat aac aga att ggg ctt ctg gat tct gag	472
Lys Arg Leu Asp Leu Ser Tyr Asn Arg Ile Gly Leu Leu Asp Ser Glu	
71 76 81 86	
tgg att cca gta tcg ttt gca aag ctg aac acc cta att ctt cgt cat	520
Trp Ile Pro Val Ser Phe Ala Lys Leu Asn Thr Leu Ile Leu Arg His	
87 92 97 102	
aac aac atc acc agc att tcc acg ggc agt ttt tcc aca act cca aat	568
Asn Asn Ile Thr Ser Ile Ser Thr Gly Ser Phe Ser Thr Thr Pro Asn	
103 108 113 118	
ttg aag tgt ctt gac tta tcg tcc aat aag ctg aag acg gtg aaa aat	616
Leu Lys Cys Leu Asp Leu Ser Ser Asn Lys Leu Lys Thr Val Lys Asn	
119 124 129 134	
gct gta ttc caa gag ttg aag gtt ctg gaa gtg ctt ctg ctt tac aac	664
Ala Val Phe Gln Glu Leu Lys Val Leu Glu Val Leu Leu Leu Tyr Asn	
135 140 145 150	
aat cac ata tcc tat ctc gat cct tca gcg ttt gga ggg ctc tcc cag	712
Asn His Ile Ser Tyr Leu Asp Pro Ser Ala Phe Gly Gly Leu Ser Gln	
151 156 161 166	
ttg cag aaa ctc tac tta agt gga aat ttt ctc aca cag ttt ccg atg	760
Leu Gln Lys Leu Tyr Leu Ser Gly Asn Phe Leu Thr Gln Phe Pro Met	
167 172 177 182	
gat ttg tat gtt gga agg ttc aag ctg gca gaa ctg atg ttt tta gat	808
Asp Leu Tyr Val Gly Arg Phe Lys Leu Ala Glu Leu Met Phe Leu Asp	
183 188 193 198	
gtt tct tat aac cga att cct tcc atg cca atg cac cac ata aat tta	856
Val Ser Tyr Asn Arg Ile Pro Ser Met Pro Met His His Ile Asn Leu	
199 204 209 214	
gtg cca gga aaa cag ctg aga ggc atc tac ctt cat gga aac cca ttt	904
Val Pro Gly Lys Gln Leu Arg Gly Ile Tyr Leu His Gly Asn Pro Phe	
215 220 225 230	

gtc tgt gac tgt tcc ctg tac tcc ttg ctg gtc ttt tgg tat cgt agg	952
Val Cys Asp Cys Ser Leu Tyr Ser Leu Leu Val Phe Trp Tyr Arg Arg	
231 236 241 246	
cac ttt agc tca gtg atg gat ttt aag aac gat tac acc tgt cgc ctg	1000
His Phe Ser Ser Val Met Asp Phe Lys Asn Asp Tyr Thr Cys Arg Leu	
247 252 257 262	
tgg tct gac tcc agg cac tcg cgt cag gta ctt ctg ctc cag gat agc	1048
Trp Ser Asp Ser Arg His Ser Arg Gln Val Leu Leu Leu Gln Asp Ser	
263 268 273 278	
ttt atg aat tgc tct gac agc atc atc aat ggt tcc ttt cgt gcg ctt	1096
Phe Met Asn Cys Ser Asp Ser Ile Ile Asn Gly Ser Phe Arg Ala Leu	
279 284 289 294	
ggc ttt att cat gag gct cag gtc ggg gaa aga ctg atg gtc cac tgt	1144
Gly Phe Ile His Glu Ala Gln Val Gly Glu Arg Leu Met Val His Cys	
295 300 305 310	
gac agc aag aca ggt aat gca aat acg gat ttc atc tgg gtg ggt cca	1192
Asp Ser Lys Thr Gly Asn Ala Asn Thr Asp Phe Ile Trp Val Gly Pro	
311 316 321 326	
gat aac aga ctg cta gag ccg gat aaa gag atg gaa aac ttt tac gtg	1240
Asp Asn Arg Leu Leu Glu Pro Asp Lys Glu Met Glu Asn Phe Tyr Val	
327 332 337 342	
ttt cac aat gga agt ctg gtt ata gaa agc cct cgt ttt gag gat gct	1288
Phe His Asn Gly Ser Leu Val Ile Glu Ser Pro Arg Phe Glu Asp Ala	
343 348 353 358	
gga gtg tat tct tgt atc gca atg aat aag caa cgc ctg tta aat gaa	1336
Gly Val Tyr Ser Cys Ile Ala Met Asn Lys Gln Arg Leu Leu Asn Glu	
359 364 369 374	
act gtg gac gtc aca ata aat gtg agc aat ttc act gta agc aga tcc	1384
Thr Val Asp Val Thr Ile Asn Val Ser Asn Phe Thr Val Ser Arg Ser	
375 380 385 390	
cat gct cat gag gca ttt aac aca gct ttt acc act ctt gct gct tgc	1432
His Ala His Glu Ala Phe Asn Thr Ala Phe Thr Thr Leu Ala Ala Cys	
391 396 401 406	
gtg gcc agt atc gtt ttg gta ctt ttg tac ctc tat ctg act cca tgc	1480
Val Ala Ser Ile Val Leu Val Leu Leu Tyr Leu Tyr Leu Thr Pro Cys	
407 412 417 422	
ccc tgc aag tgt aaa acc aag aga cag aaa aat atg cta cac caa agc	1528
Pro Cys Lys Cys Lys Thr Lys Arg Gln Lys Asn Met Leu His Gln Ser	
423 428 433 438	
aat gcc cat tca tcg att ctc agt cct ggc ccc gct agt gat gcc tcc	1576
Asn Ala His Ser Ser Ile Leu Ser Pro Gly Pro Ala Ser Asp Ala Ser	
439 444 449 454	
gct gat gaa cgg aag gca ggt gca ggt aaa aga gtg gtg ttt ttg gaa	1624

Ala Asp Glu Arg Lys	Ala Gly Ala Gly Lys	Arg Val Val Phe Leu Glu	
455	460	465	470
ccc ctg aag gat act	gca gca ggg cag aac	ggg aaa gtc agg ctc ttt	1672
Pro Leu Lys Asp Thr	Ala Ala Gly Gln Asn	Gly Lys Val Arg Leu Phe	
471	476	481	486
ccc agc gag gca gtg	ata gct gag ggc atc	cta aag tcc acg agg ggg	1720
Pro Ser Glu Ala Val	Ile Ala Glu Gly Ile	Leu Lys Ser Thr Arg Gly	
487	492	497	502
aaa tct gac tca gat	tca gtc aat tca gtg	ttt tct gac aca cct ttt	1768
Lys Ser Asp Ser Asp	Ser Val Asn Ser Val	Phe Ser Asp Thr Pro Phe	
503	508	513	518
gtg gcg tcc act taa	tttgtgccta tatttgtatg	atgtcataat ttaatctgtt	1823
Val Ala Ser Thr *			
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		Met Pro Glu	
		1	
gat gta cga gaa aaa	aag gaa aat ctt cta	ctc aat tct gag aga tct	165
Asp Val Arg Glu Lys	Lys Glu Asn Leu Leu	Leu Asn Ser Glu Arg Ser	
4	9	14	19
act agg ctc tta aca	aag acc agt cat tca	caa gga ggg gat caa gct	213
Thr Arg Leu Leu Thr	Lys Thr Ser His Ser	Gln Gly Gly Asp Gln Ala	
20	25	30	35
tta agt aag tcc aca	ggg tca cca aca gag	aag ttg att gaa aaa cgt	261
Leu Ser Lys Ser Thr	Gly Ser Pro Thr Glu	Lys Leu Ile Glu Lys Arg	
36	41	46	51
caa gga gct aag act	gtt ttt aac aag ttc	agc aac atg aat tgg cca	309
Gln Gly Ala Lys Thr	Val Phe Asn Lys Phe	Ser Asn Met Asn Trp Pro	
52	57	62	67
gtg gac att cac cct	tta aac aaa agt tta	gtc aaa gat aat aaa tgg	357

Val	Asp	Ile	His	Pro	Leu	Asn	Lys	Ser	Leu	Val	Lys	Asp	Asn	Lys	Trp	
68					73					78					83	
aag	aaa	act	gag	gag	acc	caa	gag	aaa	cga	agg	tct	ttc	ctt	cag	gag	405
Lys	Lys	Thr	Glu	Glu	Thr	Gln	Glu	Lys	Arg	Arg	Ser	Phe	Leu	Gln	Glu	
84					89					94					99	
ttt	tgc	aag	aaa	tac	ggg	ggg	gtg	agt	cat	cat	cag	tca	cat	ctt	ttt	453
Phe	Cys	Lys	Lys	Tyr	Gly	Gly	Val	Ser	His	His	Gln	Ser	His	Leu	Phe	
100					105					110					115	
cat	aca	gta	tcc	aga	atc	tat	gta	gaa	gat	aaa	cac	aaa	atc	tta	tat	501
His	Thr	Val	Ser	Arg	Ile	Tyr	Val	Glu	Asp	Lys	His	Lys	Ile	Leu	Tyr	
116					121					126					131	
tgt	gag	gta	cct	aag	gct	ggc	tgt	tcc	aat	tgg	aaa	aga	att	ctg	atg	549
Cys	Glu	Val	Pro	Lys	Ala	Gly	Cys	Ser	Asn	Trp	Lys	Arg	Ile	Leu	Met	
132					137					142					147	
gta	cta	aat	gga	ttg	gct	tcc	tct	gca	tac	aac	atc	tcc	cac	aat	gct	597
Val	Leu	Asn	Gly	Leu	Ala	Ser	Ser	Ala	Tyr	Asn	Ile	Ser	His	Asn	Ala	
148					153					158					163	
gtc	cac	tac	ggg	aag	cat	ttg	aag	aag	cta	gat	agc	ttt	gac	cta	aaa	645
Val	His	Tyr	Gly	Lys	His	Leu	Lys	Lys	Leu	Asp	Ser	Phe	Asp	Leu	Lys	
164					169					174					179	
ggg	ata	tat	acc	cgc	tta	aat	act	tac	acc	aaa	gct	gtg	ttt	gtt	cgt	693
Gly	Ile	Tyr	Thr	Arg	Leu	Asn	Thr	Tyr	Thr	Lys	Ala	Val	Phe	Val	Arg	
180					185					190					195	
gat	ccc	atg	gaa	aga	tta	gta	tca	gcc	ttt	agg	gac	aaa	ttt	gaa	cac	741
Asp	Pro	Met	Glu	Arg	Leu	Val	Ser	Ala	Phe	Arg	Asp	Lys	Phe	Glu	His	
196					201					206					211	
ccc	aat	agt	tat	tac	cat	cca	gta	ttc	gga	aag	gca	att	atc	aag	aaa	789
Pro	Asn	Ser	Tyr	Tyr	His	Pro	Val	Phe	Gly	Lys	Ala	Ile	Ile	Lys	Lys	
212					217					222					227	
tat	cga	cca	aat	gcc	tgt	gaa	gaa	gca	tta	att	aat	gga	tct	gga	gtc	837
Tyr	Arg	Pro	Asn	Ala	Cys	Glu	Glu	Ala	Leu	Ile	Asn	Gly	Ser	Gly	Val	
228					233					238					243	
aag	ttc	aaa	gag	ttt	atc	cac	tac	ttg	ctg	gat	tcc	cac	cgt	cca	gta	885
Lys	Phe	Lys	Glu	Phe	Ile	His	Tyr	Leu	Leu	Asp	Ser	His	Arg	Pro	Val	
244					249					254					259	
gga	atg	gac	att	cac	tgg	gaa	aag	gtc	agc	aaa	ctc	tgc	tat	ccg	tgt	933
Gly	Met	Asp	Ile	His	Trp	Glu	Lys	Val	Ser	Lys	Leu	Cys	Tyr	Pro	Cys	
260					265					270					275	
ttg	atc	aac	tat	gat	ttt	gta	ggg	aaa	ttt	gag	act	ttg	gaa	gaa	gat	981
Leu	Ile	Asn	Tyr	Asp	Phe	Val	Gly	Lys	Phe	Glu	Thr	Leu	Glu	Glu	Asp	
276					281					286					291	
gcc	aat	tac	ttt	tta	cag	atg	atc	ggg	gct	cca	aag	gag	ctg	aaa	ttt	1029
Ala	Asn	Tyr	Phe	Leu	Gln	Met	Ile	Gly	Ala	Pro	Lys	Glu	Leu	Lys	Phe	

292	297	302	307	
ccc aac ttt aag gat	agg cac tct tcc gat	gaa aga acc aat gct	caa	1077
Pro Asn Phe Lys Asp	Arg His Ser Ser Asp	Glu Arg Thr Asn Ala	Gln	
308	313	318	323	
gtc gtg aga cag tat	tta aag gat ctg act	aga act gag aga	caa tta	1125
Val Val Arg Gln Tyr	Leu Lys Asp Leu Thr	Arg Thr Glu Arg	Gln Leu	
324	329	334	339	
atc tat gac ttt tat	tac ttg gac tat tta	atg ttt aat tat	aca act	1173
Ile Tyr Asp Phe Tyr	Tyr Leu Asp Tyr Leu	Met Phe Asn Tyr	Thr Thr	
340	345	350	355	
cca ttt ttg tag ttt	gcattcattt tctaaaaccc	tgtatatact	taatgatgat	1228
Pro Phe Leu *				
356				
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aaa				1291

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aactaactgc cccaaccaat tttgtctagg	aagcatatat gggttttaaag tgttgattta	660

ccc gcc cca ctt gcc cct ctt gaa ccg gat tct ggt acc agc tct gct	2088
Pro Ala Pro Leu Ala Pro Leu Glu Pro Asp Ser Gly Thr Ser Ser Ala	
79 84 89 94	
gct gat ggt cct tgg aca cag aga ggg gag gag gag gca gag gcc	2136
Ala Asp Gly Pro Trp Thr Gln Arg Gly Glu Glu Glu Glu Ala Glu Ala	
95 100 105 110	
aga gcc aag ctg gcc cca ggg agg gag ccc cct agt ccc tgc cac tca	2184
Arg Ala Lys Leu Ala Pro Gly Arg Glu Pro Pro Ser Pro Cys His Ser	
111 116 121 126	
gag gac agc ctt ggg ctg ggg gca gca ccc ctt ggc agc gaa cca ccc	2232
Glu Asp Ser Leu Gly Leu Gly Ala Ala Pro Leu Gly Ser Glu Pro Pro	
127 132 137 142	
ctg agc cag ctg gtg tcc gac tca gac tca gag ctg gac agc aca gag	2280
Leu Ser Gln Leu Val Ser Asp Ser Asp Ser Glu Leu Asp Ser Thr Glu	
143 148 153 158	
cgg ctg gcc ctg gga agc aca gac acc ttg tcc aat ggg cag aaa gcg	2328
Arg Leu Ala Leu Gly Ser Thr Asp Thr Leu Ser Asn Gly Gln Lys Ala	
159 164 169 174	
gac ctg gag gct gcg cag cgc ctg gcc aag agg ctg tac cga cta gat	2376
Asp Leu Glu Ala Ala Gln Arg Leu Ala Lys Arg Leu Tyr Arg Leu Asp	
175 180 185 190	
ggc ttc agg aag gcc gat gtg gcc cgg cac ctg ggc aag aac aat gac	2424
Gly Phe Arg Lys Ala Asp Val Ala Arg His Leu Gly Lys Asn Asn Asp	
191 196 201 206	
ttc agc aaa ctg gtg gct ggg gag tac ctc aag ttc ttt gtc ttc acg	2472
Phe Ser Lys Leu Val Ala Gly Glu Tyr Leu Lys Phe Phe Val Phe Thr	
207 212 217 222	
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Gly Met Thr Leu Asp Gln Ala Leu Arg Val Phe Leu Lys Glu Leu Ala	
223 228 233 238	
tta atg ggt gag acc cag gaa cga gag cgc gtg ctg gcc cac ttc tcc	2568
Leu Met Gly Glu Thr Gln Glu Arg Glu Arg Val Leu Ala His Phe Ser	
239 244 249 254	
cag cga tac ttc cag tgc aat cct gaa gcc ctg tcc tca gag gac ggc	2616
Gln Arg Tyr Phe Gln Cys Asn Pro Glu Ala Leu Ser Ser Glu Asp Gly	
255 260 265 270	
gcc cac acg ctg acc tgt gcg ctc atg ctg ctc aac acg gat ctc cac	2664
Ala His Thr Leu Thr Cys Ala Leu Met Leu Leu Asn Thr Asp Leu His	
271 276 281 286	
ggc cat aac atc ggg aag cgc atg acc tgc ggg gac ttc atc ggg aac	2712
Gly His Asn Ile Gly Lys Arg Met Thr Cys Gly Asp Phe Ile Gly Asn	
287 292 297 302	

ctg gag ggc ctc aat gat ggc ggc gac ttc cct agg gag ctg ctc aag Leu Glu Gly Leu Asn Asp Gly Gly Asp Phe Pro Arg Glu Leu Leu Lys 303 308 313 318	2760
gcc ttg tac agc tcc atc aag aat gag aag ctg cag tgg gcc ata gac Ala Leu Tyr Ser Ser Ile Lys Asn Glu Lys Leu Gln Trp Ala Ile Asp 319 324 329 334	2808
gag gag gag ctg aga cgc tct ctg tct gag ttg gcc gac ccc aac ccc Glu Glu Glu Leu Arg Arg Ser Leu Ser Glu Leu Ala Asp Pro Asn Pro 335 340 345 350	2856
aag gtc atc aag cgg atc agc ggg ggc agt ggc agt ggc tcc agc cct Lys Val Ile Lys Arg Ile Ser Gly Gly Ser Gly Ser Gly Ser Ser Pro 351 356 361 366	2904
ttc ctg gac ctg act ccc gag cct ggg gct gcc gtc tac aag cac ggg Phe Leu Asp Leu Thr Pro Glu Pro Gly Ala Ala Val Tyr Lys His Gly 367 372 377 382	2952
gcc ctg gtg cga aag gtg cac gca gac cct gac tgc agg aag aca cct Ala Leu Val Arg Lys Val His Ala Asp Pro Asp Cys Arg Lys Thr Pro 383 388 393 398	3000
cgg ggc aag cgg ggc tgg aag agc ttc cac ggg atc ctc aag ggc atg Arg Gly Lys Arg Gly Trp Lys Ser Phe His Gly Ile Leu Lys Gly Met 399 404 409 414	3048
atc ctc tac ctg cag aag gag gag tac aag cct ggg aag gcc ctt tca Ile Leu Tyr Leu Gln Lys Glu Glu Tyr Lys Pro Gly Lys Ala Leu Ser 415 420 425 430	3096
gag acg gag ctc aag aat gcc atc agc atc cac cat gcc ctg gcc act Glu Thr Glu Leu Lys Asn Ala Ile Ser Ile His His Ala Leu Ala Thr 431 436 441 446	3144
cgt gcc agt gac tac agc aag agg ccc cac gtc ttc tac ctg cgc aca Arg Ala Ser Asp Tyr Ser Lys Arg Pro His Val Phe Tyr Leu Arg Thr 447 452 457 462	3192
gct gac tgg cgg gtc ttc ctc ttc cag gcc ccg agc ctg gag cag atg Ala Asp Trp Arg Val Phe Leu Phe Gln Ala Pro Ser Leu Glu Gln Met 463 468 473 478	3240
cag tcc tgg atc act cgc atc aat gta gta gcc gct atg ttc tct gcg Gln Ser Trp Ile Thr Arg Ile Asn Val Val Ala Ala Met Phe Ser Ala 479 484 489 494	3288
ccc ccc ttc cca gct gct gtt agc tcc caa aag aag ttc agc cgc cct Pro Pro Phe Pro Ala Ala Val Ser Ser Gln Lys Lys Phe Ser Arg Pro 495 500 505 510	3336
ctc ctg ccc agc gct gcc acc cgc ctc tcc cag gag gag cag gtg cgg Leu Leu Pro Ser Ala Ala Thr Arg Leu Ser Gln Glu Glu Gln Val Arg 511 516 521 526	3384
acc cac gag gcc aag ctg aag gcc atg gca agt gag ctg cgg gag cac	3432

Thr	His	Glu	Ala	Lys	Leu	Lys	Ala	Met	Ala	Ser	Glu	Leu	Arg	Glu	His	
527					532					537					542	
cgg	gcc	gcc	cag	ctg	ggc	aag	aag	ggc	cgg	ggc	aag	aag	gct	gaa	gag	3480
Arg	Ala	Ala	Gln	Leu	Gly	Lys	Lys	Gly	Arg	Gly	Lys	Lys	Ala	Glu	Glu	
543					548					553					558	
cag	cgg	cag	aag	gag	gcc	tac	ctg	gag	ttt	gag	aaa	tcc	cgc	tac	agc	3528
Gln	Arg	Gln	Lys	Glu	Ala	Tyr	Leu	Glu	Phe	Glu	Lys	Ser	Arg	Tyr	Ser	
559					564					569					574	
acc	tat	gca	gcg	ctg	ctt	cgg	gtc	aag	ctg	aag	gca	ggc	agt	gag	gag	3576
Thr	Tyr	Ala	Ala	Leu	Leu	Arg	Val	Lys	Leu	Lys	Ala	Gly	Ser	Glu	Glu	
575					580					585					590	
ctg	gat	gca	gtg	gag	gca	gca	ctg	gcc	cag	gcc	ggg	agc	aca	gag	gat	3624
Leu	Asp	Ala	Val	Glu	Ala	Ala	Leu	Ala	Gln	Ala	Gly	Ser	Thr	Glu	Asp	
591					596					601					606	
gga	ctc	cct	cct	tct	cac	tcc	agt	ccc	tcc	ctg	cag	ccc	aaa	ccc	tcc	3672
Gly	Leu	Pro	Pro	Ser	His	Ser	Ser	Pro	Ser	Leu	Gln	Pro	Lys	Pro	Ser	
607					612					617					622	
agc	cag	ccc	cgg	gct	cag	cgt	cac	agc	tca	gag	cct	cgg	cca	ggg	gca	3720
Ser	Gln	Pro	Arg	Ala	Gln	Arg	His	Ser	Ser	Glu	Pro	Arg	Pro	Gly	Ala	
623					628					633					638	
ggc	agt	ggg	cgg	cgg	aag	ccc	tga	gatgaggttt								3754
Gly	Ser	Gly	Arg	Arg	Lys	Pro	*									
639					644											

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gtcccggggc ccgggggtccc gtctggcggc ccgggattac cgtgacgtca cattgagcct	180
ctggccacct tggactggga cacctccgga gcctcacagc cccgcgccgc gccgcgcctc	240
acctcgccac cacgcgcctt tgggaacccg catcttcttc cttcccctgc ccatccatgg	300
gcccttctgt cttccggacc ccacgggccc gaggggccc ttccggagcg cagggtcgg	360

cagccgggct gccctcggt ctgctccac tggggccaac caggcgaagg aaccggcgct	420
gggcatccgc agcgggtgtaa ggaactgaga cacctcactg ctgggggscgc ggaacagctg	480
ggctgagacg ggaactcgac aggggaagaga gagacggggc agggacagcc acc atg Met 1	536
tcc ttc cca cac ttt gga cac ccg tac cgc ggc gct tcc cag ttt ctg Ser Phe Pro His Phe Gly His Pro Tyr Arg Gly Ala Ser Gln Phe Leu 2 7 12 17	584
gcg tcg gca agt tcc agc acc aca tgc tgc gaa tct acc caa cgc tct Ala Ser Ala Ser Ser Ser Thr Thr Cys Cys Glu Ser Thr Gln Arg Ser 18 23 28 33	632
gtc tca gat gtg gca tca ggc tcc acc cca gcg ccc gct ctc tgc tgc Val Ser Asp Val Ala Ser Gly Ser Thr Pro Ala Pro Ala Leu Cys Cys 34 39 44 49	680
gca ccc tac gat agt cga ctg ctg ggc agt gcg cga ccg gag ctg ggc Ala Pro Tyr Asp Ser Arg Leu Leu Gly Ser Ala Arg Pro Glu Leu Gly 50 55 60 65	728
gcc gcc ttg ggc atc tat gga gca ccc tat gcg gcc gct gca gct gcc Ala Ala Leu Gly Ile Tyr Gly Ala Pro Tyr Ala Ala Ala Ala Ala Ala 66 71 76 81	776
cag agc tac cct ggc tac ctg ccc tat agc cca gag ccc ccc tca ctg Gln Ser Tyr Pro Gly Tyr Leu Pro Tyr Ser Pro Glu Pro Pro Ser Leu 82 87 92 97	824
tat ggg gca ctg aat cca cag tat gaa ttt aag gag gct gca ggg agt Tyr Gly Ala Leu Asn Pro Gln Tyr Glu Phe Lys Glu Ala Ala Gly Ser 98 103 108 113	872
ttt aca tcc agc ctg gca caa cca gga gcc tat tat ccc tat gag cgg Phe Thr Ser Ser Leu Ala Gln Pro Gly Ala Tyr Tyr Pro Tyr Glu Arg 114 119 124 129	920
act ctg ggg cag tac caa tat gaa cgg tat ggc gca gtg gaa ttg agt Thr Leu Gly Gln Tyr Gln Tyr Glu Arg Tyr Gly Ala Val Glu Leu Ser 130 135 140 145	968
ggc gcc ggt cgc cga aag aac gcg acc cgg gag acc acc agt aca ctc Gly Ala Gly Arg Arg Lys Asn Ala Thr Arg Glu Thr Thr Ser Thr Leu 146 151 156 161	1016
aag gcc tgg ctc aac gag cac cgc aaa aac ccc tac ccc act aag ggt Lys Ala Trp Leu Asn Glu His Arg Lys Asn Pro Tyr Pro Thr Lys Gly 162 167 172 177	1064
gag aag atc atg ctg gcc atc atc acc aag atg acc ctc acc cag gtg Glu Lys Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln Val 178 183 188 193	1112
tcc acc tgg ttc gcc aac gca cgc cgg cgc ctc aag aaa gag aac aaa	1160

Ser	Thr	Trp	Phe	Ala	Asn	Ala	Arg	Arg	Arg	Leu	Lys	Lys	Glu	Asn	Lys		
194					199					204					209		
atg	aca	tgg	gcg	ccc	aag	aac	aaa	ggt	ggg	gag	gag	agg	aag	gca	gag	1208	
Met	Thr	Trp	Ala	Pro	Lys	Asn	Lys	Gly	Gly	Glu	Glu	Arg	Lys	Ala	Glu		
210					215					220					225		
gga	gga	gag	gag	gac	tca	cta	ggc	tgc	cta	act	gct	gac	acc	aaa	gaa	1256	
Gly	Gly	Glu	Glu	Asp	Ser	Leu	Gly	Cys	Leu	Thr	Ala	Asp	Thr	Lys	Glu		
226					231					236					241		
gtt	act	gct	agc	cag	gag	gcc	cgg	ggg	ctc	cgg	ctg	agt	gac	ctg	gaa	1304	
Val	Thr	Ala	Ser	Gln	Glu	Ala	Arg	Gly	Leu	Arg	Leu	Ser	Asp	Leu	Glu		
242					247					252					257		
gac	ctg	gag	gaa	gag	gag	gag	gag	gag	gag	gaa	gct	gaa	gac	gag	gag	1352	
Asp	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ala	Glu	Asp	Glu	Glu		
258					263					268					273		
gta	gtg	gcc	aca	gct	ggg	gac	agg	ctg	acg	gag	ttc	cga	aag	ggc	gcg	1400	
Val	Val	Ala	Thr	Ala	Gly	Asp	Arg	Leu	Thr	Glu	Phe	Arg	Lys	Gly	Ala		
274					279					284					289		
cag	tca	ctg	cct	ggg	ccg	tgc	gct	gca	gct	cga	gag	ggc	cga	ttg	gag	1448	
Gln	Ser	Leu	Pro	Gly	Pro	Cys	Ala	Ala	Ala	Arg	Glu	Gly	Arg	Leu	Glu		
290					295					300					305		
cgc	agg	gag	tgc	ggc	ctg	gct	gcg	ccc	cgc	ttc	tcc	ttc	aat	gac	cct	1496	
Arg	Arg	Glu	Cys	Gly	Leu	Ala	Ala	Pro	Arg	Phe	Ser	Phe	Asn	Asp	Pro		
306					311					316					321		
tcc	gga	tcg	gaa	gaa	gct	gac	ttc	ctc	tcg	gcg	gag	aca	ggc	agc	cct	1544	
Ser	Gly	Ser	Glu	Glu	Ala	Asp	Phe	Leu	Ser	Ala	Glu	Thr	Gly	Ser	Pro		
322					327					332					337		
agg	ttg	acc	atg	cac	tac	cca	tgc	ttg	gag	aaa	ccg	cgc	atc	tggt	tct	1592	
Arg	Leu	Thr	Met	His	Tyr	Pro	Cys	Leu	Glu	Lys	Pro	Arg	Ile	Trp	Ser		
338					343					348					353		
ctg	gcg	cac	acc	gcg	aca	gcc	agc	gct	gtt	gaa	ggg	gca	ccc	cca	gcc	1640	
Leu	Ala	His	Thr	Ala	Thr	Ala	Ser	Ala	Val	Glu	Gly	Ala	Pro	Pro	Ala		
354					359					364					369		
cgg	cct	agg	cca	cga	agt	cct	gag	tgc	cgt	atg	att	cct	gga	cag	cct	1688	
Arg	Pro	Arg	Pro	Arg	Ser	Pro	Glu	Cys	Arg	Met	Ile	Pro	Gly	Gln	Pro		
370					375					380					385		
cct	gcc	tct	gcc	cgg	cga	ctc	tca	gtc	ccc	aga	gac	tcc	gcg	tgc	gac	1736	
Pro	Ala	Ser	Ala	Arg	Arg	Leu	Ser	Val	Pro	Arg	Asp	Ser	Ala	Cys	Asp		
386					391					396					401		
gag	tct	tcc	tgc	ata	ccc	aaa	gcc	ttt	gga	aac	ccc	aag	ttt	gcc	ctg	1784	
Glu	Ser	Ser	Cys	Ile	Pro	Lys	Ala	Phe	Gly	Asn	Pro	Lys	Phe	Ala	Leu		
402					407					412					417		
cag	gga	cta	ccg	ctg	aac	tgt	gcg	ccg	tgc	ccg	cgg	agg	agc	gag	cct	1832	
Gln	Gly	Leu	Pro	Leu	Asn	Cys	Ala	Pro	Cys	Pro	Arg	Arg	Ser	Glu	Pro		

418	423	428	433	
gta gtg cag tgc cag tac ccg tct gga gca gaa ggt agt ggg ccc cca				1880
Val Val Gln Cys Gln Tyr Pro Ser Gly Ala Glu Gly Ser Gly Pro Pro				
434	439	444	449	
gcg gcg ctg gga gta tct atg caa aag aca ccc acc tac cgc ccc gcc				1928
Ala Ala Leu Gly Val Ser Met Gln Lys Thr Pro Thr Tyr Arg Pro Ala				
450	455	460	465	
cgg caa ttg cac acc ctc tgc cat tcc agt ctg ccc aga gga gac tcg				1976
Arg Gln Leu His Thr Leu Cys His Ser Ser Leu Pro Arg Gly Asp Ser				
466	471	476	481	
ctg gtc cct gct gtg ctg ctc aga gag ttt act agg gtt ggg cag gca				2024
Leu Val Pro Ala Val Leu Leu Arg Glu Phe Thr Arg Val Gly Gln Ala				
482	487	492	497	
cca ggg ctt tta gag aag tct aag act gtg ggc cag acg cac acc aca				2072
Pro Gly Leu Leu Glu Lys Ser Lys Thr Val Gly Gln Thr His Thr Thr				
498	503	508	513	
gat tta agg gga ccc tcc agt cgc cct cgc tga cccgcggc ttaggggtccg				2123
Asp Leu Arg Gly Pro Ser Ser Arg Pro Arg *				
514	519	524		
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gcggaggagc agcaagcctc cctgtgagtc ggtgggagac aagacggagc ggcggttaagg	120
gcggtaggga agtgaagcgc ctctctccac cttgttagaa gcgcgctgaa agcggcctgc	180
ctaccacccc catcgctgcc gttttgcagt cgtcgctccc accttccgct gccgcctgga	240
gggaagccgg agcgacgggg gtcacggcgg cggtcagagg gtaaaggctc tgctcccagc	300
agcctccgcg gtggatacgt cgccatcttg gatccgcggg acaagaaaat tcatgcgagg	360
gagacgtggt gggcggtcct tcctgtgaca cgacccttga gtgacagttc tatttgattg	420
cctccggtac tgtgaggaaa ggacacgact ct atg gtg agg act gat gga cat	473
Met Val Arg Thr Asp Gly His	

aca tta tct gag aaa aga aac tac cag gtg	aca aac agc atg ttt ggt	521
Thr Leu Ser Glu Lys Arg Asn Tyr Gln Val	Thr Asn Ser Met Phe Gly	
8 13 18 23		
gct tca aga aag aag ttt gta gag ggg gtc	gac agt gac tac cat gac	569
Ala Ser Arg Lys Lys Phe Val Glu Gly Val	Asp Ser Asp Tyr His Asp	
24 29 34 39		
gaa aac atg tac tac agc cag tct tct atg	ttt cca cat cgg tca gaa	617
Glu Asn Met Tyr Tyr Ser Gln Ser Ser Met	Phe Pro His Arg Ser Glu	
40 45 50 55		
aaa gat atg ctg gca tca cca tct aca tca	ggt cag ctg tct cag ttt	665
Lys Asp Met Leu Ala Ser Pro Ser Thr Ser	Gly Gln Leu Ser Gln Phe	
56 61 66 71		
ggg gca agt tta tac ggg caa caa agt gca	cta ggc ctt cca atg agg	713
Gly Ala Ser Leu Tyr Gly Gln Gln Ser Ala	Leu Gly Leu Pro Met Arg	
72 77 82 87		
ggg atg agc aac aat acc cct cag tta aat	cgc agc tta tca caa ggc	761
Gly Met Ser Asn Asn Thr Pro Gln Leu Asn	Arg Ser Leu Ser Gln Gly	
88 93 98 103		
act cag tta ccg agc cac gtc acg cca aca	aca ggg gta cca aca atg	809
Thr Gln Leu Pro Ser His Val Thr Pro Thr	Thr Gly Val Pro Thr Met	
104 109 114 119		
tca ctt cac acg cct cca tct cca agc agg	ggt att ttg cct atg aat	857
Ser Leu His Thr Pro Pro Ser Pro Ser Arg	Gly Ile Leu Pro Met Asn	
120 125 130 135		
cct agg aat atg atg aac cac tcc cag gtt	ggt cag ggc att gga att	905
Pro Arg Asn Met Met Asn His Ser Gln Val	Gly Gln Gly Ile Gly Ile	
136 141 146 151		
cct agc agg aca aat agc atg agc agt tca	ggg tta ggt agc ccc aac	953
Pro Ser Arg Thr Asn Ser Met Ser Ser Ser	Gly Leu Gly Ser Pro Asn	
152 157 162 167		
aga agc tcg cca agc ata ata tgt atg cca	aag cag cag cct tct cga	1001
Arg Ser Ser Pro Ser Ile Ile Cys Met Pro	Lys Gln Gln Pro Ser Arg	
168 173 178 183		
cag cct ttt act gtg aac agt atg tct gga	ttt gga atg aac agg aat	1049
Gln Pro Phe Thr Val Asn Ser Met Ser Gly	Phe Gly Met Asn Arg Asn	
184 189 194 199		
cag gca ttt gga atg aat aac tcc tta tca	agt aac att ttt aat gga	1097
Gln Ala Phe Gly Met Asn Asn Ser Leu Ser	Ser Asn Ile Phe Asn Gly	
200 205 210 215		
aca gac gga agt gaa aat gtg aca gga ttg	gac ctt tca gat ttc cca	1145
Thr Asp Gly Ser Glu Asn Val Thr Gly Leu	Asp Leu Ser Asp Phe Pro	
216 221 226 231		

gca tta gca gac cga aac agg agg gaa gga agt ggt aac cca act cca	1193
Ala Leu Ala Asp Arg Asn Arg Arg Glu Gly Ser Gly Asn Pro Thr Pro	
232 237 242 247	
tta ata aac ccc ttg gct gga aga gct cct tat gtt gga atg gta aca	1241
Leu Ile Asn Pro Leu Ala Gly Arg Ala Pro Tyr Val Gly Met Val Thr	
248 253 258 263	
aaa cca gca aat gaa caa tcc cag gac ttc tca ata cac aat gaa gat	1289
Lys Pro Ala Asn Glu Gln Ser Gln Asp Phe Ser Ile His Asn Glu Asp	
264 269 274 279	
ttt cca gca tta cca ggc tcc agc tat aaa gat cca aca tca agt aat	1337
Phe Pro Ala Leu Pro Gly Ser Ser Tyr Lys Asp Pro Thr Ser Ser Asn	
280 285 290 295	
gat gac agt aaa tct aat ttg aat aca tct ggc aag aca act tca agt	1385
Asp Asp Ser Lys Ser Asn Leu Asn Thr Ser Gly Lys Thr Thr Ser Ser	
296 301 306 311	
aca gat gga ccc aaa ttc cct gga gat aaa agt tca aca aca caa aat	1433
Thr Asp Gly Pro Lys Phe Pro Gly Asp Lys Ser Ser Thr Thr Gln Asn	
312 317 322 327	
aat aac cag cag aaa aaa ggg atc cag gtg tta cct gat ggt cgg gtt	1481
Asn Asn Gln Gln Lys Lys Gly Ile Gln Val Leu Pro Asp Gly Arg Val	
328 333 338 343	
act aac att cct caa ggg atg gtg acg gac caa ttt gga atg att ggc	1529
Thr Asn Ile Pro Gln Gly Met Val Thr Asp Gln Phe Gly Met Ile Gly	
344 349 354 359	
ctg tta aca ttt atc agg gca gca gag aca gac cca gga atg gta cat	1577
Leu Leu Thr Phe Ile Arg Ala Ala Glu Thr Asp Pro Gly Met Val His	
360 365 370 375	
ctt gca tta gga agt gac tta aca aca tta ggc ctc aat ctg aac tct	1625
Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly Leu Asn Leu Asn Ser	
376 381 386 391	
cct gaa aat ctc tac ccc aaa ttt gcg tca ccc tgg gca tct tca cct	1673
Pro Glu Asn Leu Tyr Pro Lys Phe Ala Ser Pro Trp Ala Ser Ser Pro	
392 397 402 407	
tgt cga cct caa gac ata gac ttc cat gtt cca tct gag tac tta acg	1721
Cys Arg Pro Gln Asp Ile Asp Phe His Val Pro Ser Glu Tyr Leu Thr	
408 413 418 423	
aac att cac att agg gat aag tta ttt ttc ttt ttc agc tgg ctg caa	1769
Asn Ile His Ile Arg Asp Lys Leu Phe Phe Phe Phe Ser Trp Leu Gln	
424 429 434 439	
taa aact tggccgatat ggtgaagacc ttctcttcta tctctattac atgaatggag	1826
*	
440	

gagacgtatt acaactttta gctgcagtgg agctttttta ccgtagattgg agataccaca 1886
aagaagaacg agtatggatt accagggcac caggcatgga gccacaatg aaaaccaata 1946
cctatgagag gggaacatat tactttcttg actgtcttaa ctggaggaaa gtagctaagg 2006
agttccatct ggaatatgac aaattagaag aacggcctca cctgccatcc accttcaact 2066
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Met Ala Thr Ser Gln Tyr Phe Asp Phe Ala Gln Gly Gly Gly Pro
1 5 10
cag tac agc acc cag gct ccg acc ctt ccc ctg ccc act gtg ggg gcc 157
Gln Tyr Ser Thr Gln Ala Pro Thr Leu Pro Leu Pro Thr Val Gly Ala
16 21 26 31
agc tat act gga caa ccc act cct ggg atg gac cct gcc gtg aac ccg 205
Ser Tyr Thr Gly Gln Pro Thr Pro Gly Met Asp Pro Ala Val Asn Pro
32 37 42 47
gcc ttt ccc cca gct gcc ccg gca ggg tac ggt gga tac cag ccc cac 253
Ala Phe Pro Pro Ala Ala Pro Ala Gly Tyr Gly Gly Tyr Gln Pro His
48 53 58 63
tcc ggc cag gac ttc gcc tac ggc agc cga ccc cag gag ccc gtc ccc 301
Ser Gly Gln Asp Phe Ala Tyr Gly Ser Arg Pro Gln Glu Pro Val Pro
64 69 74 79
acg gcc acc acc atg gct acc tac cag gac agt tac agc tac gga cag 349
Thr Ala Thr Thr Met Ala Thr Tyr Gln Asp Ser Tyr Ser Tyr Gly Gln
80 85 90 95
tca gca gct gcc agg agc tat gag gac agg ccg tac ttc cag tct gct 397
Ser Ala Ala Ala Arg Ser Tyr Glu Asp Arg Pro Tyr Phe Gln Ser Ala
96 101 106 111
gcc ctc cag tct ggg cgc atg aca gcc gca gac tcc ggc cag cca ggg 445
Ala Leu Gln Ser Gly Arg Met Thr Ala Ala Asp Ser Gly Gln Pro Gly
112 117 122 127

acc caa gaa gcc tgc ggg cag ccc agc ccc cat ggc agt cac agc cac	493
Thr Gln Glu Ala Cys Gly Gln Pro Ser Pro His Gly Ser His Ser His	
128 133 138 143	
gct cag ccc cca cag cag gcg ccc ata gtg gag tcc gga cag cca gcg	541
Ala Gln Pro Pro Gln Gln Ala Pro Ile Val Glu Ser Gly Gln Pro Ala	
144 149 154 159	
agc acc ttg tcc tgc gga tac acc tac ccc acg gcg aca ggc gtc cag	589
Ser Thr Leu Ser Ser Gly Tyr Thr Tyr Pro Thr Ala Thr Gly Val Gln	
160 165 170 175	
ccc gag tcg tca gct tcc atc gtg acc tcc tac ccc ccg ccc tcc tac	637
Pro Glu Ser Ser Ala Ser Ile Val Thr Ser Tyr Pro Pro Pro Ser Tyr	
176 181 186 191	
aac ccc acc tgc acc gcc tac acg gca cca agc tac ccg aac tat gac	685
Asn Pro Thr Cys Thr Ala Tyr Thr Ala Pro Ser Tyr Pro Asn Tyr Asp	
192 197 202 207	
gcg tcg gtg tac tcc gct gcc agc cct ttc tat cct cca gcg cag ccc	733
Ala Ser Val Tyr Ser Ala Ala Ser Pro Phe Tyr Pro Pro Ala Gln Pro	
208 213 218 223	
ccg cct ccc ccg gga ccc ccg cag cag ctg ccc ccg ccg ccc gcg cct	781
Pro Pro Pro Pro Gly Pro Pro Gln Gln Leu Pro Pro Pro Pro Ala Pro	
224 229 234 239	
gca ggc tca gga agc agc ccc agg gcc gac tcg aag cca ccg ctt ccc	829
Ala Gly Ser Gly Ser Ser Pro Arg Ala Asp Ser Lys Pro Pro Leu Pro	
240 245 250 255	
agc aag ctg ccg aga ccc aag gcg ggg ccc agg cag ctc cag ctt cac	877
Ser Lys Leu Pro Arg Pro Lys Ala Gly Pro Arg Gln Leu Gln Leu His	
256 261 266 271	
tac tgc gac atc tgc aag atc agc tgc gct ggc ccc cag acc tac cgg	925
Tyr Cys Asp Ile Cys Lys Ile Ser Cys Ala Gly Pro Gln Thr Tyr Arg	
272 277 282 287	
gaa cat ctg gga ggg cag aag cac aga aag aag gag gcg gcc cag aag	973
Glu His Leu Gly Gly Gln Lys His Arg Lys Lys Glu Ala Ala Gln Lys	
288 293 298 303	
aca ggc gtg cag ccc aac ggg agc ccg cgc ggg gtg cag gcg cag ctg	1021
Thr Gly Val Gln Pro Asn Gly Ser Pro Arg Gly Val Gln Ala Gln Leu	
304 309 314 319	
cat tgc gac ctg tgc gcc gtg tcc tgc acc ggg gcg gac gcc tac gcg	1069
His Cys Asp Leu Cys Ala Val Ser Cys Thr Gly Ala Asp Ala Tyr Ala	
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gcc cac atc cgg gga tcc aag cac cag aag gtc ttc aag ctg cac gcc	1117
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Arg	Arg	Leu	Glu	Glu	Glu	Pro	Pro	Gln	Asp	Val	Pro	Pro	His	Ala	Pro	
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Pro	Asp	Trp	Ala	Gln	Pro	Leu	Leu	Met	Gly	Arg	Pro	Glu	Ser	Pro	Ala	
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Leu Ala Val Gln Arg	Ala Val Ser His Ala	Glu Arg Ala Leu Lys	Leu	
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Val Pro Thr Leu Glu Arg Leu Arg Ala Ala Gln Lys Arg Arg Ala Gln	
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Gln Leu Lys Lys Trp Ala Gln Tyr Glu Gln Asp Leu Gln His Arg Lys	
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Cys Asn Glu Asp Gly Leu Thr Ala Leu His Gln Cys Cys Ile Asp Asn	
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Gly His Ile Asn Leu Val Lys Ile Leu Val Gln Tyr Gly Ala Asp Leu	
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Glu Pro Thr Leu Asp Val Ile Glu Thr Cys Met Ala Tyr Gln Gly Ile	
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Val Lys Asp Trp Asp Gly Trp Glu Pro Leu His Ala Ala Ala Phe Trp	
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Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala
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Tyr	Leu	Leu	Tyr	Ser	Leu	Ile	Phe	Val	Asn	Ser	Tyr	Pro	Val	Thr	Met	
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Gly Ser Ala Ser Ala Ser Gly Ala Gln Arg Gly Ser Leu Glu Glu Tyr	
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Glu Asp Thr Pro Trp Ser Asp Gln Arg Pro Arg Glu Gly Glu Gly Glu	
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Glu Pro Arg Arg Thr Val Ser Glu Ser Val Ile Ala Val Lys Ala Ser	
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Phe Pro Ser Ser Ala Leu Pro Pro Arg Thr Gly Val Ala Leu Gly Arg	
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Lys Leu Gly Ser His Ser Val Ala Ser Cys Ala Pro Gln Leu Leu Gly	
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Asp Arg Arg Val Asp Ala Gly His Thr Asp Gln Pro Val Pro Ser Gly	
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Ser Val Gly Gly Pro Ala Arg Pro Ala Ser Gly Pro Arg Gln Ala Arg	
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Glu Ala Ser Leu Val Val Thr Cys Arg Thr Asn Lys Phe Arg Lys Asn	
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Asn Tyr Lys Trp Val Ala Ala Ser Ser Lys Ser Pro Arg Val Ala Arg	
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Arg Ala Leu Ser Pro Arg Val Ala Ala Glu Asn Val Cys Lys Ala Ser	
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Ala Gly Met Ala Asn Lys Val Glu Lys Pro Gln Leu Ile Ala Asp Pro	
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Pro Ser Lys Tyr Lys Trp Lys Ala Ser Ser Pro Ser Ala Ser Ser	
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Gln Leu Ser Pro Val Leu Ser Arg Ser Pro Ser Gly Asp Arg Pro Ala	
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Val Gly His Ser Gly Leu Lys Pro Leu Ser Gly Glu Thr Pro Leu Ser	
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Ala Tyr Lys Val Lys Ser Arg Thr Lys Ile Ile Arg Arg Arg Gly Ser	
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Lys	Val	Ile	Lys	Thr	Arg	Tyr	Arg	Ile	Val	Lys	Lys	Thr	Pro	Ala	Ser	
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Ser	Leu	Ala	Ser	Arg	Ala	Val	Gln	Arg	Ser	Leu	Ala	Ile	Ile	Arg	Gln	
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Cys	Pro	Tyr	Ser	His	Val	Tyr	Val	Ser	Arg	Lys	Ala	Glu	Val	Cys	Ser	

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His Thr Leu Leu Cys Pro Asp Phe Ala Arg Arg Gly Ala Cys Pro Arg				
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Gly Ala Gln Cys Gln Leu Leu His Arg Thr Gln Lys Arg His Ser Arg				
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Arg Ala Ala Thr Ser Pro Ala Pro Gly Pro Ser Asp Ala Thr Ala Arg				
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Arg Pro Thr Arg Gln Thr Pro Ser Ser Ala Ala Leu Thr Ala Ala Ala				
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Val Ala Ala Pro Pro His Cys Pro Gly Gly Ser Ala Ser Pro Ser Ser				
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Ser Lys Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Pro Ala Ser				
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Cys Ser Asn Arg Leu Cys Lys Leu Pro Ser Phe Ile Ser Leu Gln Ser				
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Leu Thr Lys Asp Ser Gly Lys Pro Leu His Ile Lys Pro Arg Leu *				
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Ser	Thr	Glu	Pro	Gly	Glu	Pro	Pro	Cys	Ile	Thr	Ser	Ala	Gly	Phe	Gln		
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Phe	Leu	Leu	Leu	Asp	Thr	Pro	Ala	Gln	Leu	Trp	Tyr	Phe	Met	Leu	Gln		
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Tyr	Leu	Gln	Thr	Ala	Gln	Ser	Arg	Gly	Met	Asp	Leu	Val	Glu	Ile	Leu		
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Gln Ile Ile His Phe Leu Arg Thr Arg Ala His Pro Val Met Leu Lys				
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Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile Arg Leu Trp				
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Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val Leu Tyr Asn				
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Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala His Ala Arg				
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Ala Arg Leu Leu Pro Val Ala His Gln Arg Phe Ser Thr Ala Ser Ala
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Cys Leu Thr Val Val Gln Arg Leu Met Glu Arg Ile Gln Leu Pro Trp
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Asp Ser Val Gly Arg Leu Glu Val Gly Thr Glu Thr Ile Ile Asp Lys
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aat act gat att gag ggc ata gat acc acc aat gcc tgc tac ggt ggt      591

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Ser Gly Asn Ala Arg Pro Thr Gly Gly Ala Gly Ala Val Ala Met Leu	
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Ile Gly Pro Lys Ala Pro Leu Ala Leu Glu Arg Gly Leu Arg Gly Thr	
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His Met Glu Asn Val Tyr Asp Phe Tyr Lys Pro Asn Leu Ala Ser Glu	
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Tyr Pro Ile Val Asp Gly Lys Leu Ser Ile Gln Cys Tyr Leu Arg Ala	
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Arg Pro Val *				
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Pro Thr Glu Val Pro Gln Ser His Pro Gly Pro Ser Ala Leu Leu Leu	
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Pro Gly Arg Pro Pro Leu Arg Leu Glu Asp Phe Leu Gly Arg Thr Leu	
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Val Gln Gly Arg Ala Arg Arg Glu Ile Leu Ser Pro Leu Arg Phe Glu				
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Lys Asp Gln His Ile Arg Asp Val Ala Ala Ile Val Gly Glu Ser Met				
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Met Glu Asp Gly Pro His Pro Gly Leu Tyr Pro Leu Thr Gln Pro Val				
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Arg Ala Tyr Gly Ile	Leu Met Ala Thr Thr	Ser Arg Asp Ser Ala	Asp	
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acc ctc cgc ctg gag	cta gac gca gga cgt	gtg aaa ctg acg gtc	aat	2103
Thr Leu Arg Leu Glu	Leu Asp Ala Gly Arg	Val Lys Leu Thr Val	Asn	
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cta gat tgt atc agg	att aac tgt aat tcc	agc aaa ggt ccc gag	act	2151
Leu Asp Cys Ile Arg	Ile Asn Cys Asn Ser	Ser Lys Gly Pro Glu	Thr	
632	637	642	647	
ctt ttt gct ggc tat	aac ctc aat gat aac	gag tgg cac aca gtg	cgt	2199
Leu Phe Ala Gly Tyr	Asn Leu Asn Asp Asn	Glu Trp His Thr Val	Arg	
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gta gtt cgg cgt gga	aaa agt tta aag tta	aca gtg cat gac caa	cag	2247
Val Val Arg Arg Gly	Lys Ser Leu Lys Leu	Thr Val His Asp Gln	Gln	
664	669	674	679	
gcc atg aca ggt caa	atg gca ggt gat cat	act agg ctg gag ttc	cat	2295
Ala Met Thr Gly Gln	Met Ala Gly Asp His	Thr Arg Leu Glu Phe	His	
680	685	690	695	
aac ata gag act ggc	atc atc aca gaa cga	cgg tat ctt tct tct	gtc	2343
Asn Ile Glu Thr Gly	Ile Ile Thr Glu Arg	Arg Tyr Leu Ser Ser	Val	
696	701	706	711	
ccc tcc aac ttc att	gga cac ctg cag agc	ttg aca ttt aat gga	atg	2391
Pro Ser Asn Phe Ile	Gly His Leu Gln Ser	Leu Thr Phe Asn Gly	Met	
712	717	722	727	
gca tac att gac ctg	tgt aaa aat ggc gac	ata gat tac tgt gag	ctt	2439
Ala Tyr Ile Asp Leu	Cys Lys Asn Gly Asp	Ile Asp Tyr Cys Glu	Leu	
728	733	738	743	

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Asn Ala Arg Phe Gly Phe Arg Asn Ile Ile Ala Asp Pro Val Thr Phe	
744 749 754 759	
aag acc aaa tcg agc tat gtt gcc tta gct acc ttg caa gcc tac act	2535
Lys Thr Lys Ser Ser Tyr Val Ala Leu Ala Thr Leu Gln Ala Tyr Thr	
760 765 770 775	
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Ser Met His Leu Phe Phe Gln Phe Lys Thr Thr Ser Leu Asp Gly Leu	
776 781 786 791	
att cta tat aac agt ggg gat gga aat gac ttt att gtg gtt gaa tta	2631
Ile Leu Tyr Asn Ser Gly Asp Gly Asn Asp Phe Ile Val Val Glu Leu	
792 797 802 807	
gtt aaa ggg tac tta cat tac gtg ttt gat ttg gga aat ggt gct aac	2679
Val Lys Gly Tyr Leu His Tyr Val Phe Asp Leu Gly Asn Gly Ala Asn	
808 813 818 823	
ctc atc aaa gga agc tca aat aaa cct ctc aat gac aat cag tgg cac	2727
Leu Ile Lys Gly Ser Ser Asn Lys Pro Leu Asn Asp Asn Gln Trp His	
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aac gtg atg ata tca agg gac acc agc aac ctc cac act gta aag att	2775
Asn Val Met Ile Ser Arg Asp Thr Ser Asn Leu His Thr Val Lys Ile	
840 845 850 855	
gac aca aaa atc aca acg caa atc acc gcc gga gcc agg aac tta gac	2823
Asp Thr Lys Ile Thr Thr Gln Ile Thr Ala Gly Ala Arg Asn Leu Asp	
856 861 866 871	
ctc aag agt gac tta tat ata gga gga gta gct aaa gaa aca tac aaa	2871
Leu Lys Ser Asp Leu Tyr Ile Gly Gly Val Ala Lys Glu Thr Tyr Lys	
872 877 882 887	
tcc tta cca aaa ctt gta cat gcc aaa gaa ggc ttt caa ggc tgc ctg	2919
Ser Leu Pro Lys Leu Val His Ala Lys Glu Gly Phe Gln Gly Cys Leu	
888 893 898 903	
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Ala Ser Val Asp Leu Asn Gly Arg Leu Pro Asp Leu Ile Ser Asp Ala	
904 909 914 919	
ctt ttc tgc aac gga cag atc gag aga gga tgt gaa ggg ccc agc aca	3015
Leu Phe Cys Asn Gly Gln Ile Glu Arg Gly Cys Glu Gly Pro Ser Thr	
920 925 930 935	
acc tgc caa gag gac tca tgt tcc aat caa ggt gtg tgc ttg caa caa	3063
Thr Cys Gln Glu Asp Ser Cys Ser Asn Gln Gly Val Cys Leu Gln Gln	
936 941 946 951	
tgg gat ggc ttc agc tgt gac tgt agt atg act tcc ttc agt gga cca	3111
Trp Asp Gly Phe Ser Cys Asp Cys Ser Met Thr Ser Phe Ser Gly Pro	
952 957 962 967	

ctc tgc aat gac cct ggg acg aca tat atc ttt agc aaa ggt ggt gga Leu Cys Asn Asp Pro Gly Thr Thr Tyr Ile Phe Ser Lys Gly Gly Gly 968 973 978 983	3159
caa atc acg tat aag tgg cct cct aat gac cga ccc agt acg cga gca Gln Ile Thr Tyr Lys Trp Pro Pro Asn Asp Arg Pro Ser Thr Arg Ala 984 989 994 999	3207
gac aga ctg gcc ata ggt ttt agc act gtt cag aaa gaa gct gta ttg Asp Arg Leu Ala Ile Gly Phe Ser Thr Val Gln Lys Glu Ala Val Leu 1000 1005 1010 1015	3255
gtg cga gtg gac agt tct tca ggc ttg ggt gac tac cta gaa ctg cat Val Arg Val Asp Ser Ser Ser Gly Leu Gly Asp Tyr Leu Glu Leu His 1016 1021 1026 1031	3303
ata cac cag gga aaa att gga gtt aag ttt aat gtt ggg aca gat gac Ile His Gln Gly Lys Ile Gly Val Lys Phe Asn Val Gly Thr Asp Asp 1032 1037 1042 1047	3351
atc gcc att gaa gaa tcc aat gca atc att aat gat ggg aaa tac cat Ile Ala Ile Glu Glu Ser Asn Ala Ile Ile Asn Asp Gly Lys Tyr His 1048 1053 1058 1063	3399
gta gtt cgt ttc acg agg agt ggt ggc aat gcc acg ttg cag gtg gac Val Val Arg Phe Thr Arg Ser Gly Gly Asn Ala Thr Leu Gln Val Asp 1064 1069 1074 1079	3447
agc tgg cca gtg atc gag cgc tac cct gca ggg cgt cag ctc aca atc Ser Trp Pro Val Ile Glu Arg Tyr Pro Ala Gly Arg Gln Leu Thr Ile 1080 1085 1090 1095	3495
ttc aat agc caa gca acc ata ata att ggc ggg aaa gag cag ggc cag Phe Asn Ser Gln Ala Thr Ile Ile Ile Gly Gly Lys Glu Gln Gly Gln 1096 1101 1106 1111	3543
ccc ttc cag ggc cag ctc tct ggg ctg tac tac aat ggc ttg aaa gtt Pro Phe Gln Gly Gln Leu Ser Gly Leu Tyr Tyr Asn Gly Leu Lys Val 1112 1117 1122 1127	3591
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gtg aga ctg gtt ggt gaa gtg cct tcc tct atg aca act gag tca aca Val Arg Leu Val Gly Glu Val Pro Ser Ser Met Thr Thr Glu Ser Thr 1144 1149 1154 1159	3687
gcc act gcc atg caa tca gag atg tcc aca tca att atg gag act acc Ala Thr Ala Met Gln Ser Glu Met Ser Thr Ser Ile Met Glu Thr Thr 1160 1165 1170 1175	3735
acg acc ctg gct act agc aca gcc aga aga gga aag ccc ccg aca aaa Thr Thr Leu Ala Thr Ser Thr Ala Arg Arg Gly Lys Pro Pro Thr Lys 1176 1181 1186 1191	3783
gaa ccc att agc cag acc aca gat gac atc ctt gtg gcc tca gca gag	3831

Glu Pro Ile Ser Gln Thr Thr Asp Asp Ile Leu Val Ala Ser Ala Glu	
1192	1197 1202 1207
tgt ccc agc gat gat gag gac att gac ccc tgt gag ccg agc tca ggt	3879
Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro Cys Glu Pro Ser Ser Gly	
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Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly Arg Glu Pro Tyr Pro Gly	
1224	1229 1234 1239
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Ser Ala Glu Val Ile Arg Glu Ser Ser Ser Thr Thr Gly Met Val Val	
1240	1245 1250 1255
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Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Tyr Ala	
1256	1261 1266 1271
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Met Tyr Lys Tyr Arg Asn Arg Asp Glu Gly Ser Tyr His Val Asp Glu	
1272	1277 1282 1287
agt cga aac tac atc agt aac tca gca cag tcc aat ggg gct gtt gta	4119
Ser Arg Asn Tyr Ile Ser Asn Ser Ala Gln Ser Asn Gly Ala Val Val	
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Lys Glu Lys Gln Pro Ser Ser Ala Lys Ser Ser Asn Lys Asn Lys Lys	
1304	1309 1314 1319
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Asn Lys Asp Lys Glu Tyr Tyr Val *	
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Met Pro Lys Arg Lys Pro Ser Glu Gly Ala Met Ser Asp Lys Val Lys	
1 5 10 15	
gct agt ttg agt tac aga gga gat cag cag gat tat ttt cta aac cta	154
Ala Ser Leu Ser Tyr Arg Gly Asp Gln Gln Asp Tyr Phe Leu Asn Leu	
17 22 27 32	
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Pro Leu Gln Asn Gln Arg Pro Gly Leu Arg Arg Thr Leu Gln Ile Arg	
33 38 43 48	
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Asp Arg Ser Cys Leu Lys *	
49 54	
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atctccctgg gccggaggcc actgtcttct ctctctctc caccgagtcg tgctctcgcc	180
ccaacccgcg cgccagacac tgccctaacc atc atg gag gtg gcc gag gtg gaa	234

Met Glu Val Ala Glu Val Glu
1 5

agt cct ctg aac ccc agc tgt aag ata atg acc ttc aga ccc tcc atg	282
Ser Pro Leu Asn Pro Ser Cys Lys Ile Met Thr Phe Arg Pro Ser Met	
8 13 18 23	
gag gag ttc cgg gag ttc aac aaa tac ctt gca tac atg gag tct aaa	330
Glu Glu Phe Arg Glu Phe Asn Lys Tyr Leu Ala Tyr Met Glu Ser Lys	
24 29 34 39	
gga gcc cat cgt gcg ggt ctt gca aag gtg att cct cct aag gag tgg	378
Gly Ala His Arg Ala Gly Leu Ala Lys Val Ile Pro Pro Lys Glu Trp	
40 45 50 55	
aag cca aga cag tgc tat gat gac att gat aat ttg ctc att cca gca	426
Lys Pro Arg Gln Cys Tyr Asp Asp Ile Asp Asn Leu Leu Ile Pro Ala	
56 61 66 71	
cca att cag cag atg gtc aca ggg cag tca gga ctg ttc act cag tac	474
Pro Ile Gln Gln Met Val Thr Gly Gln Ser Gly Leu Phe Thr Gln Tyr	
72 77 82 87	
aac atc cag aaa aaa gcg atg act gtg aag gag ttc agg cag ctg gcc	522
Asn Ile Gln Lys Lys Ala Met Thr Val Lys Glu Phe Arg Gln Leu Ala	
88 93 98 103	
aac agt ggc aaa tat tgt act cca aga tac ttg gat tac gaa gat ttg	570
Asn Ser Gly Lys Tyr Cys Thr Pro Arg Tyr Leu Asp Tyr Glu Asp Leu	
104 109 114 119	
gag cgc aag tac tgg aag aac tta act ttt gtg gca cct atc tat ggt	618
Glu Arg Lys Tyr Trp Lys Asn Leu Thr Phe Val Ala Pro Ile Tyr Gly	
120 125 130 135	
gca gat att aat ggg agc ata tat gat gag ggt gtg gat gaa tgg aac	666
Ala Asp Ile Asn Gly Ser Ile Tyr Asp Glu Gly Val Asp Glu Trp Asn	
136 141 146 151	
ata gct cgc ctc aat aca gtc ttg gat gtg gtt gaa gaa gag tgt ggc	714
Ile Ala Arg Leu Asn Thr Val Leu Asp Val Glu Glu Glu Cys Gly	
152 157 162 167	
att tct att gag ggt gta aat acc cca tat ctc tat ttt ggc atg tgg	762
Ile Ser Ile Glu Gly Val Asn Thr Pro Tyr Leu Tyr Phe Gly Met Trp	
168 173 178 183	
aag acc acg ttt gca tgg cac acc gaa gac atg gac ctc tat agc att	810
Lys Thr Thr Phe Ala Trp His Thr Glu Asp Met Asp Leu Tyr Ser Ile	
184 189 194 199	
aat tat ctc cac ttt gga gag ccc aag tct tgg tat gct ata cct ccg	858
Asn Tyr Leu His Phe Gly Glu Pro Lys Ser Trp Tyr Ala Ile Pro Pro	
200 205 210 215	
gag cat gga aaa cga ctt gaa aga cta gct caa ggt ttt ttc cca agc	906
Glu His Gly Lys Arg Leu Glu Arg Leu Ala Gln Gly Phe Phe Pro Ser	

216	221	226	231	
agc tcc caa ggg tgt gat gca ttt ctt cgc cac aag atg aca ttg att				954
Ser Ser Gln Gly Cys Asp Ala Phe Leu Arg His Lys Met Thr Leu Ile				
232	237	242	247	
tct cca tca gta ttg aag aaa tat ggt att ccc ttt gac aag ata acc				1002
Ser Pro Ser Val Leu Lys Lys Tyr Gly Ile Pro Phe Asp Lys Ile Thr				
248	253	258	263	
cag gag gct gga gaa ttc atg atc act ttc cca tat ggc tac cat gct				1050
Gln Glu Ala Gly Glu Phe Met Ile Thr Phe Pro Tyr Gly Tyr His Ala				
264	269	274	279	
ggc ttt aat cat ggt ttc aac tgt gca gaa tct aca aat ttt gct act				1098
Gly Phe Asn His Gly Phe Asn Cys Ala Glu Ser Thr Asn Phe Ala Thr				
280	285	290	295	
gtc aga tgg att gac tat gga aaa gtt gcc aaa ttg tgc act tgc agg				1146
Val Arg Trp Ile Asp Tyr Gly Lys Val Ala Lys Leu Cys Thr Cys Arg				
296	301	306	311	
aaa gac atg gtg aag att tca atg gat atc ttt gtg agg aaa ttt cag				1194
Lys Asp Met Val Lys Ile Ser Met Asp Ile Phe Val Arg Lys Phe Gln				
312	317	322	327	
cca gac aga tat cag ctt tgg aaa caa gga aag gat ata tac acc att				1242
Pro Asp Arg Tyr Gln Leu Trp Lys Gln Gly Lys Asp Ile Tyr Thr Ile				
328	333	338	343	
gat cac acg aag cct act cca gca tcc acc cct gaa gta aaa gca tgg				1290
Asp His Thr Lys Pro Thr Pro Ala Ser Thr Pro Glu Val Lys Ala Trp				
344	349	354	359	
ctg cag agg agg agg aaa gta aga aaa gca tcc cga agc ttc cag tgt				1338
Leu Gln Arg Arg Arg Lys Val Arg Lys Ala Ser Arg Ser Phe Gln Cys				
360	365	370	375	
gct agg tct acc tct aaa agg cct aag gct gat gag gaa gag gaa gtg				1386
Ala Arg Ser Thr Ser Lys Arg Pro Lys Ala Asp Glu Glu Glu Glu Val				
376	381	386	391	
tca gat gaa gtc gat ggg gca gag gtc cct aac ccc gac tca gtc aca				1434
Ser Asp Glu Val Asp Gly Ala Glu Val Pro Asn Pro Asp Ser Val Thr				
392	397	402	407	
gat gac ctc aag gtc agt gaa aag tca gaa gca gca gtg aag ctg agg				1482
Asp Asp Leu Lys Val Ser Glu Lys Ser Glu Ala Ala Val Lys Leu Arg				
408	413	418	423	
aac aca gaa gca tct tca gaa gaa gag tca tct gct agc agg atg cag				1530
Asn Thr Glu Ala Ser Ser Glu Glu Glu Ser Ser Ala Ser Arg Met Gln				
424	429	434	439	
gtg gag cag aat tta tca gat cat atc aaa ctc tca gga aac agc tgc				1578
Val Glu Gln Asn Leu Ser Asp His Ile Lys Leu Ser Gly Asn Ser Cys				
440	445	450	455	

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Leu Ser Thr Ser Val Thr Glu Asp Ile Lys Thr Glu Asp Asp Lys Ala	
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tat gca tat aga agt gta cct tct ata tcc agt gag gct gat gat tcc	1674
Tyr Ala Tyr Arg Ser Val Pro Ser Ile Ser Ser Glu Ala Asp Asp Ser	
472 477 482 487	
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Ile Pro Leu Ser Thr Gly Tyr Glu Lys Pro Glu Lys Ser Asp Pro Ser	
488 493 498 503	
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Glu Leu Ser Trp Pro Lys Ser Pro Glu Ser Cys Ser Ser Val Ala Glu	
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Ser Asn Gly Val Leu Thr Glu Gly Glu Glu Ser Asp Val Glu Ser His	
520 525 530 535	
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Gly Asn Gly Leu Glu Pro Gly Glu Ile Pro Ala Val Pro Ser Gly Glu	
536 541 546 551	
aga aat agc ttc aaa gtc ccc agt ata gca gag gga gag aac aaa acc	1914
Arg Asn Ser Phe Lys Val Pro Ser Ile Ala Glu Gly Glu Asn Lys Thr	
552 557 562 567	
tct aag agt tgg cgc cat cca ctt agc agg cct cca gca aga tct ccg	1962
Ser Lys Ser Trp Arg His Pro Leu Ser Arg Pro Pro Ala Arg Ser Pro	
568 573 578 583	
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gtt ctg tcc att gag gag gaa gtg gaa gaa aca gag tct tgg gcg aaa	2058
Val Leu Ser Ile Glu Glu Glu Val Glu Glu Thr Glu Ser Trp Ala Lys	
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Pro Leu Ile His Leu Trp Gln Thr Lys Ser Pro Asn Phe Ala Ala Glu	
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Cys Thr Leu Leu Met Pro Tyr His Lys Pro Asp Ser Ser Asn Glu Glu	
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Gln Ile Trp Ile Asp Lys Thr Val Ile Asn Asp His Ile Cys Leu Thr	
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<400> 203
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208		213		218		223	
att aat ggc tgg aaa gtt tat gat cca gta tct gaa tat aag aga cag							838
Ile Asn Gly Trp Lys Val Tyr Asp Pro Val Ser Glu Tyr Lys Arg Gln							
224		229		234		239	
ggc ttg cca aat gag agt tgg aaa ata tcc aaa ata aac agt aat tat							886
Gly Leu Pro Asn Glu Ser Trp Lys Ile Ser Lys Ile Asn Ser Asn Tyr							
240		245		250		255	
gag ttc tgt gac acc tac cct gcc atc att gtt gtg cca act agt gta							934
Glu Phe Cys Asp Thr Tyr Pro Ala Ile Ile Val Val Pro Thr Ser Val							
256		261		266		271	
aaa gat gat gac ctt tca aaa gtg gca gct ttt cga gca aaa ggc aga							982
Lys Asp Asp Asp Leu Ser Lys Val Ala Ala Phe Arg Ala Lys Gly Arg							
272		277		282		287	
gtc cct gtg ttg tca tgg att cat ccg gaa agt caa gca acg att acc							1030
Val Pro Val Leu Ser Trp Ile His Pro Glu Ser Gln Ala Thr Ile Thr							
288		293		298		303	
cgt tgc agc cag cca ctt gtg ggt ccc aat gat aag cgc tgc aaa gag							1078
Arg Cys Ser Gln Pro Leu Val Gly Pro Asn Asp Lys Arg Cys Lys Glu							
304		309		314		319	
gat gaa aaa tac ttg caa aca ata atg gat gct aac gca cag tca cac							1126
Asp Glu Lys Tyr Leu Gln Thr Ile Met Asp Ala Asn Ala Gln Ser His							
320		325		330		335	
aag ctt atc atc ttt gat gct cga caa aac agt gtc gct gat acc aac							1174
Lys Leu Ile Ile Phe Asp Ala Arg Gln Asn Ser Val Ala Asp Thr Asn							
336		341		346		351	
aag aca aag ggt gga gga tat gaa agt gaa agt gct tac cca aat gca							1222
Lys Thr Lys Gly Gly Gly Tyr Glu Ser Glu Ser Ala Tyr Pro Asn Ala							
352		357		362		367	
gaa ctt gtg ttc ttg gag atc cac aac att cat gtc atg cga gag tca							1270
Glu Leu Val Phe Leu Glu Ile His Asn Ile His Val Met Arg Glu Ser							
368		373		378		383	
cta cgc aaa tta aaa gag att gtg tac cct tcg atc gat gag gcg cgg							1318
Leu Arg Lys Leu Lys Glu Ile Val Tyr Pro Ser Ile Asp Glu Ala Arg							
384		389		394		399	
tgg ctc tcc aat gtg gat ggg acg cat tgg ctg gaa tat ata agg atg							1366
Trp Leu Ser Asn Val Asp Gly Thr His Trp Leu Glu Tyr Ile Arg Met							
400		405		410		415	
ctg ctt gct ggg gca gta aga att gct gat aaa ata gaa tct ggg aaa							1414
Leu Leu Ala Gly Ala Val Arg Ile Ala Asp Lys Ile Glu Ser Gly Lys							
416		421		426		431	
aca tct gtg gtg gtg cat tgc agc gac ggt tgg gac cga aca gcc cag							1462
Thr Ser Val Val Val His Cys Ser Asp Gly Trp Asp Arg Thr Ala Gln							
432		437		442		447	

ctc	aca	tct	ctg	gct	atg	cta	atg	ttg	gac	agt	tac	tac	agg	acc	att	1510
Leu	Thr	Ser	Leu	Ala	Met	Leu	Met	Leu	Asp	Ser	Tyr	Tyr	Arg	Thr	Ile	
448					453					458					463	
aaa	gga	ttt	gaa	act	ctc	gta	gaa	aag	gag	tgg	ata	agc	ttt	gga	cac	1558
Lys	Gly	Phe	Glu	Thr	Leu	Val	Glu	Lys	Glu	Trp	Ile	Ser	Phe	Gly	His	
464					469					474					479	
agg	ttt	gca	ctg	cga	gtg	ggc	cat	ggt	aat	gac	aac	cat	gcg	gat	gct	1606
Arg	Phe	Ala	Leu	Arg	Val	Gly	His	Gly	Asn	Asp	Asn	His	Ala	Asp	Ala	
480					485					490					495	
gac	cga	tct	ccc	ata	ttt	ctg	cag	ttt	gtt	gat	tgt	gtt	tgg	caa	atg	1654
Asp	Arg	Ser	Pro	Ile	Phe	Leu	Gln	Phe	Val	Asp	Cys	Val	Trp	Gln	Met	
496					501					506					511	
aca	agg	cag	ttt	cct	tca	gca	ttc	gag	ttt	aat	gag	cta	ttc	ttg	att	1702
Thr	Arg	Gln	Phe	Pro	Ser	Ala	Phe	Glu	Phe	Asn	Glu	Leu	Phe	Leu	Ile	
512					517					522					527	
aca	att	ttg	gat	cac	ctt	tat	agc	tgt	ctt	ttt	ggg	acc	ttt	ttg	tgc	1750
Thr	Ile	Leu	Asp	His	Leu	Tyr	Ser	Cys	Leu	Phe	Gly	Thr	Phe	Leu	Cys	
528					533					538					543	
aac	tgt	gaa	cag	cag	cga	ttc	aaa	gag	gat	gta	tat	aca	aag	acg	ata	1798
Asn	Cys	Glu	Gln	Gln	Arg	Phe	Lys	Glu	Asp	Val	Tyr	Thr	Lys	Thr	Ile	
544					549					554					559	
tct	tta	tgg	tcg	tat	atc	aat	agc	cag	cta	gac	gag	ttt	tct	aat	ccc	1846
Ser	Leu	Trp	Ser	Tyr	Ile	Asn	Ser	Gln	Leu	Asp	Glu	Phe	Ser	Asn	Pro	
560					565					570					575	
ttc	ttt	gtg	aat	tat	gaa	aac	cac	gtg	tta	tat	cct	gtt	gct	agt	ctg	1894
Phe	Phe	Val	Asn	Tyr	Glu	Asn	His	Val	Leu	Tyr	Pro	Val	Ala	Ser	Leu	
576					581					586					591	
agt	cat	ttg	gaa	ttg	tgg	gta	aat	tat	tat	gta	cga	tgg	aat	cca	cgg	1942
Ser	His	Leu	Glu	Leu	Trp	Val	Asn	Tyr	Tyr	Val	Arg	Trp	Asn	Pro	Arg	
592					597					602					607	
atg	aga	cct	cag	atg	ccc	att	cac	cag	aat	ctc	aag	gag	ctg	ctg	gcc	1990
Met	Arg	Pro	Gln	Met	Pro	Ile	His	Gln	Asn	Leu	Lys	Glu	Leu	Leu	Ala	
608					613					618					623	
gtc	agg	gcg	gag	ctg	cag	aag	cgt	gtg	gag	ggc	cta	cag	cgg	gag	gtg	2038
Val	Arg	Ala	Glu	Leu	Gln	Lys	Arg	Val	Glu	Gly	Leu	Gln	Arg	Glu	Val	
624					629					634					639	
gcc	acg	cgc	gcc	gtc	tca	tcc	tca	tct	gag	cgg	ggc	tcc	tcg	ccc	tcc	2086
Ala	Thr	Arg	Ala	Val	Ser	Ser	Ser	Ser	Glu	Arg	Gly	Ser	Ser	Pro	Ser	
640					645					650					655	
cac	tcc	gcc	acc	tcc	gtc	cac	acc	tcg	gtc	tga	tgggcgag	aaatatgtaa				2137
His	Ser	Ala	Thr	Ser	Val	His	Thr	Ser	Val	*						
656					661					666						

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ccccctggct gactaggact gttaaacata gtgtggactg gatgatgcct tcgacaaacc 2197
agagaagcca agttgggggg agctggtgcc tggagtgggc cctgtgcacc tcacctggcg 2257
gaggctgggg gggctctgtc agcaggaccc tagaggagac tctcattcga ttttaaagaa 2317
gcacaacggg tcattttcct ttgtatgttc ctagegcaga actgtttcta aaacaacttg 2377
aagtatagtt ttgttatcta agcaatTTTT gttttaagta agtaagtgtg ctagaatgcg 2437
aagccgttat gggttcagggt tttaaaaact ggtacagtat tgtatttgtc tcatctgttg 2497
cactgtatTT caatcatctg taattaaaat gatcatatgt ttgctccctg gtctttttta 2557
agtaagtaag taagtatcct agtagatTTT tcctttgagg aaaatcggta ataaaataac 2617
atggattgaa tgtttactgt gcgtcaagca cagttaatat atgatgatgt aaagtaacta 2677
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<210> 204
<211> 2411
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (463)..(1470)

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<220>
<221> misc_feature
<222> (1)...(2411)
<223> n = a,t,c or g

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<400> 204
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accggatgta agaaccaaaac actttcctgc ctcttaatgc aaccaaagaa agcttaggag 180
gcatcgTTTT ttgttttgat cgctgaatac tgaattcctg ccttcctccc tagttcacgt 240
tccttggggt aagttttgaa ttgtttgttt acagaccagc gtttggatct atgcaaacta 300
aaccctcag atactgatgc agttcgtggc cagatagtgg tcagtttaca gacacgagac 360
agaataggaa ccggcggctc ggtggtggac tgcagaggac tgtagaaaaa tgaaggaacg 420
gtgtatgaag actccgggcc tgggaggccg ctcagctgct tc atg gag gaa cca 474
Met Glu Glu Pro
1
gcc cct tac aca gat agc acc ggt gct gct gct gga gga ggg aat tgc 522

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Ala	Pro	Tyr	Thr	Asp	Ser	Thr	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Asn	Cys	
5					10					15					20	
agg	ttc	gtg	gag	tcc	cca	agt	caa	gat	caa	aga	ctt	cag	gca	cag	cgg	570
Arg	Phe	Val	Glu	Ser	Pro	Ser	Gln	Asp	Gln	Arg	Leu	Gln	Ala	Gln	Arg	
21					26					31					36	
ctt	cga	aac	cct	gat	gtg	cga	ggt	tca	cta	cag	acg	ccc	cag	aac	cga	618
Leu	Arg	Asn	Pro	Asp	Val	Arg	Gly	Ser	Leu	Gln	Thr	Pro	Gln	Asn	Arg	
37					42					47					52	
cca	cac	ggc	cac	cag	tcc	ccg	gaa	ctg	ccc	gaa	ggc	tac	gaa	caa	aga	666
Pro	His	Gly	His	Gln	Ser	Pro	Glu	Leu	Pro	Glu	Gly	Tyr	Glu	Gln	Arg	
53					58					63					68	
aca	aca	gtc	cag	ggc	caa	gtt	tac	ttt	ttg	cat	aca	cag	act	gga	gtt	714
Thr	Thr	Val	Gln	Gly	Gln	Val	Tyr	Phe	Leu	His	Thr	Gln	Thr	Gly	Val	
69					74					79					84	
agc	acg	tgg	cac	gac	ccc	agg	ata	cca	aga	gac	ctt	aac	agt	gtg	aac	762
Ser	Thr	Trp	His	Asp	Pro	Arg	Ile	Pro	Arg	Asp	Leu	Asn	Ser	Val	Asn	
85					90					95					100	
tgt	gat	gaa	ctt	gga	cca	ctg	ccg	cca	ggc	tgg	gaa	gtc	aga	agt	aca	810
Cys	Asp	Glu	Leu	Gly	Pro	Leu	Pro	Pro	Gly	Trp	Glu	Val	Arg	Ser	Thr	
101					106					111					116	
gtt	tct	ggg	agg	ata	tat	ttt	gta	gat	cat	aat	aac	cga	aca	acc	cag	858
Val	Ser	Gly	Arg	Ile	Tyr	Phe	Val	Asp	His	Asn	Asn	Arg	Thr	Thr	Gln	
117					122					127					132	
ttt	aca	gac	cca	agg	tta	cac	cac	atc	atg	aat	cac	cag	tgc	caa	ctc	906
Phe	Thr	Asp	Pro	Arg	Leu	His	His	Ile	Met	Asn	His	Gln	Cys	Gln	Leu	
133					138					143					148	
aag	gag	ccc	agc	cag	ccg	ctg	cca	ctg	ccc	agt	gag	ggc	tct	ctg	gag	954
Lys	Glu	Pro	Ser	Gln	Pro	Leu	Pro	Leu	Pro	Ser	Glu	Gly	Ser	Leu	Glu	
149					154					159					164	
gac	gag	gag	ctt	cct	gcc	cag	aga	tac	gaa	aga	gat	cta	gtc	cag	aag	1002
Asp	Glu	Glu	Leu	Pro	Ala	Gln	Arg	Tyr	Glu	Arg	Asp	Leu	Val	Gln	Lys	
165					170					175					180	
ctg	aaa	gtc	ctc	aga	cac	gaa	ctg	tcg	ctt	cag	cag	ccc	caa	gct	ggt	1050
Leu	Lys	Val	Leu	Arg	His	Glu	Leu	Ser	Leu	Gln	Gln	Pro	Gln	Ala	Gly	
181					186					191					196	
cat	tgc	cgc	atc	gaa	gtg	tcc	aga	gaa	gaa	atc	ttt	gag	gag	tct	tac	1098
His	Cys	Arg	Ile	Glu	Val	Ser	Arg	Glu	Glu	Ile	Phe	Glu	Glu	Ser	Tyr	
197					202					207					212	
cgc	cag	ata	atg	aag	atg	cga	ccg	aaa	gac	ttg	aaa	aaa	cgg	ctg	atg	1146
Arg	Gln	Ile	Met	Lys	Met	Arg	Pro	Lys	Asp	Leu	Lys	Lys	Arg	Leu	Met	
213					218					223					228	
gtg	aaa	ttc	cgt	ggg	gaa	gaa	ggt	ttg	gat	tac	ggt	ggt	gtg	gcc	agg	1194
Val	Lys	Phe	Arg	Gly	Glu	Glu	Gly	Leu	Asp	Tyr	Gly	Gly	Val	Ala	Arg	

229	234	239	244	
gag tgg ctt tac ttg ctg tgc cat gaa atg ctg aat cct tat tac ggg				1242
Glu Trp Leu Tyr Leu Leu Cys His Glu Met Leu Asn Pro Tyr Tyr Gly				
245	250	255	260	
ctc ttc cag tat tct acg gac aat att tac atg ttg caa ata aat ccg				1290
Leu Phe Gln Tyr Ser Thr Asp Asn Ile Tyr Met Leu Gln Ile Asn Pro				
261	266	271	276	
gat tct tca atc aac ccc gac cac ttg tct tat ttc cac ttt gtg ggg				1338
Asp Ser Ser Ile Asn Pro Asp His Leu Ser Tyr Phe His Phe Val Gly				
277	282	287	292	
cgg atc atg ggg ctg ggc tgt gtt cca tgg aca cta cat caa cgg ggg				1386
Arg Ile Met Gly Leu Gly Cys Val Pro Trp Thr Leu His Gln Arg Gly				
293	298	303	308	
ctt cac agt gcc ctt cta caa gca gct gct ggg gaa gcc cat cca gct				1434
Leu His Ser Ala Leu Leu Gln Ala Ala Ala Gly Glu Ala His Pro Ala				
309	314	319	324	
ctc aga tct gga atc tgt gga ccc aga gct gca taa gaggc ttggtgtgga				1484
Leu Arg Ser Gly Ile Cys Gly Pro Arg Ala Ala *				
325	330	335		
tcctagagaa cgacatcacg cctgtactgg accacacctt ctgcgtggaa cacaacgcct				1544
tcggggcggat cctgcagcat gaactgaaac ccaatgggca gaaatgtgcc agtcacagag				1604
gagaataaga aagaatacgt ccggttgtat gtaaactgga gggtttatgag aggaatcgaa				1664
gcccagttct tagctctgca gaaggggttc aatgagctca tccctcaaca tctgctgaag				1724
ccttttgacc agaaggaact ggagctgac ataggcggcc tggataaaat agacttgaac				1784
gactggaagt cgaacacgcg gctgaagcac tgtgtggccg acagcaacat cgtgcggtgg				1844
ttctggcaag cgggtggagac gttcgatgaa gaaaggaggg ccaggctcct gcagtttgtg				1904
actgggtcca cgcgagtccc gctccaaggc ttcaaggctt tgcaagggtc tacaggcgcg				1964
gcagggcccc ggctgttcac catccacctg atagacgcga acacagacaa ccttccgaag				2024
gcccatacct gctttaaccg gatcgacatt ccaccatatg agtcctatga gaagctctac				2084
gagaagctgc tgacagccgt ggaggagacc tgcgggtttg ctgtggagtg aaaagcaacc				2144
aaaggcaaca gagtctagct catggccacc agaccaaag catccagctt ctgtgcacct				2204
cctgcaaagc tggcagaggc cctggaattc cagatcacct gaggggaaag ggttgtctct				2264
ctcctttctg ttgggggagg gggatggggg acttttggtg gtggctcca cccatatatc				2324
cctcctttac catagtactc ccaccactt ccatcaccca tccaataaaa tgcagccagg				2384
tttagccttt ggctttggtc acacagg				2411

<210> 205
 <211> 6865
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (183)..(6386)

<400> 205

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agaagaggga aatccagaca gagagagcca acttaaccat tttgttcgac aagtatcttc      120
caacctgcct agacacactc agaaccaggt ttaagaagat cattcccatc ccagagcaga      180
gc  atg gtt cag atg gtg tgt cac ctt ctg gaa tgt ctc ctg acc acg      227
    Met Val Gln Met Val Cys His Leu Leu Glu Cys Leu Leu Thr Thr
      1             5             10

gag gac atc cct gca gac tgc cct aag gaa att tat gag cat tat ttt      275
Glu Asp Ile Pro Ala Asp Cys Pro Lys Glu Ile Tyr Glu His Tyr Phe
  16             21             26             31

gtg ttt gct gcc atc tgg gct ttc ggc gga gca atg gtc caa gat cag      323
Val Phe Ala Ala Ile Trp Ala Phe Gly Gly Ala Met Val Gln Asp Gln
  32             37             42             47

ctt gtg gac tac cgg gca gag ttc agc aaa tgg tgg ctg act gag ttc      371
Leu Val Asp Tyr Arg Ala Glu Phe Ser Lys Trp Trp Leu Thr Glu Phe
  48             53             58             63

aaa aca gtc aag ttt cct tcc caa gga acc atc ttt gac tat tac atc      419
Lys Thr Val Lys Phe Pro Ser Gln Gly Thr Ile Phe Asp Tyr Tyr Ile
  64             69             74             79

gac cca gag acc aag aaa ttc gag cct tgg tcc aag ctc gtc ccc cag      467
Asp Pro Glu Thr Lys Lys Phe Glu Pro Trp Ser Lys Leu Val Pro Gln
  80             85             90             95

ttc gaa ttt gac ccc gag atg ccc ttg cag gcg tgt ttg gtg cac acg      515
Phe Glu Phe Asp Pro Glu Met Pro Leu Gln Ala Cys Leu Val His Thr
  96             101            106            111

agt gag acc atc cgt gtg tgc tac ttc atg gag cgg ttg atg gcg cgg      563
Ser Glu Thr Ile Arg Val Cys Tyr Phe Met Glu Arg Leu Met Ala Arg
  112            117            122            127

cag cgg cct gtc atg ctg gtg ggc acg gct ggc act ggc aag tcg gtg      611
Gln Arg Pro Val Met Leu Val Gly Thr Ala Gly Thr Gly Lys Ser Val
  128            133            138            143

ctg gtg gga gct aag ctg gcc agc ctt gac ccc gag gca tac ctg gtg      659

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Leu Val Gly Ala Lys	Leu Ala Ser Leu Asp	Pro Glu Ala Tyr Leu Val	
144	149	154	159
aaa aac gtg cca ttc	aac tac tac acc acg	tca gca atg ctg cag gct	707
Lys Asn Val Pro Phe	Asn Tyr Tyr Thr Thr	Ser Ala Met Leu Gln Ala	
160	165	170	175
gtc ctg gag aag cct	ctg gaa aag aag gct	ggc aga aac tat ggc cct	755
Val Leu Glu Lys Pro	Leu Glu Lys Lys Ala	Gly Arg Asn Tyr Gly Pro	
176	181	186	191
cca ggg aac aag aaa	ctc atc tat ttc att	gat gac atg aac atg cct	803
Pro Gly Asn Lys Lys	Leu Ile Tyr Phe Ile	Asp Asp Met Asn Met Pro	
192	197	202	207
gag gtg gat gcc tac	ggg acg gtg cag ccc	cac acc atc atc cgg cag	851
Glu Val Asp Ala Tyr	Gly Thr Val Gln Pro	His Thr Ile Ile Arg Gln	
208	213	218	223
cat ctg gac tat ggc	cac tgg tat gat cgg	agc aag ctg tcc cta aag	899
His Leu Asp Tyr Gly	His Trp Tyr Asp Arg	Ser Lys Leu Ser Leu Lys	
224	229	234	239
gag atc aca aat gta	cag tat gtt tcc tgt	atg aac ccc acg gca ggc	947
Glu Ile Thr Asn Val	Gln Tyr Val Ser Cys	Met Asn Pro Thr Ala Gly	
240	245	250	255
agc ttc acc atc aac	ccc cgg ctt cag cgt	cac ttc agc gtg ttt gtc	995
Ser Phe Thr Ile Asn	Pro Arg Leu Gln Arg	His Phe Ser Val Phe Val	
256	261	266	271
ctc tcc ttc ccg ggg	gca gat gcc ctg tcc	tct atc tac agc atc atc	1043
Leu Ser Phe Pro Gly	Ala Asp Ala Leu Ser	Ser Ile Tyr Ser Ile Ile	
272	277	282	287
ctc act cag cat ctg	aag ctc gga aac ttc	ccg gcg tcc ctg cag aaa	1091
Leu Thr Gln His Leu	Lys Leu Gly Asn Phe	Pro Ala Ser Leu Gln Lys	
288	293	298	303
tcc atc ccc cca ctg	atc gat ctg gcc ctc	gcc ttc cac cag aaa att	1139
Ser Ile Pro Pro Leu	Ile Asp Leu Ala Leu	Ala Phe His Gln Lys Ile	
304	309	314	319
gct acc acc ttc cta	ccc aca gga atc aaa	ttc cac tac atc ttc aac	1187
Ala Thr Thr Phe Leu	Pro Thr Gly Ile Lys	Phe His Tyr Ile Phe Asn	
320	325	330	335
ctc aga gat ttt gcc	aac att ttc cag ggc	att ctc ttc tcc tca gtg	1235
Leu Arg Asp Phe Ala	Asn Ile Phe Gln Gly	Ile Leu Phe Ser Ser Val	
336	341	346	351
gaa tgt gtg aaa tcc	aca tgg gat ctt ata	agg ctc tat ctg cat gaa	1283
Glu Cys Val Lys Ser	Thr Trp Asp Leu Ile	Arg Leu Tyr Leu His Glu	
352	357	362	367
tca aat cga gtt tat	cgg gat aag atg gta	gaa gaa aag gac ttt gat	1331
Ser Asn Arg Val Tyr	Arg Asp Lys Met Val	Glu Glu Lys Asp Phe Asp	

368	373	378	383	
ctt ttt gat aaa atc cag aca gaa gtg ctc aag aaa act ttt gat gat				1379
Leu Phe Asp Lys Ile Gln Thr Glu Val Leu Lys Lys Thr Phe Asp Asp				
384	389	394	399	
att gaa gac cct gtg gag cag acc caa agc ccg aac ctg tat tgt cac				1427
Ile Glu Asp Pro Val Glu Gln Thr Gln Ser Pro Asn Leu Tyr Cys His				
400	405	410	415	
ttt gca aat ggt att ggg gag ccc aaa tac atg cct gta cag tct tgg				1475
Phe Ala Asn Gly Ile Gly Glu Pro Lys Tyr Met Pro Val Gln Ser Trp				
416	421	426	431	
gaa ctt ttg acc cag act ctg gtg gag gcc ttg gag aac cac aat gaa				1523
Glu Leu Leu Thr Gln Thr Leu Val Glu Ala Leu Glu Asn His Asn Glu				
432	437	442	447	
gtc aac aca gtg atg gac cta gtt ctc ttt gag gat gcc atg cgc cat				1571
Val Asn Thr Val Met Asp Leu Val Leu Phe Glu Asp Ala Met Arg His				
448	453	458	463	
gtc tgc cat atc aat cgc atc ttg gag tcc ccg cgg gga aat gct ctg				1619
Val Cys His Ile Asn Arg Ile Leu Glu Ser Pro Arg Gly Asn Ala Leu				
464	469	474	479	
ctg gtt ggt gta ggt ggg agc ggc aag cag agc ctg aca agg ctg gca				1667
Leu Val Gly Val Gly Gly Ser Gly Lys Gln Ser Leu Thr Arg Leu Ala				
480	485	490	495	
gct ttc atc agc tcc atg gat gtc ttc cag atc aca ctg cgc aaa ggc				1715
Ala Phe Ile Ser Ser Met Asp Val Phe Gln Ile Thr Leu Arg Lys Gly				
496	501	506	511	
tac cag atc cag gac ttc aag atg gac ctg gcc agc ctg tgt ctg aaa				1763
Tyr Gln Ile Gln Asp Phe Lys Met Asp Leu Ala Ser Leu Cys Leu Lys				
512	517	522	527	
gct gga gtg aag aat ctc aac aca gtg ttt ctc atg act gat gcc caa				1811
Ala Gly Val Lys Asn Leu Asn Thr Val Phe Leu Met Thr Asp Ala Gln				
528	533	538	543	
gtg gct gat gag agg ttc ctt gtg ctc atc aat gat ctt ttg gca tct				1859
Val Ala Asp Glu Arg Phe Leu Val Leu Ile Asn Asp Leu Leu Ala Ser				
544	549	554	559	
ggg gag atc cca gat ctc tac tct gat gat gaa gtt gaa aac atc ata				1907
Gly Glu Ile Pro Asp Leu Tyr Ser Asp Asp Glu Val Glu Asn Ile Ile				
560	565	570	575	
agc aat gtg agg aat gaa gtc aag agc cag ggt ctg gtt gac aac aga				1955
Ser Asn Val Arg Asn Glu Val Lys Ser Gln Gly Leu Val Asp Asn Arg				
576	581	586	591	
gag aac tgt tgg aag ttc ttt ata gat cgg atc cgg cga cag ctg aag				2003
Glu Asn Cys Trp Lys Phe Phe Ile Asp Arg Ile Arg Arg Gln Leu Lys				
592	597	602	607	

gtg act ctc tgt ttc tcc cct gtg gga aac aag cta aga gtc cgc agc	2051
Val Thr Leu Cys Phe Ser Pro Val Gly Asn Lys Leu Arg Val Arg Ser	
608 613 618 623	
agg aag ttc cca gcc att gtg aac tgc aca gcc atc cac tgg ttc cac	2099
Arg Lys Phe Pro Ala Ile Val Asn Cys Thr Ala Ile His Trp Phe His	
624 629 634 639	
gag tgg cct cag caa gca ttg gag tct gtc agc ctc cgc ttc ttg cag	2147
Glu Trp Pro Gln Gln Ala Leu Glu Ser Val Ser Leu Arg Phe Leu Gln	
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aac aca gag ggc att gag ccc aca gta aag cag tgc att agc aaa ttc	2195
Asn Thr Glu Gly Ile Glu Pro Thr Val Lys Gln Ser Ile Ser Lys Phe	
656 661 666 671	
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Met Ala Phe Val His Thr Ser Val Asn Gln Thr Ser Gln Ser Tyr Leu	
672 677 682 687	
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Ser Asn Glu Gln Arg Tyr Asn Tyr Thr Thr Pro Lys Ser Phe Leu Glu	
688 693 698 703	
ttc atc aga ctc tac cag agc ttg ttg cac agg cac aga aaa gag ctc	2339
Phe Ile Arg Leu Tyr Gln Ser Leu Leu His Arg His Arg Lys Glu Leu	
704 709 714 719	
aag tgc aag aca gag cgg ttg gag aac ggg ctg ctg aag ctg cat agc	2387
Lys Cys Lys Thr Glu Arg Leu Glu Asn Gly Leu Leu Lys Leu His Ser	
720 725 730 735	
acc tct gcc cag gtg gat gat ctg aaa gca aag ctg gct gcc cag gaa	2435
Thr Ser Ala Gln Val Asp Asp Leu Lys Ala Lys Leu Ala Ala Gln Glu	
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Val Glu Leu Lys Gln Lys Asn Glu Asp Ala Asp Lys Leu Ile Gln Val	
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768 773 778 783	
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Gln Lys Asp Cys Glu Glu Asp Leu Ala Lys Ala Glu Pro Ala Leu Thr	
800 805 810 815	
gca gcg cag gca gct ctc aac acc ctg aac aag acc aac ctg aca gag	2675
Ala Ala Gln Ala Ala Leu Asn Thr Leu Asn Lys Thr Asn Leu Thr Glu	
816 821 826 831	

ctg aag tca ttt ggc tct ccg cct ctg gcc gtc agc aat gtc agc gct	2723
Leu Lys Ser Phe Gly Ser Pro Pro Leu Ala Val Ser Asn Val Ser Ala	
832 837 842 847	
gcg gtg atg gta ctg atg gct ccc agg ggt agg gtg ccc aag gac cgg	2771
Ala Val Met Val Leu Met Ala Pro Arg Gly Arg Val Pro Lys Asp Arg	
848 853 858 863	
agc tgg aag gct gct aag gtc acc atg gcc aaa gtg gat ggc ttc ctg	2819
Ser Trp Lys Ala Ala Lys Val Thr Met Ala Lys Val Asp Gly Phe Leu	
864 869 874 879	
gac tcg cta ata aac ttc aac aaa gag aac att cac gag aac tgc ctc	2867
Asp Ser Leu Ile Asn Phe Asn Lys Glu Asn Ile His Glu Asn Cys Leu	
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Lys Ala Ile Arg Pro Tyr Leu Gln Asp Pro Glu Phe Asn Pro Glu Phe	
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gtg gcc acc aaa tcc tat gcg gct gca ggc ctc tgc tcc tgg gtc atc	2963
Val Ala Thr Lys Ser Tyr Ala Ala Ala Gly Leu Cys Ser Trp Val Ile	
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Asn Ile Val Arg Phe Tyr Glu Val Phe Cys Asp Val Glu Pro Lys Arg	
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Gln Ala Leu Asn Lys Ala Thr Ala Asp Leu Thr Ala Ala Gln Glu Lys	
944 949 954 959	
ctg gct gcc atc aaa gcc aag atc gct cac ctt aat gaa aac ctg gca	3107
Leu Ala Ala Ile Lys Ala Lys Ile Ala His Leu Asn Glu Asn Leu Ala	
960 965 970 975	
aag ctc aca gcc agg ttt gag aaa gca aca gca gac aaa ctc aaa tgt	3155
Lys Leu Thr Ala Arg Phe Glu Lys Ala Thr Ala Asp Lys Leu Lys Cys	
976 981 986 991	
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Gln Gln Glu Ala Glu Val Thr Ala Val Thr Ile Ser Leu Ala Asn Arg	
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Leu Val Gly Gly Leu Ala Ser Glu Asn Val Arg Trp Ala Asp Ala Val	
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Gln Asn Phe Lys Gln Gln Glu Arg Thr Leu Cys Gly Asp Ile Leu Leu	
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Ile Thr Ala Phe Ile Ser Tyr Leu Gly Phe Phe Thr Lys Lys Tyr Arg	
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Gln Ser Leu Leu Asp Arg Thr Trp Arg Pro Tyr Leu Ser Gln Leu Lys	
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Asp Asp Ala Asp Val Ala Ala Trp Gln Asn Glu Gly Leu Pro Ala Asp	
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Pro Asp Glu Ser Leu Arg Glu Arg Val Ala Asn Leu Ile Asp Ser Ile			
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ctc tcc ttc ccg ggg gca gat gcc ctg tcc tct atc tac agc atc atc	1043
Leu Ser Phe Pro Gly Ala Asp Ala Leu Ser Ser Ile Tyr Ser Ile Ile	
272 277 282 287	
ctc act cag cat ctg aag ctc gga aac ttc ccg gcg tcc ctg cag aaa	1091
Leu Thr Gln His Leu Lys Leu Gly Asn Phe Pro Ala Ser Leu Gln Lys	
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Ser Ile Pro Pro Leu Ile Asp Leu Ala Leu Ala Phe His Gln Lys Ile	
304 309 314 319	
gct acc acc ttc cta ccc aca gga atc aaa ttc cac tac atc ttc aac	1187
Ala Thr Thr Phe Leu Pro Thr Gly Ile Lys Phe His Tyr Ile Phe Asn	
320 325 330 335	
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Leu Arg Asp Phe Ala Asn Ile Phe Gln Gly Ile Leu Phe Ser Ser Val	
336 341 346 351	
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Glu Cys Val Lys Ser Thr Trp Asp Leu Ile Arg Leu Tyr Leu His Glu	
352 357 362 367	
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Ser Asn Arg Val Tyr Arg Asp Lys Met Val Glu Glu Lys Asp Phe Asp	
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Leu Phe Asp Lys Ile Gln Thr Glu Val Leu Lys Lys Thr Phe Asp Asp	
384 389 394 399	
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Ile Glu Asp Pro Val Glu Gln Thr Gln Ser Pro Asn Leu Tyr Cys His	
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Phe Ala Asn Gly Ile Gly Glu Pro Lys Tyr Met Pro Val Gln Ser Trp	
416 421 426 431	
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Glu Leu Leu Thr Gln Thr Leu Val Glu Ala Leu Glu Asn His Asn Glu	
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Val Asn Thr Val Met Asp Leu Val Leu Phe Glu Asp Ala Met Arg His	
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Val Cys His Ile Asn Arg Ile Leu Glu Ser Pro Arg Gly Asn Ala Leu	
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Tyr Gln Ile Gln Asp Phe Lys Met Asp Leu Ala Ser Leu Cys Leu Lys	
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Gly Glu Ile Pro Asp Leu Tyr Ser Asp Asp Glu Val Glu Asn Ile Ile	
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576 581 586 591	
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Val Thr Leu Cys Phe Ser Pro Val Gly Asn Lys Leu Arg Val Arg Ser	
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Arg Lys Phe Pro Ala Ile Val Asn Cys Thr Ala Ile His Trp Phe His	
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Asn Thr Glu Gly Ile Glu Pro Thr Val Lys Gln Ser Ile Ser Lys Phe	

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Val Glu Leu Lys Gln	Lys Asn Glu Asp Ala	Asp Lys Leu Ile Gln	Val	
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caa gat tca tta ggt ggc aac tgt aga acc act att gta att tgc tgc	1333
Gln Asp Ser Leu Gly Gly Asn Cys Arg Thr Thr Ile Val Ile Cys Cys	
287 292 297 302	
tct cca tca tca tac aat gag tct gaa aca aaa tct aca ctc tta ttt	1381
Ser Pro Ser Ser Tyr Asn Glu Ser Glu Thr Lys Ser Thr Leu Leu Phe	
303 308 313 318	
ggc caa agg gcc aaa aca att aag aac aca gtt tgt gtc aat gtg gag	1429
Gly Gln Arg Ala Lys Thr Ile Lys Asn Thr Val Cys Val Asn Val Glu	
319 324 329 334	
tta act gca gaa cag tgg aaa aag aag tat gaa aaa gaa aaa gaa aaa	1477
Leu Thr Ala Glu Gln Trp Lys Lys Lys Tyr Glu Lys Glu Lys Glu Lys	
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aat aag atc ctg cgg aac act att cag tgg ctt gaa aat gag ctc aac	1525
Asn Lys Ile Leu Arg Asn Thr Ile Gln Trp Leu Glu Asn Glu Leu Asn	
351 356 361 366	
aga tgg cgt aat ggg gag acg gtg cct att gat gaa cag ttt gac aaa	1573
Arg Trp Arg Asn Gly Glu Thr Val Pro Ile Asp Glu Gln Phe Asp Lys	
367 372 377 382	

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Glu Lys Ala Asn Leu Glu Ala Phe Thr Val Asp Lys Asp Ile Thr Leu	
383 388 393 398	
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Thr Asn Asp Lys Pro Ala Thr Ala Ile Gly Val Ile Gly Asn Phe Thr	
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Ser Ala Thr Leu Ala Ser Ile Asp Ala Glu Leu Gln Lys Leu Lys Glu	
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Met Thr Asn His Gln Lys Lys Arg Ala Ala Glu Met Met Ala Ser Leu	
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cta aaa gac ctt gca gaa ata gga att gct gtg gga aat aat gat gta	2149
Leu Lys Asp Leu Ala Glu Ile Gly Ile Ala Val Gly Asn Asn Asp Val	
559 564 569 574	
aag cag cct gag gga act ggc atg ata gat gaa gag ttc act gtt gca	2197
Lys Gln Pro Glu Gly Thr Gly Met Ile Asp Glu Glu Phe Thr Val Ala	
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Arg Leu Tyr Ile Ser Lys Met Lys Ser Glu Val Lys Thr Met Val Lys	
591 596 601 606	
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Arg Cys Lys Gln Leu Glu Ser Thr Gln Thr Glu Ser Asn Lys Lys Met	
607 612 617 622	
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Glu Glu Asn Glu Lys Glu Leu Ala Ala Cys Gln Leu Arg Ile Ser Gln	
623 628 633 638	
cat gaa gcc aaa atc aag tca ttg act gaa tac ctt caa aat gtg gaa	2389
His Glu Ala Lys Ile Lys Ser Leu Thr Glu Tyr Leu Gln Asn Val Glu	
639 644 649 654	
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Gln Lys Lys Arg Gln Leu Glu Glu Ser Val Asp Ala Leu Ser Glu Glu	
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cta gtc cag ctt cga gca caa gag aaa gtc cat gaa atg gaa aag gag	2485
Leu Val Gln Leu Arg Ala Gln Glu Lys Val His Glu Met Glu Lys Glu	
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His Leu Asn Lys Val Gln Thr Ala Asn Glu Val Lys Gln Ala Val Glu	
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Gln Gln Ile Gln Ser His Arg Glu Thr His Gln Lys Gln Ile Ser Ser	
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Leu Arg Asp Glu Val Glu Ala Lys Ala Lys Leu Ile Thr Asp Leu Gln	
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gac caa aac cag aaa atg atg tta gag cag gaa cgt cta aga gta gaa	2677
Asp Gln Asn Gln Lys Met Met Leu Glu Gln Glu Arg Leu Arg Val Glu	
735 740 745 750	
cat gag aag ttg aaa gcc aca gat cag gaa aag agc aga aaa cta cat	2725
His Glu Lys Leu Lys Ala Thr Asp Gln Glu Lys Ser Arg Lys Leu His	
751 756 761 766	
gaa ctt acg gtt atg caa gat aga cga gaa caa gca aga caa gac ttg	2773
Glu Leu Thr Val Met Gln Asp Arg Arg Glu Gln Ala Arg Gln Asp Leu	
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Lys Gly Leu Glu Glu Thr Val Ala Lys Glu Leu Gln Thr Leu His Asn	
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ctg cgc aaa ctc ttt gtt cag gac ctg gct aca aga gtt aaa aag agt	2869
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799 804 809 814	
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Cys Arg Gly Cys Val Asn Phe Glu Gly Ala Asp Arg Ile Glu Leu Leu				
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Ile Asp Ala Ala Arg Gln Leu Lys Arg Ser His Val Leu Pro Glu Gly				
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Arg Ser Pro Gly Pro Pro Ala Leu Lys His Pro Ala Thr Lys Asp Leu				
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gcg gcg gca gcc gca cag ggg ccc cag ctg ccg ccc ccg cag gcc cag				288
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Pro Gln Pro Ser Gly Thr Gly Gly Gly Val Ser Gly Gln Asp Arg Tyr				
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gac agg gcc aca tca tca ggc cgc ctc ccc ctg ccc tcg ccc gcc ctg				384
Asp Arg Ala Thr Ser Ser Gly Arg Leu Pro Leu Pro Ser Pro Ala Leu				
113	118	123	128	
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Glu Tyr Thr Leu Gly Ser Arg Leu Ala Asn Gly Leu Gly Arg Glu Glu				
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Arg Gly Leu Thr Leu Ala Pro Gly Leu Ser Pro Ala Arg Pro Leu Phe				
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Gly Ser Asp Phe Glu Lys Glu Lys Gln Gln Arg Asn Ala Asp Cys Leu				
193	198	203	208	
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Ala Glu Leu Asn Glu Ala Met Arg Gly Arg Ala Glu Glu Trp His Gly				
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Pro Phe Asn Val Arg Phe Lys Lys Asp His Gly Leu Val Gly Arg Val				
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Phe Ala Phe Asp Ala Thr Ala Arg Pro Pro Gly Tyr Glu Phe Glu Leu	
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Lys Leu Phe Thr Glu Tyr Pro Cys Gly Ser Gly Asn Val Tyr Ala Gly	
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Val Leu Ala Val Ala Arg Gln Met Phe His Asp Ala Leu Arg Glu Pro	
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Ala Gly Ala Glu Ala Val Ser Gly Gly Gly Ser Gly Thr Gly Ala Thr	
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Pro Gly Ala Pro Leu Cys Cys Thr Leu Cys Arg Glu Arg Leu Glu Asp	
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Met Pro Pro Gly Val Val Phe Lys Ala Pro Gly Tyr Leu	
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Lys Gln Val Phe Ala Asn Pro Ser Pro Thr Gln Lys Ser Pro Val Gln	
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Pro Val Glu Asp Leu Ala Gly Asn Leu Trp Glu Lys Leu Arg Glu Lys	
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Ile Arg Ser Phe Val Ala Tyr Ser Ile Ala Ile Asp Glu Ile Thr Asp	
174 179 184 189	
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His Leu Thr Arg Asn	Asn Leu Ala His Phe	Pro Thr Leu Lys Leu Val		
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Ser Arg Asn Glu Ser	Asp Gly Leu Asn Tyr	Ile Pro Lys Ile Ala Glu		
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ctc aag acc gaa ttc	cag aaa agg ctg tct	gat ttc aaa ctc tac gaa	1742	
Leu Lys Thr Glu Phe	Gln Lys Arg Leu Ser	Asp Phe Lys Leu Tyr Glu		
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agc gaa ctg act ctg	ttc agc tcc ccg ttc	tcc acg aag atc gac agt	1790	
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Val Leu Lys Thr Lys	Tyr Asp Lys Val Gly	Ile Pro Glu Phe Tyr Lys		
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Ser Pro Ser Ala Ser Ala Trp Pro Glu Glu Lys Asn Tyr His Gln Pro	
30 35 40 45	
gcc att ttg aat tca tgc gct ctt cgg caa att gca gaa ggc acc agt	194
Ala Ile Leu Asn Ser Ser Ala Leu Arg Gln Ile Ala Glu Gly Thr Ser	
46 51 56 61	
atc tct gaa atg tgg caa aat gac tta cag cca ttg ctg ata gag cga	242
Ile Ser Glu Met Trp Gln Asn Asp Leu Gln Pro Leu Leu Ile Glu Arg	
62 67 72 77	
tac ccg gga tcc cct gga agc tat gct gct cgt cag cac atc atg cag	290
Tyr Pro Gly Ser Pro Gly Ser Tyr Ala Ala Arg Gln His Ile Met Gln	
78 83 88 93	
cga att cag agg ctt cag gct gac tgg gtc ttg gaa ata gac acc ttc	338
Arg Ile Gln Arg Leu Gln Ala Asp Trp Val Leu Glu Ile Asp Thr Phe	
94 99 104 109	
ttg agt cag aca ccc tat ggg tac cgg tct ttc tca aat atc atc agc	386
Leu Ser Gln Thr Pro Tyr Gly Tyr Arg Ser Phe Ser Asn Ile Ile Ser	
110 115 120 125	
acc ctc aat ccc act gct aaa cga cat ttg gtc ctc gcc tgc cac tat	434
Thr Leu Asn Pro Thr Ala Lys Arg His Leu Val Leu Ala Cys His Tyr	
126 131 136 141	
gac tcc aag tat ttt tcc cac tgg aac aac aga gtg ttt gta gga gcc	482
Asp Ser Lys Tyr Phe Ser His Trp Asn Asn Arg Val Phe Val Gly Ala	
142 147 152 157	
act gat tca gcc gtg cca tgt gca atg atg ttg gaa ctt gct cgt gcc	530

Thr Asp Ser Ala Val Pro Cys Ala Met Met Leu Glu Leu Ala Arg Ala	
158 163 168 173	
tta gac aag aaa ctc ctt tcc tta aag act gtt tca gac tcc aag cca	578
Leu Asp Lys Lys Leu Leu Ser Leu Lys Thr Val Ser Asp Ser Lys Pro	
174 179 184 189	
gat ttg tca ctc cag ctg atc ttc ttt gat ggt gaa gag gct ttt ctt	626
Asp Leu Ser Leu Gln Leu Ile Phe Phe Asp Gly Glu Glu Ala Phe Leu	
190 195 200 205	
cac tgg tct cct caa gat tct ctc tat ggg tct cga cac tta gct gca	674
His Trp Ser Pro Gln Asp Ser Leu Tyr Gly Ser Arg His Leu Ala Ala	
206 211 216 221	
aag atg gca tcg acc ccg cac cca cct gga gcg aga ggc acc agc caa	722
Lys Met Ala Ser Thr Pro His Pro Pro Gly Ala Arg Gly Thr Ser Gln	
222 227 232 237	
ctg cat ggc atg gat tta ttg gtc tta ttg gat ttg att gga gct cca	770
Leu His Gly Met Asp Leu Leu Val Leu Leu Asp Leu Ile Gly Ala Pro	
238 243 248 253	
aac cca acg ttt ccc aat ttt ttt cca aac tca gcc agg tgg ttc gaa	818
Asn Pro Thr Phe Pro Asn Phe Phe Pro Asn Ser Ala Arg Trp Phe Glu	
254 259 264 269	
aga ctt caa gca att gaa cat gaa ctt cat gaa ttg ggt ttg ctc aag	866
Arg Leu Gln Ala Ile Glu His Glu Leu His Glu Leu Gly Leu Leu Lys	
270 275 280 285	
gat cac tct ttg gag ggg cgg tat ttc cag aat tac agt tat gga ggt	914
Asp His Ser Leu Glu Gly Arg Tyr Phe Gln Asn Tyr Ser Tyr Gly Gly	
286 291 296 301	
gtg att cag gat gac cat att cca ttt tta aga aga ggt gtt cca gtt	962
Val Ile Gln Asp Asp His Ile Pro Phe Leu Arg Arg Gly Val Pro Val	
302 307 312 317	
ctg cat ctg ata ccg tct cct ttc cct gaa gtc tgg cac acc atg gat	1010
Leu His Leu Ile Pro Ser Pro Phe Pro Glu Val Trp His Thr Met Asp	
318 323 328 333	
gac aat gaa gaa aat ttg gat gaa tca acc att gac aat cta aac aaa	1058
Asp Asn Glu Glu Asn Leu Asp Glu Ser Thr Ile Asp Asn Leu Asn Lys	
334 339 344 349	
atc cta caa gtc ttt gtg ttg gaa tat ctt cat ttg taa tactctgatt	1107
Ile Leu Gln Val Phe Val Leu Glu Tyr Leu His Leu *	
350 355 360	
tagtttagga taattggttc tagaattgaa ttcaaaagtc aaggcatcat ttaaaataat	1167
ctgatttcag acaaatgctg tgtggaaaca tctatcctat agatcatcct attcctatgt	1227
gtcttttggtt atcagatcaa ttacagaata attgtgttgt gatattgtgt cctaaattgc	1287

tcattaatTTT ttatttacag attgaaaaag aggcaccgtg taaagaaaat ggcaaaataa 1347
 atatctttcc aaggatcatc atcacgatag ctaaacagta cttaaatagc ggttgggaact 1407
 aggtagcctt tcgaatttta tgattttttc atatgtggaa atctattaca tgtaatacaa 1467
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<400> 211

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 1 5 10

cac ctg ctg ctg ctg gtg gcc gcc ctg ccc tgg gca tcc agg ggg gtc 98
 His Leu Leu Leu Leu Val Ala Ala Leu Pro Trp Ala Ser Arg Gly Val
 14 19 24 29

agt ccg agt gcc tca gcc tgg cca gag gag aag cac atc atg cag cga 146
 Ser Pro Ser Ala Ser Ala Trp Pro Glu Glu Lys His Ile Met Gln Arg
 30 35 40 45

att cag agg ctt cag gct gac tgg gtc ttg gaa ata gac acc ttc ttg 194
 Ile Gln Arg Leu Gln Ala Asp Trp Val Leu Glu Ile Asp Thr Phe Leu
 46 51 56 61

agt cag aca ccc tat ggg tac cgg tct ttc tca aat atc atc agc acc 242
 Ser Gln Thr Pro Tyr Gly Tyr Arg Ser Phe Ser Asn Ile Ile Ser Thr
 62 67 72 77

ctc aat ccc act gct aaa cga cat ttg gtc ctc gcc tgc cac tat gac 290
 Leu Asn Pro Thr Ala Lys Arg His Leu Val Leu Ala Cys His Tyr Asp
 78 83 88 93

tcc aag tat ttt tcc cac tgg aac aac aga gtg ttt gta gga gcc act 338
 Ser Lys Tyr Phe Ser His Trp Asn Asn Arg Val Phe Val Gly Ala Thr
 94 99 104 109

gat tca gcc gtg cca tgt gca atg atg ttg gaa ctt gct cgt gcc tta 386
 Asp Ser Ala Val Pro Cys Ala Met Met Leu Glu Leu Ala Arg Ala Leu
 110 115 120 125

gac aag aaa ctc ctt tcc tta aag act gtt tca gac tcc aag cca gat 434
 Asp Lys Lys Leu Leu Ser Leu Lys Thr Val Ser Asp Ser Lys Pro Asp

126	131	136	141	
ttg tca ctc cag ctg atc ttc ttt gat ggt gaa gag gct ttt ctt cac				482
Leu Ser Leu Gln Leu Ile Phe Phe Asp Gly Glu Glu Ala Phe Leu His				
142	147	152	157	
tggt tct cct caa gat tct ctc tat ggg tct cga cac tta gct gca aag				530
Trp Ser Pro Gln Asp Ser Leu Tyr Gly Ser Arg His Leu Ala Ala Lys				
158	163	168	173	
atg gca tgc acc ccg cac cca cct gga gcg aga ggc acc agc caa ctg				578
Met Ala Ser Thr Pro His Pro Pro Gly Ala Arg Gly Thr Ser Gln Leu				
174	179	184	189	
cat ggc atg gat tta ttg gtc tta ttg gat ttg att gga gct cca aac				626
His Gly Met Asp Leu Leu Val Leu Leu Asp Leu Ile Gly Ala Pro Asn				
190	195	200	205	
cca acg ttt ccc aat ttt ttt cca aac tca gcc agg tgg ttc gaa aga				674
Pro Thr Phe Pro Asn Phe Phe Pro Asn Ser Ala Arg Trp Phe Glu Arg				
206	211	216	221	
ctt caa gca att gaa cat gaa ctt cat gaa ttg ggt ttg ctc aag gat				722
Leu Gln Ala Ile Glu His Glu Leu His Glu Leu Gly Leu Leu Lys Asp				
222	227	232	237	
cac tct ttg gag ggg cgg tat ttc cag aat tac agt tat gga ggt gtg				770
His Ser Leu Glu Gly Arg Tyr Phe Gln Asn Tyr Ser Tyr Gly Gly Val				
238	243	248	253	
att cag gat gac cat att cca ttt tta aga aga ggt gtt cca gtt ctg				818
Ile Gln Asp Asp His Ile Pro Phe Leu Arg Arg Gly Val Pro Val Leu				
254	259	264	269	
cat ctg ata ccg tct cct ttc cct gaa gtc tgg cac acc atg gat gac				866
His Leu Ile Pro Ser Pro Phe Pro Glu Val Trp His Thr Met Asp Asp				
270	275	280	285	
aat gaa gaa aat ttg gat gaa tca acc att gac aat cta aac aaa atc				914
Asn Glu Glu Asn Leu Asp Glu Ser Thr Ile Asp Asn Leu Asn Lys Ile				
286	291	296	301	
cta caa gtc ttt gtg ttg gaa tat ctt cat ttg taa tact ctgatttagt				964
Leu Gln Val Phe Val Leu Glu Tyr Leu His Leu *				
302	307	312		
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tttcagacaa atgctgtgtg gaaacatcta tcctatagat catcctattc ttatgtgtct				1084
ttggttatca gatcaattac agaataattg tggtgtgata ttgtgtccta aattgctcat				1144
taatttttat ttacagattg aaaaagaggc accgtgtaaa gaaaatggca aaataaatat				1204
ctttccaagg atcatcatca cgatagctaa acagtactta aatagcggtt ggaactaggt				1264
agcctttoga attttatgat tttttcatat gtggaaatct attacatgta atacaaaaca				1324

aacatgtagt ttgaaggcgg tcagatttct ttgagaaatc tttgtagagt taattttatg 1384
gaaattaaaa tcagaattaa atgct 1409

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acc atg tcg agc aaa aga aca aag acc aag acc aag aag cgc cct cag 168
Met Ser Ser Lys Arg Thr Lys Thr Lys Thr Lys Lys Arg Pro Gln
1 5 10
cgt gca aca tcc aat gtg ttt gct atg ttt gac cag tca cag att cag 216
Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln
16 21 26 31
gag ttc aaa gag gcc ttc aac atg att gat cag aac aga gat ggt ttc 264
Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe
32 37 42 47
atc gac aag gaa gat ttg cat gat atg ctt gct tca ttg ggg aag aat 312
Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn
48 53 58 63
cca act gat gag tat cta gat gcc atg atg aat gag gct cca ggc ccc 360
Pro Thr Asp Glu Tyr Leu Asp Ala Met Met Asn Glu Ala Pro Gly Pro
64 69 74 79
atc aat ttc acc atg ttc ctc acc atg ttt ggt gag aag tta aat ggc 408
Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly
80 85 90 95
aca gat cct gaa gat gtc atc aga aat gcc ttt gct tgc ttt gat gaa 456
Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu
96 101 106 111
gaa gca act ggc acc ata cag gaa gat tac ttg aga gag ctg ctg aca 504
Glu Ala Thr Gly Thr Ile Gln Glu Asp Tyr Leu Arg Glu Leu Leu Thr
112 117 122 127
acc atg ggg gat cgg ttt aca gat gag gaa gtg gat gag ctg tac aga 552
Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Leu Tyr Arg
128 133 138 143

gaa gca cct att gat aaa aag ggg aat ttc aat tac atc gag ttc aca	600
Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Ile Glu Phe Thr	
144 149 154 159	
cgc atc ctg aaa cat gga gcc aaa gac aaa gat gac tga aataacttca	649
Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp *	
160 165 170	
aattccagcc aaacgttcct tgttgccact ttgggtattc tgagattttc tcttgcacgc	709
ccttagcttt acagcttttg catttcctgt tgtattttatt ctcagccatt ttgggcatat	769
gtatcttttat aatcagactg gaaacgggac tttctattaa tatcattttc agaataaaaa	829
atagggtaat ttaacctacc agcccttctc cccaataac tgtgggtctat acagagtcaa	889
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ctc tct acc tat cgg ctc cag agc cgc agt cgt cct tcc gcc cca gag	96
Leu Ser Thr Tyr Arg Leu Gln Ser Arg Ser Arg Pro Ser Ala Pro Glu	
17 22 27 32	
acc gat gat agt cga gtt ggg ggc att atg aga gga gag aaa aac tac	144
Thr Asp Asp Ser Arg Val Gly Gly Ile Met Arg Gly Glu Lys Asn Tyr	
33 38 43 48	
tac ttc cgt gga gct gcg ggg gac cac ggt tcc tgc ccc act aca act	192
Tyr Phe Arg Gly Ala Ala Gly Asp His Gly Ser Cys Pro Thr Thr Thr	
49 54 59 64	
tcg cct ctg gcc tcg gcc ctc ttg atg ccc tcg gag gca gtc tca agc	240
Ser Pro Leu Ala Ser Ala Leu Leu Met Pro Ser Glu Ala Val Ser Ser	
65 70 75 80	
agc tgg tct gag tct gga ggc ggt ttg tca ggg gga gat gaa gag gac	288
Ser Trp Ser Glu Ser Gly Gly Gly Leu Ser Gly Gly Asp Glu Glu Asp	
81 86 91 96	

act cgg ctc ctt caa ctc ctc cgc act gcc cgg gat cct tct gag gcc	336
Thr Arg Leu Leu Gln Leu Leu Arg Thr Ala Arg Asp Pro Ser Glu Ala	
97 102 107 112	
ttc cag gct ttg caa gct gct ttg ccg cgg cgg ggc ggt cga ctt ggc	384
Phe Gln Ala Leu Gln Ala Ala Leu Pro Arg Arg Gly Gly Arg Leu Gly	
113 118 123 128	
ttc ccc cga cgc aag gaa gct ttg tat cgg gca ctg ggc cga gtg ctt	432
Phe Pro Arg Arg Lys Glu Ala Leu Tyr Arg Ala Leu Gly Arg Val Leu	
129 134 139 144	
gtg gaa gga ggt agt gat gag aag cgg ctc tgc ttg caa ctt ctc tcg	480
Val Glu Gly Gly Ser Asp Glu Lys Arg Leu Cys Leu Gln Leu Leu Ser	
145 150 155 160	
gac gtt ctc cgg ggt cag ggg gag gca ggc cag ctt gaa gag gcc ttt	528
Asp Val Leu Arg Gly Gln Gly Glu Ala Gly Gln Leu Glu Glu Ala Phe	
161 166 171 176	
agc tta gca ctt ttg cct caa cta gtt gtc tcg tta cgg gaa gag aat	576
Ser Leu Ala Leu Leu Pro Gln Leu Val Val Ser Leu Arg Glu Glu Asn	
177 182 187 192	
cca gcc ctg cgg aaa gat gcg ctg cag atc ctt cat ata tgt ctg aaa	624
Pro Ala Leu Arg Lys Asp Ala Leu Gln Ile Leu His Ile Cys Leu Lys	
193 198 203 208	
cgt agt cct gga gag gtg ctg aga acg ctt ata caa caa gga ctg gaa	672
Arg Ser Pro Gly Glu Val Leu Arg Thr Leu Ile Gln Gln Gly Leu Glu	
209 214 219 224	
agt acc gat gcc cga ctt aga gct tcc aca gca cta ctg ctt ccc atc	720
Ser Thr Asp Ala Arg Leu Arg Ala Ser Thr Ala Leu Leu Leu Pro Ile	
225 230 235 240	
ttg ctt act act gag gac ttg ttg ctt ggt ctg gat ctc acc gag gtg	768
Leu Leu Thr Thr Glu Asp Leu Leu Leu Gly Leu Asp Leu Thr Glu Val	
241 246 251 256	
ata ata tcc cta gcc cga aag ctt ggt gat cag gag aca gaa gaa gaa	816
Ile Ile Ser Leu Ala Arg Lys Leu Gly Asp Gln Glu Thr Glu Glu Glu	
257 262 267 272	
tct gag aca gct ttc tcc gca ctt caa caa att ggg gag cga ctt ggc	864
Ser Glu Thr Ala Phe Ser Ala Leu Gln Gln Ile Gly Glu Arg Leu Gly	
273 278 283 288	
caa gac agg ttt caa tct tac att tct cgt ctg ccc tct gcc ctg agg	912
Gln Asp Arg Phe Gln Ser Tyr Ile Ser Arg Leu Pro Ser Ala Leu Arg	
289 294 299 304	
aga cac tac aat cgc cgc ctg gag tcc cag ttt gga agt cag gtt cct	960
Arg His Tyr Asn Arg Arg Leu Glu Ser Gln Phe Gly Ser Gln Val Pro	
305 310 315 320	

tat tat ttg gaa ctt gaa gcc tct gga ttt cct gaa gat ccc ctt ccc	1008
Tyr Tyr Leu Glu Leu Glu Ala Ser Gly Phe Pro Glu Asp Pro Leu Pro	
321 326 331 336	
tggt gca gtg act ctt tcc aac agc aat ctt aaa ttt ggg att att cct	1056
Cys Ala Val Thr Leu Ser Asn Ser Asn Leu Lys Phe Gly Ile Ile Pro	
337 342 347 352	
cag gag ctg cat tca cga tta ttg gat cag gaa gac tat aag aac cgg	1104
Gln Glu Leu His Ser Arg Leu Leu Asp Gln Glu Asp Tyr Lys Asn Arg	
353 358 363 368	
acc cag gcc gtc gaa gaa cta aag cag gtg ctg gga aaa ttt aac cct	1152
Thr Gln Ala Val Glu Glu Leu Lys Gln Val Leu Gly Lys Phe Asn Pro	
369 374 379 384	
agt tct act cct cat tct agt ctt gtt ggc ttc att agt ttg cta tat	1200
Ser Ser Thr Pro His Ser Ser Leu Val Gly Phe Ile Ser Leu Leu Tyr	
385 390 395 400	
aat ttg tta gac gat tct aac ttc aaa gtg gtg cat ggc aca ctt gaa	1248
Asn Leu Leu Asp Asp Ser Asn Phe Lys Val Val His Gly Thr Leu Glu	
401 406 411 416	
gtc ctg cat tta ctg gtt att cgc ctt gga gag cag gta cag cag ttc	1296
Val Leu His Leu Leu Val Ile Arg Leu Gly Glu Gln Val Gln Gln Phe	
417 422 427 432	
ttg gga cca gtt ata gca gct tct gtc aaa gtg ctg gcg gac aac aag	1344
Leu Gly Pro Val Ile Ala Ala Ser Val Lys Val Leu Ala Asp Asn Lys	
433 438 443 448	
ttg gtg atc aaa caa gaa tac atg aaa atc ttc ctc aag cta atg aag	1392
Leu Val Ile Lys Gln Glu Tyr Met Lys Ile Phe Leu Lys Leu Met Lys	
449 454 459 464	
gaa gta gga cct cag cag gtg ctt tgt tta ctc ctg gaa cat ctc aaa	1440
Glu Val Gly Pro Gln Gln Val Leu Cys Leu Leu Leu Glu His Leu Lys	
465 470 475 480	
cat aag cat tcc aga gtg aga gag gag gtg gtg aac att tgc atc tgc	1488
His Lys His Ser Arg Val Arg Glu Glu Val Val Asn Ile Cys Ile Cys	
481 486 491 496	
tcc ctg ctg acc tat cct agt gag gat ttt gac ttg ccc aaa ctg tcc	1536
Ser Leu Leu Thr Tyr Pro Ser Glu Asp Phe Asp Leu Pro Lys Leu Ser	
497 502 507 512	
ttt gat ctt gcc cca gct ctt gta gat agc aaa cgc agg gta cgc caa	1584
Phe Asp Leu Ala Pro Ala Leu Val Asp Ser Lys Arg Arg Val Arg Gln	
513 518 523 528	
gca gct tta gaa gct ttt gcc gta ttg gca tca tca atg ggc tca ggt	1632
Ala Ala Leu Glu Ala Phe Ala Val Leu Ala Ser Ser Met Gly Ser Gly	
529 534 539 544	
aaa acc agc atc ctt ttt aaa gct gtg gat aca gtt gaa ctg caa gat	1680

Lys Thr Ser Ile Leu Phe Lys Ala Val Asp Thr Val Glu Leu Gln Asp	
545 550 555 560	
aat gga gat gga gtg atg aat gct gtg cag gcc aga ttg gct agg aaa	1728
Asn Gly Asp Gly Val Met Asn Ala Val Gln Ala Arg Leu Ala Arg Lys	
561 566 571 576	
acc tta cca agg ctc aca gag cag gga ttt gtg gaa tat gca gta ctg	1776
Thr Leu Pro Arg Leu Thr Glu Gln Gly Phe Val Glu Tyr Ala Val Leu	
577 582 587 592	
atg cca tct tct gcc ggg ggt agg tca aac cat ttg gca cat gga gca	1824
Met Pro Ser Ser Ala Gly Gly Arg Ser Asn His Leu Ala His Gly Ala	
593 598 603 608	
gat acg gac tgg ctt ttg gct ggt aac aga act cag agt gca cac tgt	1872
Asp Thr Asp Trp Leu Leu Ala Gly Asn Arg Thr Gln Ser Ala His Cys	
609 614 619 624	
cac tgt ggt gac cac gtg agg gat agc atg cac att tat gga tct tac	1920
His Cys Gly Asp His Val Arg Asp Ser Met His Ile Tyr Gly Ser Tyr	
625 630 635 640	
agc cca act atc tgt acc cga agg gta tta agt gca gga aaa gga aaa	1968
Ser Pro Thr Ile Cys Thr Arg Arg Val Leu Ser Ala Gly Lys Gly Lys	
641 646 651 656	
aat aaa tta cca tgg gaa aat gag caa cct gga atc atg gga gaa aac	2016
Asn Lys Leu Pro Trp Glu Asn Glu Gln Pro Gly Ile Met Gly Glu Asn	
657 662 667 672	
cag acc tcc act tcc aag gat ata gag cag ttt tca aca tat gat ttc	2064
Gln Thr Ser Thr Ser Lys Asp Ile Glu Gln Phe Ser Thr Tyr Asp Phe	
673 678 683 688	
atc cca tct gca aaa tta aag ctt tct caa gga atg cca gtc aat gat	2112
Ile Pro Ser Ala Lys Leu Lys Leu Ser Gln Gly Met Pro Val Asn Asp	
689 694 699 704	
gat tta tgt ttt agc aga aaa aga gta tca aga aac tta ttt cag aat	2160
Asp Leu Cys Phe Ser Arg Lys Arg Val Ser Arg Asn Leu Phe Gln Asn	
705 710 715 720	
agt cgg gat ttt aac cca gat tgt ctt cct tta tgt gct gct ggt act	2208
Ser Arg Asp Phe Asn Pro Asp Cys Leu Pro Leu Cys Ala Ala Gly Thr	
721 726 731 736	
act ggg act cat caa aca aat ctt tct ggg aaa tgt gca caa ctt gga	2256
Thr Gly Thr His Gln Thr Asn Leu Ser Gly Lys Cys Ala Gln Leu Gly	
737 742 747 752	
ttt tca caa ata tgt ggt aaa act ggc agt gtg ggt tct gac tta caa	2304
Phe Ser Gln Ile Cys Gly Lys Thr Gly Ser Val Gly Ser Asp Leu Gln	
753 758 763 768	
ttc cta ggg aca act agc agt cat caa gaa aaa gtg tat gct agc ctc	2352
Phe Leu Gly Thr Thr Ser Ser His Gln Glu Lys Val Tyr Ala Ser Leu	

769	774	779	784	
aat ttt ggc agt aag aca cag caa aca ttt ggt agt caa aca gag tgt				2400
Asn Phe Gly Ser Lys Thr Gln Gln Thr Phe Gly Ser Gln Thr Glu Cys				
785	790	795	800	
act tcc tca aat ggt caa aat cca agt cca gga gct tac atc ctt cca				2448
Thr Ser Ser Asn Gly Gln Asn Pro Ser Pro Gly Ala Tyr Ile Leu Pro				
801	806	811	816	
tcc tat cct gtc tca tca cct cga act agt cca aag cat aca tct cct				2496
Ser Tyr Pro Val Ser Ser Pro Arg Thr Ser Pro Lys His Thr Ser Pro				
817	822	827	832	
ctt att ata tct cca aag aag tct caa gat aat tct gtt aat ttc tca				2544
Leu Ile Ile Ser Pro Lys Lys Ser Gln Asp Asn Ser Val Asn Phe Ser				
833	838	843	848	
aat tcc tgg cct ctt aaa agc ttc gaa gga cta tca aag cca agt cca				2592
Asn Ser Trp Pro Leu Lys Ser Phe Glu Gly Leu Ser Lys Pro Ser Pro				
849	854	859	864	
cag aag aag ctt gtc agc caa aaa tcg tct gat cct acg ggt aga aat				2640
Gln Lys Lys Leu Val Ser Gln Lys Ser Ser Asp Pro Thr Gly Arg Asn				
865	870	875	880	
cat gga gaa aat tct caa gaa aaa cct cca gtt cag ctt aca cct gcc				2688
His Gly Glu Asn Ser Gln Glu Lys Pro Pro Val Gln Leu Thr Pro Ala				
881	886	891	896	
ttg gtg aga tcg cca tct tcc cga cga ggt cta aat ggg aca aag cct				2736
Leu Val Arg Ser Pro Ser Ser Arg Arg Gly Leu Asn Gly Thr Lys Pro				
897	902	907	912	
gtt cct ccc ata cca agg gga ata agc ctt ttg cct gat aaa gct gat				2784
Val Pro Pro Ile Pro Arg Gly Ile Ser Leu Leu Pro Asp Lys Ala Asp				
913	918	923	928	
tta agc aca gtg gga cac aaa aag aaa gag cct gat gat att tgg aag				2832
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Arg Asn Ser Ala Ala Lys Lys Arg Ala Lys Leu Ser Gly Ser Thr Ser				
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Asp Leu Glu Ser Pro Asp Ser Ala Met Lys Leu Asp Leu Thr Met Asp				
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Gln Gly Lys Arg Ile Met Ser Asp Ile Phe Pro Thr Phe Gly Ser Lys	
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Pro Cys Pro Thr Arg Leu Ser Ser Ala Lys Lys Lys Ile Ser His Ile	
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Gln Asp Leu Val Val Gly Asn Ile Val Lys Ile Phe Asp Ala Phe Lys	
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Asp Met Thr Ile Leu Asn Glu Leu *				
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 aatatttagc catttaccta aaa atg gta ttt ttt aca tgc aat gca tgt 530
 Met Val Phe Phe Thr Cys Asn Ala Cys
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 Gly Glu Ser Val Lys Lys Ile Gln Val Glu Lys His Val Ser Val Cys
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 Arg Asn Cys Glu Cys Leu Ser Cys Ile Asp Cys Gly Lys Asp Phe Trp
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 Gly Asp Asp Tyr Lys Asn His Val Lys Cys Ile Ser Glu Asp Gln Lys
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 tat ggt ggc aaa ggc tat gaa ggt aaa acc cac aaa ggc gac atc aaa 722
 Tyr Gly Gly Lys Gly Tyr Glu Gly Lys Thr His Lys Gly Asp Ile Lys
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 Val Ser Pro Lys Val Arg Glu Leu Leu Glu Gln Ile Ser Ala Phe Asp
 90 95 100 105
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 Asn Val Pro Arg Lys Lys Ala Lys Phe Gln Asn Trp Met Lys Asn Ser
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 Pro Leu His Pro Val Ala Asn Pro His Ala Glu Ile Ser Thr Lys Val
 154 159 164 169
 cca gcc tcc aaa gtg aaa gac gcc gtg gaa cag caa ggg gag gtg aag 1058

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Gln	Lys	Pro	Lys	Lys	Arg	Lys	Lys	Gly	Gln	Glu	Ala	Asp	Leu	Glu	Ala	
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Lys	Lys	Lys	Lys	Gln	Arg	Lys	Asp	Ser	Ala	Ser	Glu	Glu	Glu	Ala	Arg	
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Val	Gly	Ala	Gly	Lys	Arg	Lys	Arg	Arg	His	Ser	Glu	Val	Glu	Thr	Asp	
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Ser	Lys	Lys	Lys	Lys	Met	Lys	Leu	Pro	Glu	His	Pro	Glu	Gly	Gly	Glu	
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Pro	Glu	Asp	Asp	Glu	Ala	Pro	Ala	Lys	Asp	Pro	Trp	Gln	Met	Leu	Leu	
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Ile	Lys	Cys	Ser	Ile	Tyr	Phe	Pro	Leu	Thr	Ala	Arg	Trp	Lys	Pro	Gln	
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Met Ser Asp Ser Gly Ala Ser Arg Leu Arg Arg Gln Leu Glu Ser Gly
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Gly Phe Glu Ala Arg Leu Tyr Val Lys Gln Leu Ser Gln Gln Ser Asp
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Gly Asp Arg Asp Leu Gln Glu His Arg Gln Arg Ile Gln Ala Leu Ala
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gag gag acg gcg cag aac ctg aag cgc aac gtc tac cag aac tac cgg      305
Glu Glu Thr Ala Gln Asn Leu Lys Arg Asn Val Tyr Gln Asn Tyr Arg
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cag ttc ata gag acg gcc cgc gag atc tcc tac ctg gag agc gag atg      353
Gln Phe Ile Glu Thr Ala Arg Glu Ile Ser Tyr Leu Glu Ser Glu Met
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tac cag ctc agc cat ttg ctg acc gag cag aaa agc agc ctg gag agc      401
Tyr Gln Leu Ser His Leu Leu Thr Glu Gln Lys Ser Ser Leu Glu Ser
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atc ccg ctt acg ttg ctg cct gcc gct gct gcc gcc gga gcc gcc gcc      449
Ile Pro Leu Thr Leu Leu Pro Ala Ala Ala Ala Ala Gly Ala Ala Ala
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gcc tct gga ggg gag gag gga gtc ggt ggg gcg ggg ggc cga gac cac      497
Ala Ser Gly Gly Glu Glu Gly Val Gly Gly Ala Gly Gly Arg Asp His
 117                      122                      127                      132

ctc cga ggc cag gcc ggc ttt ttc tcc acc ccc ggg ggt gcc tcc cgc      545
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 133                      138                      143                      148

gac ggc tcc ggt cca ggc gag gaa gga aag cag cgc act ctc acc acc      593
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ctg ctt gag aag gtg gaa ggc tgc agg cat ctg ctg gag acg ccg gga      641
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Met Ala Gln Leu Gln Arg Val His Gly Phe Leu Met Asn Asp Cys Leu				
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Leu Val Ala Thr Trp Leu Pro Gln Arg Arg Gly Met Tyr Arg Tyr Asn				
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Ala Leu Tyr Ser Leu Asp Gly Leu Ala Val Val Asn Val Lys Asp Asn				
229	234	239	244	
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357	362	367	372	
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Gln Leu Thr Glu Val Leu Val Phe Glu Leu Ser Pro Asp Arg Ser Leu				
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gcc gct gtt cat act gca att cgt cag ctt cgc atc gaa ggt gcc act	1457
Ala Ala Val His Thr Ala Ile Arg Gln Leu Arg Ile Glu Gly Ala Thr	
437 442 447 452	
tta ctc tat att cat aag ctg tgc cat gtc ttc ttt acc agc ctt ctc	1505
Leu Leu Tyr Ile His Lys Leu Cys His Val Phe Phe Thr Ser Leu Leu	
453 458 463 468	
gag act gca aga gaa ttt gag atc gat ttt gca ggc act gac agc ggc	1553
Glu Thr Ala Arg Glu Phe Glu Ile Asp Phe Ala Gly Thr Asp Ser Gly	
469 474 479 484	
tgc tac tct gcc ttt gtg gtc tgg gca aga tca gcc atg ggc atg ttc	1601
Cys Tyr Ser Ala Phe Val Val Trp Ala Arg Ser Ala Met Gly Met Phe	
485 490 495 500	
gtg gat gct ttt agc aag cag gtg ttt gat agt aag gag agc ctc tct	1649
Val Asp Ala Phe Ser Lys Gln Val Phe Asp Ser Lys Glu Ser Leu Ser	
501 506 511 516	
aca gca gct gag tgt gta aaa gtg gct aag gag cat tgc cag caa ctg	1697
Thr Ala Ala Glu Cys Val Lys Val Ala Lys Glu His Cys Gln Gln Leu	
517 522 527 532	
ggt gat atc gga ctg gat ctc acc ttc atc atc cat gcc ctt ctg gtg	1745
Gly Asp Ile Gly Leu Asp Leu Thr Phe Ile Ile His Ala Leu Leu Val	
533 538 543 548	
aaa gac atc caa ggg gcc ttg cac agt tac aaa gaa atc atc att gaa	1793
Lys Asp Ile Gln Gly Ala Leu His Ser Tyr Lys Glu Ile Ile Ile Glu	
549 554 559 564	
gcc act aaa cat cgc aac tct gaa gag atg tgg agg agg atg aac ttg	1841
Ala Thr Lys His Arg Asn Ser Glu Glu Met Trp Arg Arg Met Asn Leu	
565 570 575 580	
atg acg cca gaa gcc ctg ggt aag ctc aaa gaa gag atg aaa agt tgt	1889
Met Thr Pro Glu Ala Leu Gly Lys Leu Lys Glu Glu Met Lys Ser Cys	
581 586 591 596	
ggg gta agt aac ttt gag cag tac aca ggg gat gac tgc tgg gtg aac	1937
Gly Val Ser Asn Phe Glu Gln Tyr Thr Gly Asp Asp Cys Trp Val Asn	
597 602 607 612	
cta agt tac aca gtg gtt gct ttc acc aaa cag acc atg ggc ttc ttg	1985
Leu Ser Tyr Thr Val Val Ala Phe Thr Lys Gln Thr Met Gly Phe Leu	
613 618 623 628	

gaa gag gcc ctg aag ctg tat ttc cca gag ctg cac atg gta ctt ttg	2033
Glu Glu Ala Leu Lys Leu Tyr Phe Pro Glu Leu His Met Val Leu Leu	
629 634 639 644	
 gag agc ctg gtg gaa atc att ttg gtt gct gtt cag cat gtg gat tat	2081
Glu Ser Leu Val Glu Ile Ile Leu Val Ala Val Gln His Val Asp Tyr	
645 650 655 660	
 agt ctt cga tgt gag cag gat cca gag aag aaa gct ttt atc aga cag	2129
Ser Leu Arg Cys Glu Gln Asp Pro Glu Lys Lys Ala Phe Ile Arg Gln	
661 666 671 676	
 aat gca tcc ttt tta tat gaa aca gtc ctc cct gtg gtg gag aaa agg	2177
Asn Ala Ser Phe Leu Tyr Glu Thr Val Leu Pro Val Val Glu Lys Arg	
677 682 687 692	
 ttt gaa gaa ggt gtg ggg aaa cct gcc aag caa ctc caa gat ctg agg	2225
Phe Glu Glu Gly Val Gly Lys Pro Ala Lys Gln Leu Gln Asp Leu Arg	
693 698 703 708	
 aat gca tct aga ctt att cgt gtg aat cct gaa agt aca aca tca gtg	2273
Asn Ala Ser Arg Leu Ile Arg Val Asn Pro Glu Ser Thr Thr Ser Val	
709 714 719 724	
 gtc taa tgcttgggtc tgtttatatg tgtatatatg cagagagctt tatattattt	2329
Val *	
725	
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 cggcgac atg gag gac ggc gtg ctc aag gag ggc ttc ctg gtc aag agg	109
Met Glu Asp Gly Val Leu Lys Glu Gly Phe Leu Val Lys Arg	
1 5 10	
 ggc cac att gtc cac aac tgg aag gcg cga tgg ttc atc ctt cgg cag	157
Gly His Ile Val His Asn Trp Lys Ala Arg Trp Phe Ile Leu Arg Gln	
15 20 25 30	
 aac acg ctg gtg tac tac aag ctt gag ggg ggt cgg aga gtg acc cct	205
Asn Thr Leu Val Tyr Tyr Lys Leu Glu Gly Gly Arg Arg Val Thr Pro	

31	36	41	46	
ccc aag ggc cgg atc ctc ctg gat ggc tgc acc atc acc tgc ccc tgc				253
Pro Lys Gly Arg Ile Leu Leu Asp Gly Cys Thr Ile Thr Cys Pro Cys				
47	52	57	62	
ctg gag tat gaa aac cga ccg ctc ctc att aag ctg aag act caa aca				301
Leu Glu Tyr Glu Asn Arg Pro Leu Leu Ile Lys Leu Lys Thr Gln Thr				
63	68	73	78	
tcc acg gag tac ttc ctg gag gcc tgt tct cga gag gag cgg gat gcc				349
Ser Thr Glu Tyr Phe Leu Glu Ala Cys Ser Arg Glu Glu Arg Asp Ala				
79	84	89	94	
tgg gcc ttt gag atc acc ggg gct att cat gca ggg cag ccg ggg aag				397
Trp Ala Phe Glu Ile Thr Gly Ala Ile His Ala Gly Gln Pro Gly Lys				
95	100	105	110	
gtc cag cag ctg cac agc ctg aga aac tcc ttc aag ctg ccc ccg cac				445
Val Gln Gln Leu His Ser Leu Arg Asn Ser Phe Lys Leu Pro Pro His				
111	116	121	126	
atc agc ctg cat cgc att gtg gac aag atg cac gat agc aac acc gga				493
Ile Ser Leu His Arg Ile Val Asp Lys Met His Asp Ser Asn Thr Gly				
127	132	137	142	
atc cgt tca agc ccc aac atg gag cag gga agc acc tat aaa aag acc				541
Ile Arg Ser Ser Pro Asn Met Glu Gln Gly Ser Thr Tyr Lys Lys Thr				
143	148	153	158	
ttc ctc ggc tcc tcc ctg gtg gac tgg ctc atc tcc aac agc ttc acg				589
Phe Leu Gly Ser Ser Leu Val Asp Trp Leu Ile Ser Asn Ser Phe Thr				
159	164	169	174	
gcc agc cgt ctg gag gcg gtg acc ctg gcc tcc atg ctc atg gag gag				637
Ala Ser Arg Leu Glu Ala Val Thr Leu Ala Ser Met Leu Met Glu Glu				
175	180	185	190	
aac ttc ctc agg cct gtg ggt gtc cga agc atg gga gcc att cgc tct				685
Asn Phe Leu Arg Pro Val Gly Val Arg Ser Met Gly Ala Ile Arg Ser				
191	196	201	206	
ggg gat ctg gcc gag cag ttc ctg gat gac tcc aca gcc ctg tac act				733
Gly Asp Leu Ala Glu Gln Phe Leu Asp Asp Ser Thr Ala Leu Tyr Thr				
207	212	217	222	
ttt gct gag agc tac aaa aag aag ata agc ccc aag gaa gaa att agc				781
Phe Ala Glu Ser Tyr Lys Lys Lys Ile Ser Pro Lys Glu Glu Ile Ser				
223	228	233	238	
ctg agc act gtg gag tta agt ggc acg gtg gtg aaa caa ggc tac ctg				829
Leu Ser Thr Val Glu Leu Ser Gly Thr Val Val Lys Gln Gly Tyr Leu				
239	244	249	254	
gcc aag cag gga cac aag agg aaa aac tgg aag gtg cgt cgc ttt gtt				877
Ala Lys Gln Gly His Lys Arg Lys Asn Trp Lys Val Arg Arg Phe Val				
255	260	265	270	

cta agg aag gat cca gct ttc ctg cat tac tat gac cct tcc aaa gaa	925
Leu Arg Lys Asp Pro Ala Phe Leu His Tyr Tyr Asp Pro Ser Lys Glu	
271 276 281 286	
gag aac agg cca gtg ggt ggg ttt tct ctt cgt ggt tca ctc gtg tct	973
Glu Asn Arg Pro Val Gly Gly Phe Ser Leu Arg Gly Ser Leu Val Ser	
287 292 297 302	
gct ctg gaa gat aat ggc gtt ccc act ggg gtt aaa ggg aat gtc cag	1021
Ala Leu Glu Asp Asn Gly Val Pro Thr Gly Val Lys Gly Asn Val Gln	
303 308 313 318	
gga aac ctc ttc aaa gtg att act aag gat gac aca cac tat tac att	1069
Gly Asn Leu Phe Lys Val Ile Thr Lys Asp Asp Thr His Tyr Tyr Ile	
319 324 329 334	
cag gcc agc agc aag gct gag cga gcc gag tgg att gaa gct atc aaa	1117
Gln Ala Ser Ser Lys Ala Glu Arg Ala Glu Trp Ile Glu Ala Ile Lys	
335 340 345 350	
aag cta aca tga caa ggacctgagg gaaccaggat tcctccctcc taccagatga	1172
Lys Leu Thr *	
351	
cacagacaag agttcctgga gaatgggagt gttaagactt ttgacttctt tgtaagtttt	1232
gtactgcttt ggagagtga tgctgccaa agttcctcag attacaaaca gcagtgggtgc	1292
catttccttc cccatcttca tgttacaaac ctggaaaggc tagaacagcc attaggcgtc	1352
agcatcttga cttttcccca gcatcacaaa cagccatttc ctggggcacc aaagtagggt	1412
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atcaggtgag agacacctgt ccctgttcag ttcccatca gtaaa atg ggg aga	114
	Met Gly Arg
	1
aat tcc aag cac act tct cag agc aga gca gaa gag gtt gac tat gga	162

Asn	Ser	Lys	His	Thr	Ser	Gln	Ser	Arg	Ala	Glu	Glu	Val	Asp	Tyr	Gly	
4					9					14					19	
gag gag aat gaa gat ggg acc cag gtg agc ccg ggt gcc cac tac tgc																210
Glu	Glu	Asn	Glu	Asp	Gly	Thr	Gln	Val	Ser	Pro	Gly	Ala	His	Tyr	Cys	
20					25					30					35	
agc ccc act ggc gca ggc tgc ccc agg ccc tgt gca gac aca cca ggc																258
Ser	Pro	Thr	Gly	Ala	Gly	Cys	Pro	Arg	Pro	Cys	Ala	Asp	Thr	Pro	Gly	
36					41					46					51	
cct cag ccg cag ccc atg gac ctg cgg gtg ggc cag cgg ccc cca gtg																306
Pro	Gln	Pro	Gln	Pro	Met	Asp	Leu	Arg	Val	Gly	Gln	Arg	Pro	Pro	Val	
52					57					62					67	
gag ccc cca cca gag ccc aca ttg ctg gcc ctg cag cgt ccc cag cgc																354
Glu	Pro	Pro	Pro	Glu	Pro	Thr	Leu	Leu	Ala	Leu	Gln	Arg	Pro	Gln	Arg	
68					73					78					83	
ctg cac cac cac ctc ttc cta gca ggc ctg cag cag cag cgc tcg gtg																402
Leu	His	His	His	Leu	Phe	Leu	Ala	Gly	Leu	Gln	Gln	Gln	Arg	Ser	Val	
84					89					94					99	
gag ccc atg agg ctc tcc atg gac acg ccg atg ccc gag ttg cag gtg																450
Glu	Pro	Met	Arg	Leu	Ser	Met	Asp	Thr	Pro	Met	Pro	Glu	Leu	Gln	Val	
100					105					110					115	
gga ccc cag gaa caa gag ctg cgg cag ctt ctc cac aag gac aag agc																498
Gly	Pro	Gln	Glu	Gln	Glu	Leu	Arg	Gln	Leu	Leu	His	Lys	Asp	Lys	Ser	
116					121					126					131	
aag cga agt gct gta gcc agc agc gtg gtc aag cag aag cta gcg gag																546
Lys	Arg	Ser	Ala	Val	Ala	Ser	Ser	Val	Val	Lys	Gln	Lys	Leu	Ala	Glu	
132					137					142					147	
gtg att ctg aaa aaa cag cag gcg gcc cta gaa aga aca gtc cat ccc																594
Val	Ile	Leu	Lys	Lys	Gln	Gln	Ala	Ala	Leu	Glu	Arg	Thr	Val	His	Pro	
148					153					158					163	
aac agc ccc ggc att ccc tac aga acc ctg gag ccc ctg gag acg gaa																642
Asn	Ser	Pro	Gly	Ile	Pro	Tyr	Arg	Thr	Leu	Glu	Pro	Leu	Glu	Thr	Glu	
164					169					174					179	
gga gcc acc cgc tcc atg ctc agc agc ttt ttg cct cct gtt ccc agc																690
Gly	Ala	Thr	Arg	Ser	Met	Leu	Ser	Ser	Phe	Leu	Pro	Pro	Val	Pro	Ser	
180					185					190					195	
ctg ccc agt gac ccc cca gag cac ttc cct ctg cgc aag aca gtc tct																738
Leu	Pro	Ser	Asp	Pro	Pro	Glu	His	Phe	Pro	Leu	Arg	Lys	Thr	Val	Ser	
196					201					206					211	
gag ccc aac ctg aag ctg cgc tat aag ccc aag aag tcc ctg gag cgg																786
Glu	Pro	Asn	Leu	Lys	Leu	Arg	Tyr	Lys	Pro	Lys	Lys	Ser	Leu	Glu	Arg	
212					217					222					227	
agg aag aat cca ctg ctc cga aag gag agt gcg ccc ccc agc ctc cgg																834
Arg	Lys	Asn	Pro	Leu	Leu	Arg	Lys	Glu	Ser	Ala	Pro	Pro	Ser	Leu	Arg	

228	233	238	243	
cgg cgg ccc gca gag acc ctc gga gac tcc tcc cca agt agt agc agc				882
Arg Arg Pro Ala Glu Thr Leu Gly Asp Ser Ser Pro Ser Ser Ser Ser				
244	249	254	259	
acg ccc gca tca gga tgc agc tcc ccc aat gac agc gag cac ggc ccc				930
Thr Pro Ala Ser Gly Cys Ser Ser Pro Asn Asp Ser Glu His Gly Pro				
260	265	270	275	
aat ccc atc ctg ggc tgc gag gcg ctc ttg ggc cag cgg ctg cgg ctg				978
Asn Pro Ile Leu Gly Ser Glu Ala Leu Leu Gly Gln Arg Leu Arg Leu				
276	281	286	291	
cag gag act tct gtg gcc ccg ttc gcc ttg ccg aca gtg tcc ttg ctg				1026
Gln Glu Thr Ser Val Ala Pro Phe Ala Leu Pro Thr Val Ser Leu Leu				
292	297	302	307	
ccc gca atc act ctg ggg ctg ccc gcc cct gcc agg gct gac agt gac				1074
Pro Ala Ile Thr Leu Gly Leu Pro Ala Pro Ala Arg Ala Asp Ser Asp				
308	313	318	323	
cgc agg acc cat ccg act ctg ggc cct cgg ggg cca atc ctg ggg agc				1122
Arg Arg Thr His Pro Thr Leu Gly Pro Arg Gly Pro Ile Leu Gly Ser				
324	329	334	339	
ccc cac act ccc ctc ttc ctg ccc cat ggc ttg gag ccc gag gct ggg				1170
Pro His Thr Pro Leu Phe Leu Pro His Gly Leu Glu Pro Glu Ala Gly				
340	345	350	355	
ggc acc ttg ccc tct cgc ctg cag ccc att ctc ctc ctg gac ccc tca				1218
Gly Thr Leu Pro Ser Arg Leu Gln Pro Ile Leu Leu Leu Asp Pro Ser				
356	361	366	371	
ggc tct cat gcc ccg ctg ctg act gtg ccc ggg ctt ggg ccc ttg ccc				1266
Gly Ser His Ala Pro Leu Leu Thr Val Pro Gly Leu Gly Pro Leu Pro				
372	377	382	387	
ttc cac ttt gcc cag tcc tta atg acc acc gag cgg ctc tct ggg tca				1314
Phe His Phe Ala Gln Ser Leu Met Thr Thr Glu Arg Leu Ser Gly Ser				
388	393	398	403	
ggc ctc cac tgg cca ctg agc cgg act cgc tca gag ccc ctg ccc ccc				1362
Gly Leu His Trp Pro Leu Ser Arg Thr Arg Ser Glu Pro Leu Pro Pro				
404	409	414	419	
agt gcc acc gct ccc cca ccg ccg ggc ccc atg cag ccc cgc ctg gag				1410
Ser Ala Thr Ala Pro Pro Pro Pro Gly Pro Met Gln Pro Arg Leu Glu				
420	425	430	435	
cag ctc aaa act cac gtc cag gtg atc aag agg tca gcc aag ccg agt				1458
Gln Leu Lys Thr His Val Gln Val Ile Lys Arg Ser Ala Lys Pro Ser				
436	441	446	451	
gag aag ccc cgg ctg cgg cag ata ccc tcg gct gaa gac ctg gag aca				1506
Glu Lys Pro Arg Leu Arg Gln Ile Pro Ser Ala Glu Asp Leu Glu Thr				
452	457	462	467	

gat ggc ggg gga ccg ggc cag gtg gtg gac gat ggc ctg gag cac agg Asp Gly Gly Gly Pro Gly Gln Val Val Asp Asp Gly Leu Glu His Arg 468 473 478 483	1554
gag ctg ggc cat ggg cag cct gag gcc aga ggc ccc gct cct ctc cag Glu Leu Gly His Gly Gln Pro Glu Ala Arg Gly Pro Ala Pro Leu Gln 484 489 494 499	1602
cag cac cct cag gtg ttg ctc tgg gaa cag cag cga ctg gct ggg cgg Gln His Pro Gln Val Leu Leu Trp Glu Gln Gln Arg Leu Ala Gly Arg 500 505 510 515	1650
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ggt ggg cac cgg cct ctg tcc cgg gct cag tct tcc cca gcc gca cct Gly Gly His Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ala Pro 532 537 542 547	1746
gcc tca ctg tca gcc cca gag cct gcc agc cag gcc cga gtc ctc tcc Ala Ser Leu Ser Ala Pro Glu Pro Ala Ser Gln Ala Arg Val Leu Ser 548 553 558 563	1794
agc tca gag acc cct gcc agg acc ctg ccc ttc acc aca ggg ctg atc Ser Ser Glu Thr Pro Ala Arg Thr Leu Pro Phe Thr Thr Gly Leu Ile 564 569 574 579	1842
tat gac tcg gtc atg ctg aag cac cag tgc tcc tgc ggt gac aac agc Tyr Asp Ser Val Met Leu Lys His Gln Cys Ser Cys Gly Asp Asn Ser 580 585 590 595	1890
agg cac ccg gag cac gcc ggc cgc atc cag agc atc tgg tcc cgg ctg Arg His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg Leu 596 601 606 611	1938
cag gag cgg ggg ctc cgg agc cag tgt gag tgt ctc cga ggc cgg aag Gln Glu Arg Gly Leu Arg Ser Gln Cys Glu Cys Leu Arg Gly Arg Lys 612 617 622 627	1986
gcc tcc ctg gaa gag ctg cag tca gtc cac tct gag cgg cac gtg ctc Ala Ser Leu Glu Glu Leu Gln Ser Val His Ser Glu Arg His Val Leu 628 633 638 643	2034
ctc tac ggc acc aac ccg ctc agc cgc ctc aaa ctg gac aac ggg aag Leu Tyr Gly Thr Asn Pro Leu Ser Arg Leu Lys Leu Asp Asn Gly Lys 644 649 654 659	2082
ctg gca ggg ctc ctg gca cag cgg atg ttt gtg atg ctg ccc tgt ggt Leu Ala Gly Leu Leu Ala Gln Arg Met Phe Val Met Leu Pro Cys Gly 660 665 670 675	2130
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Asn Ala Ala Arg Trp Ala Ala Gly Ser Val Thr Asp Leu Ala Phe Lys	
692 697 702 707	
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Val Ala Ser Arg Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro	
708 713 718 723	
gga cac cat gca gat cat tca aca gcc atg ggc ttc tgc ttc ttc aac	2322
Gly His His Ala Asp His Ser Thr Ala Met Gly Phe Cys Phe Phe Asn	
724 729 734 739	
tca gtg gcc atc gcc tgc cgg cag ctg caa cag cag agc aag gcc agc	2370
Ser Val Ala Ile Ala Cys Arg Gln Leu Gln Gln Gln Ser Lys Ala Ser	
740 745 750 755	
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Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln	
756 761 766 771	
caa acc ttc tac caa gac ccc agt gtg ctc tac atc tcc ctg cat cgc	2466
Gln Thr Phe Tyr Gln Asp Pro Ser Val Leu Tyr Ile Ser Leu His Arg	
772 777 782 787	
cat gac gac ggc aac ttc ttc ccg ggg agt ggg gct gtg gat gag gta	2514
His Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Val Asp Glu Val	
788 793 798 803	
ggg gct ggc agc ggt gag ggc ttc aat gtc aat gtg gcc tgg gct gga	2562
Gly Ala Gly Ser Gly Glu Gly Phe Asn Val Asn Val Ala Trp Ala Gly	
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ggg ctg gac ccc ccc atg ggg gat cct gag tac ctg gct gct ttc agg	2610
Gly Leu Asp Pro Pro Met Gly Asp Pro Glu Tyr Leu Ala Ala Phe Arg	
820 825 830 835	
ata gtc gtg atg ccc atc gcc cga gag ttc tct cca gac cta gtc ctg	2658
Ile Val Val Met Pro Ile Ala Arg Glu Phe Ser Pro Asp Leu Val Leu	
836 841 846 851	
gtg tct gct gga ttt gat gct gct gag ggt cac ccg gcc cca ctg ggt	2706
Val Ser Ala Gly Phe Asp Ala Ala Glu Gly His Pro Ala Pro Leu Gly	
852 857 862 867	
ggc tac cat gtt tct gcc aaa tgt ttt gga tac atg acg cag caa ctg	2754
Gly Tyr His Val Ser Ala Lys Cys Phe Gly Tyr Met Thr Gln Gln Leu	
868 873 878 883	
atg aac ctg gca gga ggc gca gtg gtg ctg gcc ttg gag ggt ggc cat	2802
Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly Gly His	
884 889 894 899	
gac ctc aca gcc atc tgt gac gcc tct gag gcc tgt gtg gct gct ctt	2850
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala Ala Leu	
900 905 910 915	
ctg ggt aac agg gtg gat ccc ctt tca gaa gaa ggc tgg aaa cag aaa	2898

Leu Gly Asn Arg Val Asp Pro Leu Ser Glu Glu Gly Trp Lys Gln Lys	
916 921 926 931	
ccc aac ctc aat gcc atc cgc tct ctg gag gcc gtg atc cgg gtg cac	2946
Pro Asn Leu Asn Ala Ile Arg Ser Leu Glu Ala Val Ile Arg Val His	
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agt aaa tac tgg ggc tgc atg cag cgc ctg gcc tcc tgt cca gac tcc	2994
Ser Lys Tyr Trp Gly Cys Met Gln Arg Leu Ala Ser Cys Pro Asp Ser	
948 953 958 963	
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Trp Val Pro Arg Val Pro Gly Ala Asp Lys Glu Glu Val Glu Ala Val	
964 969 974 979	
acc gca ctg gcg tcc ctc tct gtg ggc atc ctg gct gaa gat agg ccc	3090
Thr Ala Leu Ala Ser Leu Ser Val Gly Ile Leu Ala Glu Asp Arg Pro	
980 985 990 995	
tcg gag cag ctg gtg gag gag gaa gaa cct atg aat ctc taa ggctctg	3139
Ser Glu Gln Leu Val Glu Glu Glu Glu Pro Met Asn Leu *	
996 1001 1006	
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tggggcctcc ccaccatag ctctgattcc caccacacat aggaatagcc tgactgaggg	3979
ggaaggggtg ggagagaaga tacagacatg gaggagggga ggctgctctg gcaaagtctt	4039
caaggctttt ggggggtccag gcctggggtc aagaaggaaa atgtgtgtga gcatgtgtgt	4099
gagtgaggcg tgtgtgtgag tgaggcgtgt gtgtgtgtct ttctaggac ccaccatacc	4159

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Glu Pro Val Arg Leu Glu Arg Asp Ile Cys Arg Ala Ile Glu Leu Leu
6 11 16 21

gaa aaa cta caa agg agt gga gaa gta cca cca cag aaa ctt cag gct 149
Glu Lys Leu Gln Arg Ser Gly Glu Val Pro Pro Gln Lys Leu Gln Ala
22 27 32 37

ttg caa aga gtc ctt caa agt gaa ttc tgc aat gct gtg aga gag gta 197
Leu Gln Arg Val Leu Gln Ser Glu Phe Cys Asn Ala Val Arg Glu Val
38 43 48 53

tat gaa cat gtc tat gag act gtg gac atc agt agc agt cct gaa gtg 245
Tyr Glu His Val Tyr Glu Thr Val Asp Ile Ser Ser Ser Pro Glu Val
54 59 64 69

aga gcg aac gct act gca aag gct act gtt gct gca ttt gct gcc agt 293
Arg Ala Asn Ala Thr Ala Lys Ala Thr Val Ala Ala Phe Ala Ala Ser
70 75 80 85

gaa gga cat tct cat cct cga gtt gtt gag cta cca aaa aca gag gag 341
Glu Gly His Ser His Pro Arg Val Val Glu Leu Pro Lys Thr Glu Glu
86 91 96 101

ggc ctt gga ttc aat att atg gga ggc aaa gaa caa aac tct cca atc 389
Gly Leu Gly Phe Asn Ile Met Gly Gly Lys Glu Gln Asn Ser Pro Ile
102 107 112 117

tat ata tcc cga ata att cca ggt gga att gct gat aga cat ggg ggc 437
Tyr Ile Ser Arg Ile Ile Pro Gly Gly Ile Ala Asp Arg His Gly Gly
118 123 128 133

ctc aaa cgt gga gat caa ctc ctc tct gtt aat gga gtg agt gtt gaa	485
Leu Lys Arg Gly Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu	
134 139 144 149	
gga gaa cat cat gaa aaa gct gta gaa ctg ctg aaa gcc gca caa gga	533
Gly Glu His His Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Gln Gly	
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Lys Val Lys Leu Val Val Arg Tyr Thr Pro Lys Val Leu Glu Glu Met	
166 171 176 181	
gag tcg cgc ttt gaa aaa atg aga tca gca aaa cgc agg caa cag acc	629
Glu Ser Arg Phe Glu Lys Met Arg Ser Ala Lys Arg Arg Gln Gln Thr	
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198	
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cgccccgcac tcccggaccc gaagccggga agattccttt cttgtctgtt agaaacgtat 180

gtcaaacgag gatacagtgt ctggaactat tggttctaag atataagtgg aatgagcctg 240

gatcaggaga agtatgctga gctagagttg aaggaagctt ctcttttctaa caagagaaaag 300

cagagttaaa tt atg gca gag aca agt ctg tta gag gct ggg gcc tct 348
Met Ala Glu Thr Ser Leu Leu Glu Ala Gly Ala Ser
1 5 10

gca gcc tct aca gct gcg gct ttg gag aac tta cag gtg gag gcg agc 396
Ala Ala Ser Thr Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser
13 18 23 28

tgc tct gtg tgc ctg gag tat ctg aag gaa cct gtc atc att gag tgt 444
Cys Ser Val Cys Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys
29 34 39 44

ggg cac aac ttc tgc aaa gct tgc atc acc cgc tgg tgg gag gac cta 492
Gly His Asn Phe Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu
45 50 55 60

gag agg gac ttc cct tgt cct gtc tgt cga aag aca tcc cgc tac cgc 540
Glu Arg Asp Phe Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg
61 66 71 76

agt ctc cga cct aat cgg caa cta ggc agt atg gtg gaa att gcc aag 588
Ser Leu Arg Pro Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys
77 82 87 92

cag ctc cag gcc gtc aag cgg aag atc cgg gat gag agc ctc tgc ccc 636
Gln Leu Gln Ala Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro
93 98 103 108

caa cac cat gag gcc ctc agc ctt ttc tgt tat gag gac cag gag gct 684
Gln His His Glu Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala
109 114 119 124

gta tgc ttg ata tgt gca att tcc cac acc cac cgg gcc cac acc gtt 732
Val Cys Leu Ile Cys Ala Ile Ser His Thr His Arg Ala His Thr Val
125 130 135 140

gtg cca ctg gac gat gct aca cag gag tac aag gaa aaa ctg cag aag 780
Val Pro Leu Asp Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys
141 146 151 156

tgt ctg gag ccc ctg gaa cag aag ctg cag gag atc act cgc tgc aag 828
Cys Leu Glu Pro Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys
157 162 167 172

tcc tct gag gag aag aag cct ggt gag ctc aag aga cta gtg gaa agt 876
Ser Ser Glu Glu Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser

173	178	183	188	
cgc cga cag cag atc ttg agg gag ttt gaa gag ctt cat agg cgg ctg				924
Arg Arg Gln Gln Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu				
189	194	199	204	
gat gaa gag cag cag gtg ttg ctt tca cga ctg gaa gaa gag gaa cag				972
Asp Glu Glu Gln Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln				
205	210	215	220	
gac att ctg cag cga ctc cga gaa aat gct gct cac ctt ggg gac aag				1020
Asp Ile Leu Gln Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys				
221	226	231	236	
cgc cgg gac ctg gcc cac ttg gct gcc gag gtg gag ggc aag tgc tta				1068
Arg Arg Asp Leu Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu				
237	242	247	252	
cag tca ggc ttc gag atg ctt aag gtt cga cct ttg ccc ctg cat agc				1116
Gln Ser Gly Phe Glu Met Leu Lys Val Arg Pro Leu Pro Leu His Ser				
253	258	263	268	
ccc tca ggc tga gtg cagcgtagct ttgcgtagcc tgggatttgt cagcctggga				1171
Pro Ser Gly *				
269				
tactcattct tctgctctcc ttctctaaat ccagttcttt ctgccaggtg tactcaaagg				1231
gtcttttgcta cggaaaagtg atttctccca tccccttcta accatttttg tgttcttata				1291
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tct				1834

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174 179 184 189

cag cac gag gcg gcg gtg ccc cag ctg gcg gcc gcc ctg gcc cga tgc	745
Gln His Glu Ala Ala Val Pro Gln Leu Ala Ala Ala Leu Ala Arg Cys	
190 195 200 205	
acc gag aac ccc atg gtg cgg cac gag tgc gcg gag gcc ctg ggc gcc	793
Thr Glu Asn Pro Met Val Arg His Glu Cys Ala Glu Ala Leu Gly Ala	
206 211 216 221	
att gcc cgg ccc gcc tgc ctg gcc gcg ctg cag gct cac gcg gac gac	841
Ile Ala Arg Pro Ala Cys Leu Ala Ala Leu Gln Ala His Ala Asp Asp	
222 227 232 237	
cca gag cgc gtg gtg cgt gag agc tgc gag gtg gct ctg gac atg tat	889
Pro Glu Arg Val Val Arg Glu Ser Cys Glu Val Ala Leu Asp Met Tyr	
238 243 248 253	
gag cac gag acc ggg cgg gcc ttc cag tac gcg gac ggc ctg gag cag	937
Glu His Glu Thr Gly Arg Ala Phe Gln Tyr Ala Asp Gly Leu Glu Gln	
254 259 264 269	
ctg cgc ggg gcc ccc tcc tag gg cccaccctc acccgagct cccggaggac	990
Leu Arg Gly Ala Pro Ser *	
270 275	
tcttgagggc cgctcctccc ccgcagagct ttggcgtcta aaccgggtgt gtgtaaatacg	1050
gtgtcatcgc ttgtgtcttg ctgggcgcac ggttgctgtc cccctcctcc gtctgggacc	1110
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gacacagggg ctgggggcct ctgactcccc caccgaggg cctgggtagg gacaggggtg	1530
tggtccctga gtgggtcagg tagggcacag gggccagggg gggacaagca gacctcagag	1590
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 <212> DNA
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<222> (939) .. (4865)

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tgaaagtgat ctattctttc cacacactga gcttcaagga agcacattct gataccctct     180
tcactattgg caactcaatc accagcatta tttccagtgt acttgggcat atttctttgc     240
cttctatgat ccgaaaaata tttgcaactt taacaagacc tctggcatta ttttatgaaa     300
actcaaagct tgatgaagtt cctaaagtat atagttgtct gaacaacaag ttagaaaagc     360
tactgggaga aattattgct tgtctgcaat tcagctacac cggaacttat gatagtgaac     420
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gaaaacagag tgctcagttc tggaatgcc a ttttgccaa agtgatgatg ttggtttatc     540
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gtttggaaac tgttgaaatg atggaggaat ccagtggacc atattctgat ggactgaaac     660
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actttgtggt tatacctcca gaaggaaaag atgcaaagga aagaatatta actgatcatc     780
aaaaagaagt tctcaaaaca aagcgggtttg aggagcaaat ggacagtgac attgtcattc     840
ctcaagatgt cacggaagac tgtggtatgg ctgaacatct tgaaaagtcc tccctttcga     900
ataatgagtg tggttctctt gacaaaacca gtccagaa      atg tca aac agt aat     953
                                   Met Ser Asn Ser Asn
                                   1

aat gat gaa aga aaa aaa gct tta att tca tca agg aaa aca tca act     1001
Asn Asp Glu Arg Lys Lys Ala Leu Ile Ser Ser Arg Lys Thr Ser Thr
   6              11              16              21

gaa tgt gca tct agt aca gaa aat tct ttc gtt gtc agc agt agt tca     1049
Glu Cys Ala Ser Ser Thr Glu Asn Ser Phe Val Val Ser Ser Ser Ser
  22              27              32              37

gtt tct aat acc act gtt gct gga act ccc cca tac cct aca agt cgg     1097
Val Ser Asn Thr Thr Val Ala Gly Thr Pro Pro Tyr Pro Thr Ser Arg
  38              43              48              53

agg caa acc ttt att act ttg gag aag ttt gat ggt tca gaa aat aga     1145
Arg Gln Thr Phe Ile Thr Leu Glu Lys Phe Asp Gly Ser Glu Asn Arg
  54              59              64              69

cct ttt agt cca tcc ccc ttg aat aat att tca tca act gtt aca gtg     1193
Pro Phe Ser Pro Ser Pro Leu Asn Asn Ile Ser Ser Thr Val Thr Val
  70              75              80              85
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aaa aat aac cag gaa acc atg att aaa aca gat ttt cta cca aaa gca	1241
Lys Asn Asn Gln Glu Thr Met Ile Lys Thr Asp Phe Leu Pro Lys Ala	
86 91 96 101	
aag caa aga gaa ggg act ttt tca aaa tct gat tct gaa aaa ata gtg	1289
Lys Gln Arg Glu Gly Thr Phe Ser Lys Ser Asp Ser Glu Lys Ile Val	
102 107 112 117	
aat gga act aag aga tca agc cgg aga gct ggt aaa gct gaa caa aca	1337
Asn Gly Thr Lys Arg Ser Ser Arg Arg Ala Gly Lys Ala Glu Gln Thr	
118 123 128 133	
ggg aat aaa agg tct aag ccc tta atg aga tct gag ccg gag aaa aat	1385
Gly Asn Lys Arg Ser Lys Pro Leu Met Arg Ser Glu Pro Glu Lys Asn	
134 139 144 149	
act gag gaa tct gtt gaa ggc att gta gtc tta gaa aat aac cca cct	1433
Thr Glu Glu Ser Val Glu Gly Ile Val Val Leu Glu Asn Asn Pro Pro	
150 155 160 165	
ggt ttg ctt aat caa aca gaa tgt gtg tca gat aat cag gtt cat ctt	1481
Gly Leu Leu Asn Gln Thr Glu Cys Val Ser Asp Asn Gln Val His Leu	
166 171 176 181	
tct gaa tct aca atg gag cat gac aat aca aag ctt aaa gca gca aca	1529
Ser Glu Ser Thr Met Glu His Asp Asn Thr Lys Leu Lys Ala Ala Thr	
182 187 192 197	
gtg gaa aat gct gta tta ttg gaa act aat act gta gag gag aaa aat	1577
Val Glu Asn Ala Val Leu Leu Glu Thr Asn Thr Val Glu Glu Lys Asn	
198 203 208 213	
gta gaa att aat ttg gaa tcc aaa gag aat aca ccc cca gta gta ata	1625
Val Glu Ile Asn Leu Glu Ser Lys Glu Asn Thr Pro Pro Val Val Ile	
214 219 224 229	
tca gca gat caa atg gta aat gag gat agt cag gtt cag ata act cca	1673
Ser Ala Asp Gln Met Val Asn Glu Asp Ser Gln Val Gln Ile Thr Pro	
230 235 240 245	
aat cag aaa acc ctt aga cgg tct tca agg cga cgt tca gaa gta gta	1721
Asn Gln Lys Thr Leu Arg Arg Ser Ser Arg Arg Arg Ser Glu Val Val	
246 251 256 261	
gag tct acc act gaa agc caa gat aag gaa aat agt cat caa aaa aag	1769
Glu Ser Thr Thr Glu Ser Gln Asp Lys Glu Asn Ser His Gln Lys Lys	
262 267 272 277	
gaa cga cgt aag gaa gaa gaa aaa cct ctt cag aag agt cca ttg cat	1817
Glu Arg Arg Lys Glu Glu Glu Lys Pro Leu Gln Lys Ser Pro Leu His	
278 283 288 293	
ata aaa gat gat gtg tta cct aaa caa aaa ctg att gct gaa caa act	1865
Ile Lys Asp Asp Val Leu Pro Lys Gln Lys Leu Ile Ala Glu Gln Thr	
294 299 304 309	
cta cag gag aat tta att gag aaa gga agt aat tta cat gag aag act	1913

Leu Gln Glu Asn Leu Ile Glu Lys Gly Ser Asn Leu His Glu Lys Thr	
310 315 320 325	
ctt ggg gaa act agt gct aat gca gaa act gaa caa aat aaa aaa aag	1961
Leu Gly Glu Thr Ser Ala Asn Ala Glu Thr Glu Gln Asn Lys Lys Lys	
326 331 336 341	
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Ala Asp Pro Glu Asn Ile Lys Ser Glu Gly Asp Gly Thr Gln Asp Ile	
342 347 352 357	
gta gat aag tcc tct gag aaa cta gtc aga ggc cga aca cgg tat caa	2057
Val Asp Lys Ser Ser Glu Lys Leu Val Arg Gly Arg Thr Arg Tyr Gln	
358 363 368 373	
act aga aga gca tct cag ggt ttg ctt tcc agc att gaa aac tca gaa	2105
Thr Arg Arg Ala Ser Gln Gly Leu Leu Ser Ser Ile Glu Asn Ser Glu	
374 379 384 389	
tct gat agt tcg gag gca aaa gaa gaa ggt tct agg aag aag aga tct	2153
Ser Asp Ser Ser Glu Ala Lys Glu Glu Gly Ser Arg Lys Lys Arg Ser	
390 395 400 405	
gga aaa tgg aaa aac aaa agc aat gaa agt gtt gac att caa gat caa	2201
Gly Lys Trp Lys Asn Lys Ser Asn Glu Ser Val Asp Ile Gln Asp Gln	
406 411 416 421	
gaa gag aaa gtg gtg aaa cag gaa tgt ata aaa gct gaa aat cag tca	2249
Glu Glu Lys Val Val Lys Gln Glu Cys Ile Lys Ala Glu Asn Gln Ser	
422 427 432 437	
cat gat tat aaa gca act tct gaa gaa gat gta agc ata aaa tct ccg	2297
His Asp Tyr Lys Ala Thr Ser Glu Glu Asp Val Ser Ile Lys Ser Pro	
438 443 448 453	
att tgc gaa aaa caa gat gaa agt aat act gta ata tgt cag gat tct	2345
Ile Cys Glu Lys Gln Asp Glu Ser Asn Thr Val Ile Cys Gln Asp Ser	
454 459 464 469	
aca gta act tca gat ttg ttg caa gtt cct gat gat tta cca aat gtg	2393
Thr Val Thr Ser Asp Leu Leu Gln Val Pro Asp Asp Leu Pro Asn Val	
470 475 480 485	
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Cys Glu Glu Lys Asn Glu Thr Ser Lys Tyr Ala Glu Tyr Ser Phe Thr	
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agt cta cct gtg cca gaa tca aat cta agg act aga aat gcc att aag	2489
Ser Leu Pro Val Pro Glu Ser Asn Leu Arg Thr Arg Asn Ala Ile Lys	
502 507 512 517	
aga tta cat aag cga gac tct ttt gat aat tgt agt ttg gga gaa tcc	2537
Arg Leu His Lys Arg Asp Ser Phe Asp Asn Cys Ser Leu Gly Glu Ser	
518 523 528 533	
tca aaa ata ggg ata tca gat att tct tcg ctt tca gaa aaa act ttt	2585
Ser Lys Ile Gly Ile Ser Asp Ile Ser Ser Leu Ser Glu Lys Thr Phe	

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ctc att ggg tta aag Leu Ile Gly Leu Lys 582	aat aca gaa aat aat Asn Thr Glu Asn Asn 587	gac gta gag att agt gaa Asp Val Glu Ile Ser Glu 592		2729
aca aaa aag gca gat Thr Lys Lys Ala Asp 598	gtg caa gca cct gta Val Gln Ala Pro Val 603	agc cca tca gaa act tct Ser Pro Ser Glu Thr Ser 608		2777
caa gct aat cca tat Gln Ala Asn Pro Tyr 614	tct gaa gga caa ttt Ser Glu Gly Gln Phe 619	tta gat gaa cat cat agt Leu Asp Glu His His Ser 624		2825
gtg aat ttt cat ttg Val Asn Phe His Leu 630	ggt ctc aaa gag gat Gly Leu Lys Glu Asp 635	aat gat act att aat gat Asn Asp Thr Ile Asn Asp 640		2873
tca tta att gtt tct Ser Leu Ile Val Ser 646	gaa acc aaa tca aaa Glu Thr Lys Ser Lys 651	gaa aac act atg caa gaa Glu Asn Thr Met Gln Glu 656		2921
tct ctt cct tct gga Ser Leu Pro Ser Gly 662	ata gta aac ttt aga Ile Val Asn Phe Arg 667	gag gaa att tgt gat atg Glu Glu Ile Cys Asp Met 672		2969
gat tct agt gaa gca Asp Ser Ser Glu Ala 678	atg tct ctt gaa agc Met Ser Leu Glu Ser 683	cag gag tca cct aat gaa Gln Glu Ser Pro Asn Glu 688		3017
aat ttt aaa act gtt Asn Phe Lys Thr Val 694	ggc ccg tgt tta gga Gly Pro Cys Leu Gly 699	gac tcg aaa aat gtt tca Asp Ser Lys Asn Val Ser 704		3065
cag gaa tct ttg gag Gln Glu Ser Leu Glu 710	aca aaa gaa gaa aaa Thr Lys Glu Glu Lys 715	cca gaa gaa acc cca aaa Pro Glu Glu Thr Pro Lys 720		3113
atg gaa ctg agt cta Met Glu Leu Ser Leu 726	gag aat gtt act gtt Glu Asn Val Thr Val 731	gaa gga aat gca tgt aaa Glu Gly Asn Ala Cys Lys 736		3161
gta aca gaa tcc aat Val Thr Glu Ser Asn 742	cta gag aaa gca aaa Leu Glu Lys Ala Lys 747	act atg gaa ttg aat gta Thr Met Glu Leu Asn Val 752		3209
gga aat gaa gct agc Gly Asn Glu Ala Ser 758	ttt cat gga caa gag Phe His Gly Gln Glu 763	aga acc aaa act ggt att Arg Thr Lys Thr Gly Ile 768		3257

tct gaa gaa gca gca ata gaa gaa aat aaa aga aat gat gac tct gaa	3305
Ser Glu Glu Ala Ala Ile Glu Glu Asn Lys Arg Asn Asp Asp Ser Glu	
774 779 784 789	
gca gac aca gct aaa ctg aat gcc aaa gaa gta gca act gag gaa ttt	3353
Ala Asp Thr Ala Lys Leu Asn Ala Lys Glu Val Ala Thr Glu Glu Phe	
790 795 800 805	
aat tca gat att agt ctt tct gat aat act aca cct gta aaa ttg aat	3401
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Gly Ala Tyr Gly Phe Arg Val Ala Ser Leu Asn Lys Ile Ala Asp Thr	
825 830 835 840	
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Lys Ser Ser Ile Asp Arg Asn Ile Ser Leu Leu His Tyr Leu Ile Met	

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atc ctg gag aag cat ttt cct gat att cta aac atg cct tca gag ctg				2825
Ile Leu Glu Lys His Phe Pro Asp Ile Leu Asn Met Pro Ser Glu Leu				
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Gln His Leu Pro Glu Ala Ala Lys Val Asn Leu Ala Glu Leu Glu Lys				
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Glu Val Gly Asn Leu Arg Arg Gly Leu Arg Ala Val Glu Val Glu Leu				
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Glu Tyr Gln Arg Arg Gln Val Arg Glu Pro Ser Asp Lys Phe Val Pro				
905	910	915	920	
gtc atg agc gac ttc atc acg gtg tcc agc ttc agc ttc tcc gag ctg				3017
Val Met Ser Asp Phe Ile Thr Val Ser Ser Phe Ser Phe Ser Glu Leu				
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Glu Asp Gln Leu Asn Glu Ala Arg Asp Lys Phe Ala Lys Ala Leu Met				
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cac ttc ggg gag cat gac agc aag atg cag cca gac gaa ttc ttt ggc				3113
His Phe Gly Glu His Asp Ser Lys Met Gln Pro Asp Glu Phe Phe Gly				
953	958	963	968	
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Ile Phe Asp Thr Phe Leu Gln Ala Phe Ser Glu Ala Arg Gln Asp Leu				
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gag gcc atg agg agg agg aag gag gag gag gag cgg cgg gcg cgc atg				3209
Glu Ala Met Arg Arg Arg Lys Glu Glu Glu Glu Arg Arg Ala Arg Met				
985	990	995	1000	
gaa gcc atg ctg aag gag cag agg gaa cgt gag cgg tgg cag cgg cag				3257
Glu Ala Met Leu Lys Glu Gln Arg Glu Arg Glu Arg Trp Gln Arg Gln				
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cgg aag gtc ctg gct gca ggc agc tcg ctg gag gag gga gga gag ttc				3305
Arg Lys Val Leu Ala Ala Gly Ser Ser Leu Glu Glu Gly Gly Glu Phe				
1017	1022	1027	1032	
gat gac ctg gtg tcg gcc ctg cgc tct ggg gag gtc ttc gac aag gac				3353
Asp Asp Leu Val Ser Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp				
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Leu Cys Lys Leu Lys Arg Ser Arg Lys Arg Ser Gly Ser Gln Ala Leu				
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<220>

<221> CDS

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Ser	Ser	Asn	Asn	Ser	Ala	Pro	Pro	Lys	Pro	Met	Ser	Leu	Lys	Ile	Glu	
202					207					212					217	
aga	att	agc	tcg	tgg	aaa	aca	cca	cca	cag	gaa	aat	aga	gat	aaa	aat	963
Arg	Ile	Ser	Ser	Trp	Lys	Thr	Pro	Pro	Gln	Glu	Asn	Arg	Asp	Lys	Asn	
218					223					228					233	
ctt	tcc	agg	aga	cgt	caa	gac	aga	aga	gca	aca	cct	act	gga	agg	cca	1011
Leu	Ser	Arg	Arg	Arg	Gln	Asp	Arg	Arg	Ala	Thr	Pro	Thr	Gly	Arg	Pro	
234					239					244					249	
act	ccc	tgt	gca	gag	aga	cgg	ggg	ggt	gtc	tga	agatggaa	aggtggcctc				1062
Thr	Pro	Cys	Ala	Glu	Arg	Arg	Gly	Gly	Val	*						
250					255					260						
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Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr																
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Val Lys Gly Leu Leu Lys Pro Ser Phe Ser Pro Arg Asn Tyr Lys Ala																
17 22 27 32																
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Leu Ser Glu Val Gln Gly Trp Lys Gln Arg Met Ala Ala Lys Glu Leu																
33 38 43 48																
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Phe	Tyr	Asn	Pro	Gly	Arg	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser		
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aca	gct	ttc	tcc	atg	ctg	tgc	ctg	ggc	gcc	cag	gac	agc	acc	ctg	gac	648	
Thr	Ala	Phe	Ser	Met	Leu	Cys	Leu	Gly	Ala	Gln	Asp	Ser	Thr	Leu	Asp		
81					86					91					96		
gag	atc	aag	cag	ggg	ttc	aac	ttc	aga	aag	atg	cca	gaa	aaa	gat	ctt	696	
Glu	Ile	Lys	Gln	Gly	Phe	Asn	Phe	Arg	Lys	Met	Pro	Glu	Lys	Asp	Leu		
97					102					107					112		
cat	gag	ggc	ttc	cat	tac	atc	atc	cac	gag	ctg	acc	cag	aag	acc	cag	744	
His	Glu	Gly	Phe	His	Tyr	Ile	Ile	His	Glu	Leu	Thr	Gln	Lys	Thr	Gln		
113					118					123					128		
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Asp	Leu	Lys	Leu	Ser	Ile	Gly	Asn	Thr	Leu	Phe	Ile	Asp	Gln	Arg	Leu		
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cag	cca	cag	cgt	aag	ttt	ttg	gaa	gat	gcc	aag	aac	ttt	tac	agt	gcc	840	
Gln	Pro	Gln	Arg	Lys	Phe	Leu	Glu	Asp	Ala	Lys	Asn	Phe	Tyr	Ser	Ala		
145					150					155					160		
gaa	acc	atc	ctt	acc	aac	ttt	cag	aat	ttg	gaa	atg	gct	cag	aag	cag	888	
Glu	Thr	Ile	Leu	Thr	Asn	Phe	Gln	Asn	Leu	Glu	Met	Ala	Gln	Lys	Gln		
161					166					171					176		
atc	aat	gac	ttt	atc	agt	caa	aaa	acc	cat	ggg	aaa	att	aac	aac	ctg	936	
Ile	Asn	Asp	Phe	Ile	Ser	Gln	Lys	Thr	His	Gly	Lys	Ile	Asn	Asn	Leu		
177					182					187					192		
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Ile	Glu	Asn	Ile	Asp	Pro	Gly	Thr	Val	Met	Leu	Leu	Ala	Asn	Tyr	Ile		
193					198					203					208		
ttc	ttt	cga	gcc	agg	tgg	aaa	cat	gag	ttt	gat	cca	aat	gta	act	aaa	1032	
Phe	Phe	Arg	Ala	Arg	Trp	Lys	His	Glu	Phe	Asp	Pro	Asn	Val	Thr	Lys		
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Glu	Glu	Asp	Phe	Phe	Leu	Glu	Lys	Asn	Ser	Ser	Val	Lys	Val	Pro	Met		
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Met	Phe	Arg	Ser	Gly	Ile	Tyr	Gln	Val	Gly	Tyr	Asp	Asp	Lys	Leu	Ser		
241					246					251					256		
tgc	acc	atc	ctg	gaa	ata	ccc	tac	cag	aaa	aat	atc	aca	gcc	atc	ttc	1176	
Cys	Thr	Ile	Leu	Glu	Ile	Pro	Tyr	Gln	Lys	Asn	Ile	Thr	Ala	Ile	Phe		
257					262					267					272		
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Ile	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Lys	His	Leu	Glu	Lys	Gly	Leu	Gln		

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Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val				
289	294	299	304	
gac gtg tct gta ccc aga ctc cac atg acg ggc acc ttc gac ctg aag				1320
Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys				
305	310	315	320	
aag act ctc tcc tac ata ggt gtc tcc aaa atc ttt gag gaa cat ggt				1368
Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly				
321	326	331	336	
gat ctc acc aag atc gcc cct cat cgc agc ctg aaa gtg ggc gag gct				1416
Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala				
337	342	347	352	
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Val Asn Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala				
353	358	363	368	
gct ggc acc gga gca cag act ctg ccc atg gag aca cca ctc gtc gtc				1512
Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val				
369	374	379	384	
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Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro				
385	390	395	400	
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acatcctctg agacagaaac agcatccact gtgggatctg aagaaacct catccagacc	240

ccttccgtag tcactcaggg gacagcaacc cgaagtagga agacagccca aaagactgca 300

atg cag tgc tgc ttg gag tat gtc caa cag ttt ctt acc aga ctt atc 348
Met Gln Cys Cys Leu Glu Tyr Val Gln Gln Phe Leu Thr Arg Leu Ile
1 5 10 15

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Asn Leu Tyr Ile Ile Gln Asn Asn Ser Phe Ser Gln Ser Leu Ala Thr
17 22 27 32

gaa cat caa ggg gat ctt ggt cga gaa caa gga gag act tca aaa tgg 444
Glu His Gln Gly Asp Leu Gly Arg Glu Gln Gly Glu Thr Ser Lys Trp
33 38 43 48

gac aga aat tca caa gga gat gta aaa gag aaa aac ata agt aaa caa 492
Asp Arg Asn Ser Gln Gly Asp Val Lys Glu Lys Asn Ile Ser Lys Gln
49 54 59 64

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Lys Thr Ser Lys Glu Tyr Leu Ser Ala Phe Leu Ala Ala Cys Gln Leu
65 70 75 80

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Phe Leu Glu Cys Ser Ser Phe Pro Val Tyr Ile Ala Glu Gly Asn His
81 86 91 96

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Thr Ser Glu Leu Arg Ser Glu Lys Leu Glu Thr Asp Cys Glu His Val
97 102 107 112

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Gln Pro Pro Gln Trp Leu Gln Thr Leu Met Asn Ala Cys Ser Gln Ala
113 118 123 128

agt gat ttc agt gtt cag agt gtt gct att tca cta gtt atg gac ctg 732
Ser Asp Phe Ser Val Gln Ser Val Ala Ile Ser Leu Val Met Asp Leu
129 134 139 144

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Val Gly Leu Thr Gln Ser Val Ala Met Val Thr Gly Glu Asn Ile Asn
145 150 155 160

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Ser Val Glu Pro Ala Gln Pro Leu Ser Pro Asn Gln Gly Arg Val Ala
161 166 171 176

gtg gtt att aga cct ccc ctc act cag ggc aat ctg agg tac ata gct 876
Val Val Ile Arg Pro Pro Leu Thr Gln Gly Asn Leu Arg Tyr Ile Ala
177 182 187 192

gag aag act gaa ttt ttc aag cat gta gct tta aca ttg tgg gac cag 924
Glu Lys Thr Glu Phe Phe Lys His Val Ala Leu Thr Leu Trp Asp Gln
193 198 203 208

ttg gga gat ggg aca cct cag cat cac cag aag agt gtg gaa cta ttt 972
Leu Gly Asp Gly Thr Pro Gln His His Gln Lys Ser Val Glu Leu Phe
209 214 219 224

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Tyr	Gln	Leu	His	Asn	Leu	Val	Pro	Ser	Ser	Ser	Ile	Cys	Glu	Asp	Val	
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ata	agt	cag	cag	tta	acc	cat	aaa	gat	aag	aaa	ata	agg	atg	gaa	gca	1068
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cat	gcc	aag	ttt	gca	gtt	ctt	tgg	cat	cta	acg	aga	gat	ctc	cat	ata	1116
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Asn	Lys	Ser	Ser	Ser	Phe	Val	Arg	Ser	Phe	Asp	Arg	Ser	Leu	Phe	Ile	
273					278					283					288	
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Met	Leu	Asp	Ser	Leu	Asn	Ser	Leu	Asp	Gly	Ser	Thr	Ser	Ser	Val	Gly	
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Gln	Ala	Trp	Leu	Asn	Gln	Val	Leu	Gln	Arg	His	Asp	Ile	Ala	Arg	Val	
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Ser	Val	Gln	Arg	Val	Gln	Ala	Glu	Arg	Tyr	Trp	Asn	Lys	Ser	Pro	Cys	
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Tyr	Pro	Gly	Glu	Glu	Ser	Asp	Lys	His	Phe	Met	Gln	Asn	Phe	Ala	Cys	
353					358					363					368	
agc	aat	gtg	agc	caa	gta	caa	ctc	atc	aca	tca	aaa	gga	aat	ggg	gaa	1452
Ser	Asn	Val	Ser	Gln	Val	Gln	Leu	Ile	Thr	Ser	Lys	Gly	Asn	Gly	Glu	
369					374					379					384	
aag	cca	ctt	acc	atg	gat	gaa	ata	gag	aac	ttt	agt	ctc	act	gtg	aat	1500
Lys	Pro	Leu	Thr	Met	Asp	Glu	Ile	Glu	Asn	Phe	Ser	Leu	Thr	Val	Asn	
385					390					395					400	
cca	tta	agt	gac	aga	ctt	tcc	ctc	cta	agt	acc	agc	agt	gag	aca	att	1548
Pro	Leu	Ser	Asp	Arg	Leu	Ser	Leu	Leu	Ser	Thr	Ser	Ser	Glu	Thr	Ile	
401					406					411					416	
cca	atg	gtt	gtg	tct	gat	ttt	gat	ctt	cca	gac	caa	cag	ata	gaa	ata	1596
Pro	Met	Val	Val	Ser	Asp	Phe	Asp	Leu	Pro	Asp	Gln	Gln	Ile	Glu	Ile	
417					422					427					432	
ctt	cag	agt	tct	gac	tcg	gga	tgt	tca	cag	tcc	tct	gct	ggg	gac	aac	1644
Leu	Gln	Ser	Ser	Asp	Ser	Gly	Cys	Ser	Gln	Ser	Ser	Ala	Gly	Asp	Asn	
433					438					443					448	

ttg agt tac gaa gtt gat cct gaa acc gtg aat gcc caa gag gat tct	1692
Leu Ser Tyr Glu Val Asp Pro Glu Thr Val Asn Ala Gln Glu Asp Ser	
449 454 459 464	
caa atg ccc aag gaa agc tcc cca gat gat gat gtt caa cag gta gta	1740
Gln Met Pro Lys Glu Ser Ser Pro Asp Asp Asp Val Gln Gln Val Val	
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Phe Asp Leu Ile Cys Lys Val Val Ser Gly Leu Glu Val Glu Ser Ala	
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Ser Val Thr Ser Gln Leu Glu Ile Glu Ala Met Pro Pro Lys Cys Ser	
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Asp Ile Asp Pro Asp Glu Glu Thr Ile Lys Ile Glu Asp Asp Ser Ile	
513 518 523 528	
cga cag agt cag aat gct ttg ctg agt aat gaa agt tct cag ttt ctg	1932
Arg Gln Ser Gln Asn Ala Leu Leu Ser Asn Glu Ser Ser Gln Phe Leu	
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tct gtg tct gca gag gga ggc cat gag tgt gtg gca aat gga atc tcc	1980
Ser Val Ser Ala Glu Gly Gly His Glu Cys Val Ala Asn Gly Ile Ser	
545 550 555 560	
agg aat agc tcc tca cct tgt att tca gga acc aca cac act ctt cat	2028
Arg Asn Ser Ser Ser Pro Cys Ile Ser Gly Thr Thr His Thr Leu His	
561 566 571 576	
gac tct tct gtt gct tcc ata gaa acc aaa tct aga caa agg agt cac	2076
Asp Ser Ser Val Ala Ser Ile Glu Thr Lys Ser Arg Gln Arg Ser His	
577 582 587 592	
agt agt att caa ttc agc ttc aaa gaa aaa tta tca gaa aaa gtt tcg	2124
Ser Ser Ile Gln Phe Ser Phe Lys Glu Lys Leu Ser Glu Lys Val Ser	
593 598 603 608	
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Glu Lys Glu Thr Ile Val Lys Glu Ser Gly Lys Gln Pro Gly Ala Lys	
609 614 619 624	
cct aaa gta aaa ctt gcc aga aaa aag gat gat gac aag aaa aaa tct	2220
Pro Lys Val Lys Leu Ala Arg Lys Lys Asp Asp Asp Lys Lys Lys Ser	
625 630 635 640	
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Ser Asn Glu Lys Leu Lys Gln Thr Ser Val Phe Phe Ser Asp Gly Leu	
641 646 651 656	
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Asp Leu Glu Asn Trp Tyr Ser Cys Gly Glu Gly Asp Ile Ser Glu Ile	
657 662 667 672	
gag agt gac atg ggt tct cca gga tct cga aaa tct ccc aat ttc aac	2364

Glu Ser Asp Met Gly Ser Pro Gly Ser Arg Lys Ser Pro Asn Phe Asn 673 678 683 688	
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tca tcc agg act ttg tat gct ttc tct gcc atc aaa gcc atc ttg aaa Ser Ser Arg Thr Leu Tyr Ala Phe Ser Ala Ile Lys Ala Ile Leu Lys 705 710 715 720	2460
act aac cct ata gct ttt gta aat gcc att tca act act agt gta aat Thr Asn Pro Ile Ala Phe Val Asn Ala Ile Ser Thr Thr Ser Val Asn 721 726 731 736	2508
aat gca tat act cct cag ttg tct ctc ctt cag aat cta ttg gcc aga Asn Ala Tyr Thr Pro Gln Leu Ser Leu Leu Gln Asn Leu Leu Ala Arg 737 742 747 752	2556
cac cgg att tct gtt atg ggc aaa gat ttt tat agt cac att cca gtg His Arg Ile Ser Val Met Gly Lys Asp Phe Tyr Ser His Ile Pro Val 753 758 763 768	2604
gac tca aat cat aac ttc cgg agt tct atg tac ata gaa att ctt att Asp Ser Asn His Asn Phe Arg Ser Ser Met Tyr Ile Glu Ile Leu Ile 769 774 779 784	2652
tct ctc tgc tta tat tac atg cgt agc cat tac cca act cat gtc aag Ser Leu Cys Leu Tyr Tyr Met Arg Ser His Tyr Pro Thr His Val Lys 785 790 795 800	2700
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ata gaa att ctg aca cta ctc ttc act gag ctg gca aaa gta ata gaa Ile Glu Ile Leu Thr Leu Leu Phe Thr Glu Leu Ala Lys Val Ile Glu 817 822 827 832	2796
agc tca gcg aag ggt ttc cct agt ttt att tct gat atg tta tct aag Ser Ser Ala Lys Gly Phe Pro Ser Phe Ile Ser Asp Met Leu Ser Lys 833 838 843 848	2844
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Leu Gln Arg Leu Ile Val Leu Glu His Arg Val Met Thr Ile Pro Glu				
913	918	923	928	
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Glu Asn Glu Thr Gly Phe Asp Phe Val Val Ser Asp Leu Glu His Ile				
929	934	939	944	
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Ser Pro His Gln Pro Met Thr Ser Leu Gln Tyr Leu His Ala Gln Pro				
945	950	955	960	
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Ile Thr Cys Gln Gly Met Phe Leu Cys Ala Val Ile Arg Ala Leu His				
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cag cac tgt gca tgt aag atg cac cca caa tgg att ggt tta atc aca				3276
Gln His Cys Ala Cys Lys Met His Pro Gln Trp Ile Gly Leu Ile Thr				
977	982	987	992	
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Ser Thr Leu Pro Tyr Met Gly Lys Val Leu Gln Arg Val Val Val Ser				
993	998	1003	1008	
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Val Thr Leu Gln Leu Cys Arg Asn Leu Asp Asn Leu Ile Gln Gln Tyr				
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aaa tac gaa aca gga tta tct gat agt agg cct ctg tgg atg gca tca				3420
Lys Tyr Glu Thr Gly Leu Ser Asp Ser Arg Pro Leu Trp Met Ala Ser				
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Ile Ile Pro Pro Asp Met Ile Leu Thr Leu Leu Glu Gly Ile Thr Ala				
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Ile Ile His Tyr Cys Leu Asp Pro Thr Thr Gln Tyr His Gln Leu				
1057	1062	1067	1072	
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Leu Val Ser Val Asp Gln Lys His Leu Phe Glu Ala Arg Ser Gly Ile				
1073	1078	1083	1088	
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Leu Ser Ile Leu His Met Ile Met Ser Ser Val Thr Leu Leu Trp Ser				
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Ile Leu His Gln Ala Asp Ser Ser Glu Lys Met Thr Ile Ala Ala Ser				
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Ala Ser Leu Thr Thr Ile Asn Leu Gly Ala Thr Lys Asn Leu Arg Gln				
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Gln Ile Leu Glu Leu Leu Gly Pro Ile Ser Met Asn His Gly Val His	
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Phe Met Ala Ala Ile Ala Phe Val Trp Asn Glu Arg Arg Gln Asn Lys	
1153 1158 1163 1168	
aca acc acc agg acc aag gtc att cct gca gcc agt gaa gaa cag ctt	3852
Thr Thr Thr Arg Thr Lys Val Ile Pro Ala Ala Ser Glu Glu Gln Leu	
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Leu Leu Val Glu Leu Val Arg Ser Ile Ser Val Met Arg Ala Glu Thr	
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Leu Glu Gln Thr Thr Trp Leu Arg Arg Asn Leu Glu Val Lys Pro Ser	
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Pro Lys Ile Met Val Asp Gly Thr Asn Leu Glu Ser Asp Val Glu Asp	
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Met Leu Ser Pro Ala Met Glu Thr Ala Asn Ile Thr Pro Ser Val Tyr	
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Val Asn Ile Met His Tyr Val Val Pro Tyr Leu Arg Asn His Ser Ala	
1393 1398 1403 1408	
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His Asn Ala Pro Ser Tyr Arg Ala Cys Val Gln Leu Leu Ser Ser Leu	
1409 1414 1419 1424	
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Ser Gly Tyr Gln Tyr Thr Arg Arg Ala Trp Lys Lys Glu Ala Phe Asp	
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Leu Phe Met Asp Pro Ser Phe Phe Gln Met Asp Ala Ser Cys Val Asn	
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Leu Lys Arg Leu Ala Phe Ala Ile Phe Ser Ser Glu Ile Asp Gln Tyr	
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Gln Lys Tyr Leu Pro Asp Ile Gln Glu Arg Leu Val Glu Ser Leu Arg	
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Leu Pro Gln Val Pro Thr Leu His Ser Gln Val Phe Leu Phe Phe Arg	
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Gly Leu Glu Thr Thr Tyr Thr Gly Gly Asn Gly Phe Ser Thr Ser Tyr	
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Arg Leu Ala Lys Leu Leu Arg Lys Arg Ala Lys Lys Asn Pro Glu Glu	
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Asp Asn Ser Gly Arg Thr Leu Gly Trp Glu Pro Gly His Leu Leu Leu	
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Thr Ile Cys Thr Val Arg Ser Met Glu Gln Leu Leu Pro Phe Phe Asn	
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Met Lys Leu Glu Asn His Lys Pro Cys Ser Ser Lys Ala Arg Gln Lys	
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Gln Pro Pro Gln Trp Leu Gln Thr Leu Met Asn Ala Cys Ser Gln Ala				
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Ser Asp Phe Ser Val Gln Ser Val Ala Ile Ser Leu Val Met Asp Leu				
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Val Gly Leu Thr Gln Ser Val Ala Met Val Thr Gly Glu Asn Ile Asn				
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Ser Val Glu Pro Ala Gln Pro Leu Ser Pro Asn Gln Gly Arg Val Ala				
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Val Val Ile Arg Pro Pro Leu Thr Gln Gly Asn Leu Arg Tyr Ile Ala				
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Glu Lys Thr Glu Phe Phe Lys His Val Ala Leu Thr Leu Trp Asp Gln				
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Leu Gly Asp Gly Thr Pro Gln His His Gln Lys Ser Val Glu Leu Phe				
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Ile Ser Gln Gln Leu Thr His Lys Asp Lys Lys Ile Arg Met Glu Ala				
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His Ala Lys Phe Ala Val Leu Trp His Leu Thr Arg Asp Leu His Ile				
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Asn Lys Ser Ser Ser Phe Val Arg Ser Phe Asp Arg Ser Leu Phe Ile				
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Leu Glu Pro Leu Leu Leu Leu Leu His Pro Lys Thr Gln Arg Val				
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Ser Val Gln Arg Val Gln Ala Glu Arg Tyr Trp Asn Lys Ser Pro Cys	
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Tyr Pro Gly Glu Glu Ser Asp Lys His Phe Met Gln Asn Phe Ala Cys	
353 358 363 368	
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Ser Asn Val Ser Gln Val Gln Leu Ile Thr Ser Lys Gly Asn Gly Glu	
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Lys Pro Leu Thr Met Asp Glu Ile Glu Asn Phe Ser Leu Thr Val Asn	
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Pro Leu Ser Asp Arg Leu Ser Leu Leu Ser Thr Ser Ser Glu Thr Ile	
401 406 411 416	
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Pro Met Val Val Ser Asp Phe Asp Leu Pro Asp Gln Gln Ile Glu Ile	
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Leu Gln Ser Ser Asp Ser Gly Cys Ser Gln Ser Ser Ala Gly Asp Asn	
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Leu Ser Tyr Glu Val Asp Pro Glu Thr Val Asn Ala Gln Glu Asp Ser	
449 454 459 464	
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Gln Met Pro Lys Glu Ser Ser Pro Asp Asp Asp Val Gln Gln Val Val	
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Phe Asp Leu Ile Cys Lys Val Val Ser Gly Leu Glu Val Glu Ser Ala	
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Ser Val Thr Ser Gln Leu Glu Ile Glu Ala Met Pro Pro Lys Cys Ser	
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Asp Ile Asp Pro Asp Glu Glu Thr Ile Lys Ile Glu Asp Asp Ser Ile	
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Arg Gln Ser Gln Asn Ala Leu Leu Ser Asn Glu Ser Ser Gln Phe Leu	
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Ser Val Ser Ala Glu Gly Gly His Glu Cys Val Ala Asn Gly Ile Ser	
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Arg Asn Ser Ser Ser Pro Cys Ile Ser Gly Thr Thr His Thr Leu His	
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Pro Lys Val Lys Leu Ala Arg Lys Lys Asp Asp Asp Lys Lys Lys Ser	
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Ser Asn Glu Lys Leu Lys Gln Thr Ser Val Phe Phe Ser Asp Gly Leu	
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Glu Ser Asp Met Gly Ser Pro Gly Ser Arg Lys Ser Pro Asn Phe Asn	
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Ile His Pro Leu Tyr Gln His Val Leu Leu Tyr Leu Gln Leu Tyr Asp	
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Thr Asn Pro Ile Ala Phe Val Asn Ala Ile Ser Thr Thr Ser Val Asn	
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Asn Ala Tyr Thr Pro Gln Leu Ser Leu Leu Gln Asn Leu Leu Ala Arg	
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His Arg Ile Ser Val Met Gly Lys Asp Phe Tyr Ser His Ile Pro Val	
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Asp Ser Asn His Asn Phe Arg Ser Ser Met Tyr Ile Glu Ile Leu Ile	
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Val	Thr	Ala	Gln	Asp	Leu	Ile	Gly	Asn	Arg	Asn	Met	Gln	Met	Met	Ser	
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Ile	Glu	Ile	Leu	Thr	Leu	Leu	Phe	Thr	Glu	Leu	Ala	Lys	Val	Ile	Glu	
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Ser	Ser	Ala	Lys	Gly	Phe	Pro	Ser	Phe	Ile	Ser	Asp	Met	Leu	Ser	Lys	
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Cys	Lys	Val	Gln	Lys	Val	Ile	Leu	His	Cys	Leu	Leu	Ser	Ser	Ile	Phe	
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Ser	Ala	Gln	Lys	Trp	His	Ser	Glu	Lys	Met	Ala	Gly	Lys	Asn	Leu	Val	
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Ala Ser Leu Thr Thr Ile Asn Leu Gly Ala Thr Lys Asn Leu Arg Gln				
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Gln Ile Leu Glu Leu Leu Gly Pro Ile Ser Met Asn His Gly Val His				
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Pro Ala Pro Ala Met Val Trp Asp Val Pro Val Glu Glu Phe Pro Leu	
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Arg Cys Pro Leu Phe Ala Gln Gln Arg Val Pro Glu Gly Gly Pro Leu	
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Leu Asp Thr Arg Lys Asn Val Gln Ala Thr Glu Gly Arg Thr Lys Ala	

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Pro Ala Arg Leu Cys Ala Gly Glu Asn Ala Ser Thr Pro Ser Glu Pro				
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gaa aag ttc ccc cag gtg cgc cgg cag cgc ggg gcg ggc gcc ggg gag				1850
Glu Lys Phe Pro Gln Val Arg Arg Gln Arg Gly Ala Gly Ala Gly Glu				
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ggc gag ttc gtg tgc ggc gag tgc ggg aag gcg ttc cgc cag agc tcc				1898
Gly Glu Phe Val Cys Gly Glu Cys Gly Lys Ala Phe Arg Gln Ser Ser				
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tcc ctc acg ctg cac cgg cgc tgg cac agc cgg gag aag gct tac aag				1946
Ser Leu Thr Leu His Arg Arg Trp His Ser Arg Glu Lys Ala Tyr Lys				
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tgc gat gaa tgc ggc aag gcc ttc acc tgg agc acc aac ctt ctg gag				1994
Cys Asp Glu Cys Gly Lys Ala Phe Thr Trp Ser Thr Asn Leu Leu Glu				
207	212	217	222	
cac cgg cgc atc cac acc ggc gag aag ccc ttc ttc tgc ggc gag tgc				2042
His Arg Arg Ile His Thr Gly Glu Lys Pro Phe Phe Cys Gly Glu Cys				
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ggg aag gcc ttc agc tgc cac tcg tcc ctc aac gtg cac cag cgc atc				2090
Gly Lys Ala Phe Ser Cys His Ser Ser Leu Asn Val His Gln Arg Ile				
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His Thr Gly Glu Arg Pro Tyr Lys Cys Ser Ala Cys Glu Lys Ala Phe				
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Ser Cys Ser Ser Leu Leu Ser Met His Leu Arg Val His Thr Gly Glu				
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Lys Pro Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Asn Gln Arg Thr				
287	292	297	302	
cac ctc aca cgc cac cac cgc atc cac acg ggc gag aag ccc tac cag				2282
His Leu Thr Arg His His Arg Ile His Thr Gly Glu Lys Pro Tyr Gln				
303	308	313	318	
tgc ggc tcc tgc ggc aag gcc ttc acc tgc cac tca tcc ctc acc gtg				2330
Cys Gly Ser Cys Gly Lys Ala Phe Thr Cys His Ser Ser Leu Thr Val				
319	324	329	334	
cat gag aag atc cac agc ggg gac aag cgg ttc aag tgc agc gac tgc				2378
His Glu Lys Ile His Ser Gly Asp Lys Pro Phe Lys Cys Ser Asp Cys				
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gag aag gcc ttc aac agc cgc tcg cgc ctc acc ctc cac cag agg acg				2426
Glu Lys Ala Phe Asn Ser Arg Ser Arg Leu Thr Leu His Gln Arg Thr				
351	356	361	366	

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His Thr Gly Glu Lys Pro Phe Lys Cys Ala Asp Cys Gly Lys Gly Phe	
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Lys Pro Phe Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Ser His Ala	
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Tyr Leu Ile Val His Arg Arg Ile His Thr Gly Glu Lys Pro Phe Asp	
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Cys Ser Gln Cys Trp Lys Ala Phe Ser Cys His Ser Ser Leu Ile Val	
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His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Glu Cys	
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His Ser Gly Glu Lys Ser Phe Lys Cys Glu Lys Cys Gly Glu Met Phe	
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Asn Trp Ser Ser His Leu Thr Glu His Gln Arg Leu His Ser Glu Gly	
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Lys Pro Leu Ala Ile Gln Phe Asn Lys His Leu Leu Ser Thr Tyr Tyr	
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Val Pro Gly Ser Leu Leu Gly Ala Gly Asp Ala Gly Leu Arg Asp Val	
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Asp Pro Ile Asp Ala Leu Asp Val Ala Lys Leu Leu Cys Val Val Pro	
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 Pro Val Gly Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys
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 Val Leu Leu His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr
 30 35 40 45

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Phe Ser Glu Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala	
46 51 56 61	
cat aaa gtt ggt atc act cct cct tgc ttc aat ctc ttt gcc ctc ttc	601
His Lys Val Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe	
62 67 72 77	
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Asp Ala Gln Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile	
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ccc aga gat gca agc ctg atg cta tat ttc cgc ata agg ttt tat ttc	697
Pro Arg Asp Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe	
94 99 104 109	
cgg aac tgg cat ggc atg aat cct cgg gaa ccg gct gtg tac cgt tgt	745
Arg Asn Trp His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys	
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Gly Pro Pro Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met	
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Gln Leu Leu Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys	
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His Glu Phe Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu	
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Glu Glu Ile His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu	
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His Leu Cys His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val	
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Ala Lys Lys Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg	
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His Ile Arg Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val	
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Phe Arg Arg Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln	
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Ala	Glu	Gly	Glu	Pro	Cys	Tyr	Ile	Arg	Asp	Ser	Gly	Val	Ala	Pro	Thr	
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Asp	Pro	Gly	Pro	Glu	Ser	Ala	Ala	Gly	Pro	Pro	Thr	His	Glu	Val	Leu	
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gtg	aca	ggc	act	ggt	ggc	atc	cag	tgg	tgg	cca	gta	gag	gag	gag	gtg	1369
Val	Thr	Gly	Thr	Gly	Gly	Ile	Gln	Trp	Trp	Pro	Val	Glu	Glu	Glu	Val	
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Asn	Lys	Glu	Glu	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Arg	Asn	Pro	Gln	Ala	
334					339					344					349	
agc	ctg	ttt	ggg	aag	aag	gcc	aag	gct	cac	aag	gca	ttc	ggc	cag	ccg	1465
Ser	Leu	Phe	Gly	Lys	Lys	Ala	Lys	Ala	His	Lys	Ala	Phe	Gly	Gln	Pro	
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gca	gac	agg	ccg	cgg	gag	cca	ctg	tgg	gcc	tac	ttc	tgt	gac	ttc	cgg	1513
Ala	Asp	Arg	Pro	Arg	Glu	Pro	Leu	Trp	Ala	Tyr	Phe	Cys	Asp	Phe	Arg	
366					371					376					381	
gac	atc	acc	cac	gtg	gtg	ctg	aaa	gag	cac	tgt	gtc	agc	atc	cac	cgg	1561
Asp	Ile	Thr	His	Val	Val	Leu	Lys	Glu	His	Cys	Val	Ser	Ile	His	Arg	
382					387					392					397	
cag	gac	aac	aag	tgc	ctg	gag	ctg	agc	ttg	cct	tcc	cgg	gct	gcg	gcg	1609
Gln	Asp	Asn	Lys	Cys	Leu	Glu	Leu	Ser	Leu	Pro	Ser	Arg	Ala	Ala	Ala	
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ctg	tcc	ttc	gtg	tcg	ctg	gtg	gac	ggc	tat	ttc	cgc	ctg	acg	gcc	gac	1657
Leu	Ser	Phe	Val	Ser	Leu	Val	Asp	Gly	Tyr	Phe	Arg	Leu	Thr	Ala	Asp	
414					419					424					429	
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Ser	Ser	His	Tyr	Leu	Cys	His	Glu	Val	Ala	Pro	Pro	Arg	Leu	Val	Met	
430					435					440					445	
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Ser	Ile	Arg	Asp	Gly	Ile	His	Gly	Pro	Leu	Leu	Glu	Pro	Phe	Val	Gln	
446					451					456					461	
gcc	aag	ctg	cgg	ccc	gag	gac	ggc	ctg	tac	ctc	att	cac	tgg	agc	acc	1801
Ala	Lys	Leu	Arg	Pro	Glu	Asp	Gly	Leu	Tyr	Leu	Ile	His	Trp	Ser	Thr	
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agc	cac	ccc	tac	cgc	ctg	atc	ctc	aca	gtg	gcc	cag	cgt	agc	cag	gca	1849
Ser	His	Pro	Tyr	Arg	Leu	Ile	Leu	Thr	Val	Ala	Gln	Arg	Ser	Gln	Ala	
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cca	gac	ggc	atg	cag	agc	ttg	cgg	ctc	cga	aag	ttc	ccc	att	gag	cag	1897
Pro	Asp	Gly	Met	Gln	Ser	Leu	Arg	Leu	Arg	Lys	Phe	Pro	Ile	Glu	Gln	

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cag gac ggg gcc ttc gtg ctg gag ggc tgg ggc cgg tcc ttc ccc agc				1945
Gln Asp Gly Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser				
510	515	520	525	
ggt cgg gaa ctt ggg gct gcc ttg cag ggc tgc ttg ctg agg gcc ggg				1993
Val Arg Glu Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly				
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Asp Asp Cys Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu				
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Thr Ser Asn Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr				
558	563	568	573	
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Leu Asn Leu Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile				
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acc cag ctg tcc cac ttg ggc cag ggc aca agg acc aac gtg tat gag				2185
Thr Gln Leu Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu				
590	595	600	605	
ggc cgc ctg cga gtg gag ggc agc ggg gac cct gag gag ggc aag atg				2233
Gly Arg Leu Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met				
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Asp Asp Glu Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu				
622	627	632	637	
cga gtg gtg ctc aaa gtg ctg gac cct agt cac cat gac atc gcc ctg				2329
Arg Val Val Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu				
638	643	648	653	
gcc ttc tac gag aca gcc agc ctc atg agc cag gtc tcc cac acg cac				2377
Ala Phe Tyr Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His				
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Leu Ala Phe Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ile Met				
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gtg aca gag tac gtg gag cac gga ccc ctg gat gtg tgg ctg cgg agg				2473
Val Thr Glu Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg				
686	691	696	701	
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Glu Arg Gly His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln				
702	707	712	717	
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Leu Ala Ser Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly				
718	723	728	733	

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Gly Thr Ser Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly	
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Gln His Arg Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr	
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Ser Gln Cys Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr	
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Ile Leu Arg Asp Leu Thr Arg Leu Gln Pro His Asn Leu Ala Asp Val	
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Gln Ile Cys Glu Gly Met Ala Tyr Leu His Ala Gln His Tyr Ile His	
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Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val	
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Lys Ile Gly Asp Phe Gly Leu Ala Lys Ala Val Pro Asp Ala Thr Ser	
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Gln Ser Ala *	
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Leu Glu Gln Asn Glu Ala Ser Arg Lys Asn Lys Lys Lys Lys Lys Lys				
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Glu Asp Ala Glu Glu Phe Pro Asn Leu Ala Val Ala Ser Glu Arg Arg				
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Gln Met Lys Thr Pro His Asn Pro Leu Asp Ser Ser Ala Pro Leu Met				
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Gly Lys Gly Asp Arg Gln Arg Phe Tyr Ser Asp Ser His His Leu Lys	
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Glu Gly His Lys Asp Lys Glu Arg Ala Arg Leu Ser His Gly Asp Arg	
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Pro Asp Lys Pro Lys Ser Glu Asp Tyr Glu Lys Asp Lys Glu Arg Glu	
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Arg Phe Ile Gly Leu Pro Leu Ser Arg Trp Leu Gly Val Arg Asp Gln		
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Thr Glu Gly His Arg Pro Lys Glu Pro Gln Leu Ser Leu Leu Ala Ala		
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Gln Cys Gly Leu Thr Leu Gln Gln Thr Gln Arg Trp Phe Arg Arg Arg		
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Lys Arg Lys Asp Phe Lys Glu Gln Val Ile His His Phe Val Ala Val		
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Ile Leu Met Thr Phe Ser Tyr Ser Ala Asn Leu Leu Arg Ile Gly Ser	
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Leu Val Leu Leu Leu His Asp Ser Ser Asp Tyr Leu Leu Glu Ala Cys	
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Lys Met Val Asn Tyr Met Gln Tyr Gln Gln Val Cys Asp Ala Leu Phe	
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Leu Ile Phe Ser Phe Val Phe Phe Tyr Thr Arg Leu Val Leu Phe Pro	
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Thr Gln Ile Leu Tyr Thr Thr Tyr Tyr Glu Ser Ile Ser Asn Arg Gly	
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Pro Phe Phe Gly Tyr Tyr Phe Phe Asn Gly Leu Leu Met Leu Leu Gln	
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Pro Arg Ser Arg Val Ala Gly Arg Leu Thr Asn Arg His Thr Thr Ala	
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Ser Ala Arg Leu Arg Thr Val Phe Gln Gly Val Gly His Trp Ala Leu
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tcc aca tgg gct ggc ctg aag ccc agc cgg cta ctg cca cag cgg gct   148
Ser Thr Trp Ala Gly Leu Lys Pro Ser Arg Leu Leu Pro Gln Arg Ala
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tct ccc agg ctg ctc tcg gtc ggc cgt gcg gac ctc gcc aag cat cag   196
Ser Pro Arg Leu Leu Ser Val Gly Arg Ala Asp Leu Ala Lys His Gln
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ggg gca agc tgc ttc cac agt gag ccc cgc aag gag ttt gga ggc cct   340
Gly Ala Ser Cys Phe His Ser Glu Pro Arg Lys Glu Phe Gly Gly Pro
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gat gga ggg gac gga ggc aac ggt gga cac gtc att ctg aga gtt gac   388
Asp Gly Gly Asp Gly Gly Asn Gly Gly His Val Ile Leu Arg Val Asp
      104                109                114                119

cag caa gtc aag tcc ctg tcg tcg gtc ctg tcg cgg tac cag ggt ttc   436
Gln Gln Val Lys Ser Leu Ser Ser Val Leu Ser Arg Tyr Gln Gly Phe
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agt gga gaa gat gga ggg agt aaa aac tgc ttc ggg cgc agt ggc gcc   484
Ser Gly Glu Asp Gly Gly Ser Lys Asn Cys Phe Gly Arg Ser Gly Ala
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gtc ctc tac atc cgg gtc ccc gtg ggc acg ctg gtg aag gag gga ggc   532
Val Leu Tyr Ile Arg Val Pro Val Gly Thr Leu Val Lys Glu Gly Gly
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184 189 194 199	
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Asn Arg Ala Pro Val Thr Cys Thr Pro Gly Gln Pro Gly Gln Gln Arg	
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Gln Ala Leu Asp Leu Leu Pro Leu Leu Ile Gln Thr Val Glu Lys Ala				
263	268	273	278	

gcc tcc caa agc act cag gtt ccc acc atc act gaa ggg gtt gcc gca	1517
Ala Ser Gln Ser Thr Gln Val Pro Thr Ile Thr Glu Gly Val Ala Ala	
279 284 289 294	
gcc ttg ttg ctc tta aag ttg tca gtg gct gac tca cag gct gag gcc	1565
Ala Leu Leu Leu Leu Lys Leu Ser Val Ala Asp Ser Gln Ala Glu Ala	
295 300 305 310	
aaa ctg agc agt ttc tgg cag ttg att gtg gat gag aaa aag cag gtt	1613
Lys Leu Ser Ser Phe Trp Gln Leu Ile Val Asp Glu Lys Lys Gln Val	
311 316 321 326	
ttc act tct gag aaa ttc ctg gtc atg gct tca gag gat gcc ctg tgt	1661
Phe Thr Ser Glu Lys Phe Leu Val Met Ala Ser Glu Asp Ala Leu Cys	
327 332 337 342	
act gtg ttg cat ctg aca gag aga ctt ttc ctt gac cac ccg cat aga	1709
Thr Val Leu His Leu Thr Glu Arg Leu Phe Leu Asp His Pro His Arg	
343 348 353 358	
ctc act ggc aac aaa gtt cag cag tac cac cgg gct ctg gtg gcg gtg	1757
Leu Thr Gly Asn Lys Val Gln Gln Tyr His Arg Ala Leu Val Ala Val	
359 364 369 374	
ctc ctg agc cgc acc tgg cac gtc cgc agg cag gct cag cag aca gtt	1805
Leu Leu Ser Arg Thr Trp His Val Arg Arg Gln Ala Gln Gln Thr Val	
375 380 385 390	
cgg aag ctg ctg tcc tct ctt ggg ggc ttt aag ctg gcg cac gga ctc	1853
Arg Lys Leu Leu Ser Ser Leu Gly Gly Phe Lys Leu Ala His Gly Leu	
391 396 401 406	
ttg gag gag ctg aag act gtc ctc agt tct cac aag gtg ctg ccc tta	1901
Leu Glu Glu Leu Lys Thr Val Leu Ser Ser His Lys Val Leu Pro Leu	
407 412 417 422	
gag gct ttg gtg act gat gct gga gag gtg act gag gca ggc aag gcc	1949
Glu Ala Leu Val Thr Asp Ala Gly Glu Val Thr Glu Ala Gly Lys Ala	
423 428 433 438	
tac gtg cct cca cgg gtc ctg cag gag gct ctg tgt gtc atc tcc ggt	1997
Tyr Val Pro Pro Arg Val Leu Gln Glu Ala Leu Cys Val Ile Ser Gly	
439 444 449 454	
gtg cca ggg ctc aag ggt gat gtc acc gac act gaa caa ctg gcc cag	2045
Val Pro Gly Leu Lys Gly Asp Val Thr Asp Thr Glu Gln Leu Ala Gln	
455 460 465 470	
gaa atg ctg atc atc tcc cac cac cca tcc tta gtt gcc gtg cag tct	2093
Glu Met Leu Ile Ile Ser His His Pro Ser Leu Val Ala Val Gln Ser	
471 476 481 486	
gga ctt tgg cca gca ctt ctt gcc agg atg aag atc gat cct gaa gcc	2141
Gly Leu Trp Pro Ala Leu Leu Ala Arg Met Lys Ile Asp Pro Glu Ala	
487 492 497 502	

ttt atc acc agg cac ctg gat cag atc att ccc agg atg acc aca cag	2189
Phe Ile Thr Arg His Leu Asp Gln Ile Ile Pro Arg Met Thr Thr Gln	
503 508 513 518	
agt ccc cta aac cag tcc tcc atg aat gcc atg ggc tcc ctt tcc gtc	2237
Ser Pro Leu Asn Gln Ser Ser Met Asn Ala Met Gly Ser Leu Ser Val	
519 524 529 534	
ctg tcg ccg gac cgg gtc ctc cca cag ctc atc agc acc atc act tcc	2285
Leu Ser Pro Asp Arg Val Leu Pro Gln Leu Ile Ser Thr Ile Thr Ser	
535 540 545 550	
tcc gtg cag aac cct gca ctg cgc ctg gtg acg cgg gag gag ttt gcc	2333
Ser Val Gln Asn Pro Ala Leu Arg Leu Val Thr Arg Glu Glu Phe Ala	
551 556 561 566	
att atg cag acc cct gct ggg gag ctg tat gac aaa tcc atc att cag	2381
Ile Met Gln Thr Pro Ala Gly Glu Leu Tyr Asp Lys Ser Ile Ile Gln	
567 572 577 582	
agt gcc cag cag gac agc ata aaa aag gcc aac atg aag cga gag aac	2429
Ser Ala Gln Gln Asp Ser Ile Lys Lys Ala Asn Met Lys Arg Glu Asn	
583 588 593 598	
aaa gct tat tcc ttc aaa gag cag atc atc gag ctg gag ctg aag gag	2477
Lys Ala Tyr Ser Phe Lys Glu Gln Ile Ile Glu Leu Glu Leu Lys Glu	
599 604 609 614	
gag ata aag aag aag aaa ggc atc aaa gag gag gtg cag ctg acc agc	2525
Glu Ile Lys Lys Lys Lys Gly Ile Lys Glu Glu Val Gln Leu Thr Ser	
615 620 625 630	
aag cag aag gag atg ctg cag gcc cag cta gac agg gag gcg cag gtc	2573
Lys Gln Lys Glu Met Leu Gln Ala Gln Leu Asp Arg Glu Ala Gln Val	
631 636 641 646	
cgg agg cgg ctg cag gag ctg gat ggg gag ctg gag gcg gcg ctt gga	2621
Arg Arg Arg Leu Gln Glu Leu Asp Gly Glu Leu Glu Ala Ala Leu Gly	
647 652 657 662	
ctg ctg gac atc atc ctg gcc aag aag tcg acc ggc ctg acc cag tac	2669
Leu Leu Asp Ile Ile Leu Ala Lys Lys Ser Thr Gly Leu Thr Gln Tyr	
663 668 673 678	
atc cct gtt ttg gtc gac tct ttt ctg ccc ttg ctg aag tct ccc ctg	2717
Ile Pro Val Leu Val Asp Ser Phe Leu Pro Leu Leu Lys Ser Pro Leu	
679 684 689 694	
gct gct ccc agg atc aag aac ccc ttc ttg tcc ttg gct gcc tgt gtc	2765
Ala Ala Pro Arg Ile Lys Asn Pro Phe Leu Ser Leu Ala Ala Cys Val	
695 700 705 710	
atg ccc tct agg ctc aag gct ttg ggc act ttg gtg agc cac gtg acc	2813
Met Pro Ser Arg Leu Lys Ala Leu Gly Thr Leu Val Ser His Val Thr	
711 716 721 726	
ctg cgc ctg ctg aag cca gag tgt gtc ctg gat aag tcc tgg tgc cag	2861

Leu	Arg	Leu	Leu	Lys	Pro	Glu	Cys	Val	Leu	Asp	Lys	Ser	Trp	Cys	Gln	
727					732					737					742	
gaa	gag	ctg	tcg	gtg	gct	gtg	aag	agg	gcg	gtg	atg	ctg	ctg	cac	acc	2909
Glu	Glu	Leu	Ser	Val	Ala	Val	Lys	Arg	Ala	Val	Met	Leu	Leu	His	Thr	
743					748					753					758	
cac	acc	atc	acc	agc	agg	gtg	ggc	aag	ggg	gag	cca	ggg	gct	gcg	ccc	2957
His	Thr	Ile	Thr	Ser	Arg	Val	Gly	Lys	Gly	Glu	Pro	Gly	Ala	Ala	Pro	
759					764					769					774	
ttg	tcc	gcg	cca	gcc	ttc	tcc	tta	gtc	ttc	ccg	ttt	ctg	aag	atg	gtg	3005
Leu	Ser	Ala	Pro	Ala	Phe	Ser	Leu	Val	Phe	Pro	Phe	Leu	Lys	Met	Val	
775					780					785					790	
ctg	acg	gag	atg	ccc	cac	cac	agt	gag	gag	gag	gag	gag	tgg	atg	gcc	3053
Leu	Thr	Glu	Met	Pro	His	His	Ser	Glu	Glu	Glu	Glu	Glu	Trp	Met	Ala	
791					796					801					806	
cag	att	ctt	cag	atc	ctc	act	gtc	caa	gcc	cag	ctg	agg	gcc	tcc	ccc	3101
Gln	Ile	Leu	Gln	Ile	Leu	Thr	Val	Gln	Ala	Gln	Leu	Arg	Ala	Ser	Pro	
807					812					817					822	
aac	acc	cca	ccc	ggg	cgg	gtg	gac	gag	aat	ggc	ccg	gag	ttg	ctg	cct	3149
Asn	Thr	Pro	Pro	Gly	Arg	Val	Asp	Glu	Asn	Gly	Pro	Glu	Leu	Leu	Pro	
823					828					833					838	
cgc	gtg	gcc	atg	ctg	cgt	ctt	ctg	act	tgg	gtg	atc	ggg	acg	ggc	tcg	3197
Arg	Val	Ala	Met	Leu	Arg	Leu	Leu	Thr	Trp	Val	Ile	Gly	Thr	Gly	Ser	
839					844					849					854	
cct	cgc	tta	cag	gtt	ctg	gct	tca	gac	acc	ctg	acc	acc	ctg	tgt	gcc	3245
Pro	Arg	Leu	Gln	Val	Leu	Ala	Ser	Asp	Thr	Leu	Thr	Thr	Leu	Cys	Ala	
855					860					865					870	
agc	agc	agt	ggg	gat	gat	ggc	tgt	gcc	ttt	gca	gag	cag	gag	gag	gtg	3293
Ser	Ser	Ser	Gly	Asp	Asp	Gly	Cys	Ala	Phe	Ala	Glu	Gln	Glu	Glu	Val	
871					876					881					886	
gac	gtg	ctg	ctc	tgt	gcc	ttg	cag	tcc	ccg	tgt	gcc	agc	gtg	cgg	gaa	3341
Asp	Val	Leu	Leu	Cys	Ala	Leu	Gln	Ser	Pro	Cys	Ala	Ser	Val	Arg	Glu	
887					892					897					902	
acc	gtg	ctc	cgg	ggg	ctg	atg	gaa	ctc	cac	atg	gta	ttg	cca	gca	cct	3389
Thr	Val	Leu	Arg	Gly	Leu	Met	Glu	Leu	His	Met	Val	Leu	Pro	Ala	Pro	
903					908					913					918	
gat	act	gat	gag	aag	aat	ggc	ctg	aac	ctt	ctg	cgg	aga	ctc	tgg	gtg	3437
Asp	Thr	Asp	Glu	Lys	Asn	Gly	Leu	Asn	Leu	Leu	Arg	Arg	Leu	Trp	Val	
919					924					929					934	
gtc	aag	ttt	gac	aag	gag	gag	gag	atc	cgg	aag	ctg	gct	gag	agg	ctc	3485
Val	Lys	Phe	Asp	Lys	Glu	Glu	Glu	Ile	Arg	Lys	Leu	Ala	Glu	Arg	Leu	
935					940					945					950	
tgg	tca	atg	atg	ggc	cta	gac	ctg	cag	cca	gac	ctc	tgc	tcc	ttg	ctg	3533
Trp	Ser	Met	Met	Gly	Leu	Asp	Leu	Gln	Pro	Asp	Leu	Cys	Ser	Leu	Leu	

951	956	961	966	
att gac gac gtg atc tat cat gag gcg gct gta agg cag gca ggg gcc				3581
Ile Asp Asp Val Ile Tyr His Glu Ala Ala Val Arg Gln Ala Gly Ala				
967	972	977	982	
gaa gcc ctc tcc caa gca gtg gca cgt tac cag cgg cag gcg gcg gag				3629
Glu Ala Leu Ser Gln Ala Val Ala Arg Tyr Gln Arg Gln Ala Ala Glu				
983	988	993	998	
gtt atg ggc agg ctc atg gag att tac cag gaa aag ctc tac cgg ccg				3677
Val Met Gly Arg Leu Met Glu Ile Tyr Gln Glu Lys Leu Tyr Arg Pro				
999	1004	1009	1014	
ccc cca gtg ctg gat gct ttg gga cga gtt att tca gaa tct cct cca				3725
Pro Pro Val Leu Asp Ala Leu Gly Arg Val Ile Ser Glu Ser Pro Pro				
1015	1020	1025	1030	
gat cag tgg gaa gcc agg tgt ggc ttg gcg ttg gcc ctc aac aag ctc				3773
Asp Gln Trp Glu Ala Arg Cys Gly Leu Ala Leu Ala Leu Asn Lys Leu				
1031	1036	1041	1046	
tcc cag tat ttg gac agc tct cag gtg aag cca ctc ttt cag ttt ttt				3821
Ser Gln Tyr Leu Asp Ser Ser Gln Val Lys Pro Leu Phe Gln Phe Phe				
1047	1052	1057	1062	
gtc cct gat gcc ctc aat gac cga cac cca gat gtc cgg aag tgc atg				3869
Val Pro Asp Ala Leu Asn Asp Arg His Pro Asp Val Arg Lys Cys Met				
1063	1068	1073	1078	
ttg gat gca gcc ctc gca acg ctc aac act cat ggg aag gag aac gtc				3917
Leu Asp Ala Ala Leu Ala Thr Leu Asn Thr His Gly Lys Glu Asn Val				
1079	1084	1089	1094	
aac tcg ctg ttg cca gta ttc gag gag ttc ctg aag aac gcg ccc aat				3965
Asn Ser Leu Leu Pro Val Phe Glu Glu Phe Leu Lys Asn Ala Pro Asn				
1095	1100	1105	1110	
gat gcc agc tac gat gct gtg cga cag agt gtg gtc ctg atg ggc				4013
Asp Ala Ser Tyr Asp Ala Val Arg Gln Ser Val Val Val Leu Met Gly				
1111	1116	1121	1126	
tct ctg gcc aag cac ctg gac aag agt gac ccc aaa gtg aag ccc att				4061
Ser Leu Ala Lys His Leu Asp Lys Ser Asp Pro Lys Val Lys Pro Ile				
1127	1132	1137	1142	
gtt gcc aag ctc atc gct gcc ctc tcc acc ccc tcc cag cag gtc cag				4109
Val Ala Lys Leu Ile Ala Ala Leu Ser Thr Pro Ser Gln Gln Val Gln				
1143	1148	1153	1158	
gag tcc gta gcc agc tgc ttg cca ccc ctc gtg cca gcc atc aag gag				4157
Glu Ser Val Ala Ser Cys Leu Pro Pro Leu Val Pro Ala Ile Lys Glu				
1159	1164	1169	1174	
gat gct gga ggg atg atc cag agg ctt atg cag cag ctg ctg gag tca				4205
Asp Ala Gly Gly Met Ile Gln Arg Leu Met Gln Gln Leu Leu Glu Ser				
1175	1180	1185	1190	

gac aag tac gca gag cgc aaa ggg gcc gcg tat ggc ctg gcg ggc ctg	4253
Asp Lys Tyr Ala Glu Arg Lys Gly Ala Ala Tyr Gly Leu Ala Gly Leu	
1191 1196 1201 1206	
gtg aag ggc ctg ggc atc ctc tcg ctg aag caa cag gag atg atg gcg	4301
Val Lys Gly Leu Gly Ile Leu Ser Leu Lys Gln Gln Glu Met Met Ala	
1207 1212 1217 1222	
gca ctg act gat gcc atc caa gat aag aag aac ttc cgc cgg cga gag	4349
Ala Leu Thr Asp Ala Ile Gln Asp Lys Lys Asn Phe Arg Arg Arg Glu	
1223 1228 1233 1238	
gga gcc ctc ttt gcc ttc gag atg ctc tgc acc atg ctg ggg aaa ctt	4397
Gly Ala Leu Phe Ala Phe Glu Met Leu Cys Thr Met Leu Gly Lys Leu	
1239 1244 1249 1254	
ttt gag ccg tat gtg gtt cac gtg ctg ccc cat ctg ctc ctg tgc ttt	4445
Phe Glu Pro Tyr Val Val His Val Leu Pro His Leu Leu Leu Cys Phe	
1255 1260 1265 1270	
ggg gat gga aac cag tat gtg cgt gag gct gca gat gac tgt gcc aag	4493
Gly Asp Gly Asn Gln Tyr Val Arg Glu Ala Ala Asp Asp Cys Ala Lys	
1271 1276 1281 1286	
gct gtg atg agc aac ttg agt gct cac ggg gtg aag ctg gtg ctc ccc	4541
Ala Val Met Ser Asn Leu Ser Ala His Gly Val Lys Leu Val Leu Pro	
1287 1292 1297 1302	
tcc tta ctg gct gcc ctg gag gag gaa tcg tgg cgg acc aaa gct ggg	4589
Ser Leu Leu Ala Ala Leu Glu Glu Glu Ser Trp Arg Thr Lys Ala Gly	
1303 1308 1313 1318	
tca gtg gag ctt ctt ggg gca atg gcg tac tgt gct cct aag cag ctg	4637
Ser Val Glu Leu Leu Gly Ala Met Ala Tyr Cys Ala Pro Lys Gln Leu	
1319 1324 1329 1334	
tca tcc tgt cta ccc aac att gtg ccc aag ctt acg gag gtg ctg acc	4685
Ser Ser Cys Leu Pro Asn Ile Val Pro Lys Leu Thr Glu Val Leu Thr	
1335 1340 1345 1350	
gac tcc cat gtc aaa gtc cag aag gct gga cag cag gcg ctc agg cag	4733
Asp Ser His Val Lys Val Gln Lys Ala Gly Gln Gln Ala Leu Arg Gln	
1351 1356 1361 1366	
atc ggc tcc gtt atc agg aac ccg gag atc ctg gcc att gct cca gtc	4781
Ile Gly Ser Val Ile Arg Asn Pro Glu Ile Leu Ala Ile Ala Pro Val	
1367 1372 1377 1382	
ctc ctg gat gcc ctg acg gat ccc tcc agg aag acc cag aag tgc ttg	4829
Leu Leu Asp Ala Leu Thr Asp Pro Ser Arg Lys Thr Gln Lys Cys Leu	
1383 1388 1393 1398	
cag acc ctg ctg gac acc aag ttt gtc cac ttc att gat gcc cca tcc	4877
Gln Thr Leu Leu Asp Thr Lys Phe Val His Phe Ile Asp Ala Pro Ser	
1399 1404 1409 1414	

ctg gcc ctc atc atg ccc att gtc cag aga gcc ttc cag gac cgt tcc	4925
Leu Ala Leu Ile Met Pro Ile Val Gln Arg Ala Phe Gln Asp Arg Ser	
1415 1420 1425 1430	
acg gac acg cgg aag atg gca gcc cag att att ggc aac atg tac tcc	4973
Thr Asp Thr Arg Lys Met Ala Ala Gln Ile Ile Gly Asn Met Tyr Ser	
1431 1436 1441 1446	
ctg aca gac cag aag gac ttg gct ccg tac ctg ccc agc gtg acg cct	5021
Leu Thr Asp Gln Lys Asp Leu Ala Pro Tyr Leu Pro Ser Val Thr Pro	
1447 1452 1457 1462	
ggc ctg aaa gca tcg ctt ttg gac cct gtg cct gag gtg cgg acc gta	5069
Gly Leu Lys Ala Ser Leu Leu Asp Pro Val Pro Glu Val Arg Thr Val	
1463 1468 1473 1478	
tct gca aag gcc ctt ggg gcc atg gtg aag ggc atg ggg gag tcg tgc	5117
Ser Ala Lys Ala Leu Gly Ala Met Val Lys Gly Met Gly Glu Ser Cys	
1479 1484 1489 1494	
ttt gag gac ttg ctg ccg tgg ctg atg gag aca ctg acc tat gag cag	5165
Phe Glu Asp Leu Leu Pro Trp Leu Met Glu Thr Leu Thr Tyr Glu Gln	
1495 1500 1505 1510	
agc tct gtg gat cgc tca ggc gct gca cag ggg ttg gct gag gtc atg	5213
Ser Ser Val Asp Arg Ser Gly Ala Ala Gln Gly Leu Ala Glu Val Met	
1511 1516 1521 1526	
gcc ggt ttg ggg gtg gag aag ttg gag aag ttg atg cca gaa atc gtg	5261
Ala Gly Leu Gly Val Glu Lys Leu Glu Lys Leu Met Pro Glu Ile Val	
1527 1532 1537 1542	
gct aca gcc agc aaa gtg gac att gca ccc cat gtc cga gat ggc tac	5309
Ala Thr Ala Ser Lys Val Asp Ile Ala Pro His Val Arg Asp Gly Tyr	
1543 1548 1553 1558	
att atg atg ttt aac tac ctg ccc atc acc ttt gga gac aag ttt act	5357
Ile Met Met Phe Asn Tyr Leu Pro Ile Thr Phe Gly Asp Lys Phe Thr	
1559 1564 1569 1574	
cct tat gtg ggg ccc atc atc ccc tgt atc ctc aaa gct ctt gct gat	5405
Pro Tyr Val Gly Pro Ile Ile Pro Cys Ile Leu Lys Ala Leu Ala Asp	
1575 1580 1585 1590	
gag aat gag ttt gtg cgt gac acc gcc ctg cgc gcg ggc cag cgg gtt	5453
Glu Asn Glu Phe Val Arg Asp Thr Ala Leu Arg Ala Gly Gln Arg Val	
1591 1596 1601 1606	
atc tcc atg tac gct gag aca gcc atc gcc ctg ctg ctg ccc cag cta	5501
Ile Ser Met Tyr Ala Glu Thr Ala Ile Ala Leu Leu Leu Pro Gln Leu	
1607 1612 1617 1622	
gag caa ggc ctc ttt gat gac ctt tgg aga atc agg ttc agc tct gtt	5549
Glu Gln Gly Leu Phe Asp Asp Leu Trp Arg Ile Arg Phe Ser Ser Val	
1623 1628 1633 1638	
cag ctc ctt ggg gat ctc ctg ttt cac atc tca gga gtc act ggg aag	5597

Gln	Leu	Leu	Gly	Asp	Leu	Leu	Phe	His	Ile	Ser	Gly	Val	Thr	Gly	Lys	
1639					1644					1649					1654	
atg	acc	aca	gaa	act	gcc	tct	gag	gat	gat	aac	ttt	gga	act	gcc	cag	5645
Met	Thr	Thr	Glu	Thr	Ala	Ser	Glu	Asp	Asp	Asn	Phe	Gly	Thr	Ala	Gln	
1655					1660					1665					1670	
tcc	aac	aag	gcg	atc	atc	act	gcc	ctg	ggg	gta	gag	cgg	cgg	aac	cgg	5693
Ser	Asn	Lys	Ala	Ile	Ile	Thr	Ala	Leu	Gly	Val	Glu	Arg	Arg	Asn	Arg	
1671					1676					1681					1686	
gtg	ttg	gca	ggg	ctg	tac	atg	ggc	cgc	tca	gac	acc	cag	ctg	gtg	gtg	5741
Val	Leu	Ala	Gly	Leu	Tyr	Met	Gly	Arg	Ser	Asp	Thr	Gln	Leu	Val	Val	
1687					1692					1697					1702	
cgg	cag	gcg	tcc	ctg	cat	gtc	tgg	aag	att	gtt	gtc	tcc	aat	acc	ccc	5789
Arg	Gln	Ala	Ser	Leu	His	Val	Trp	Lys	Ile	Val	Val	Ser	Asn	Thr	Pro	
1703					1708					1713					1718	
cgc	acc	ttg	cgt	gag	atc	cta	ccc	act	ctc	ttt	ggg	ctc	ctg	ctg	ggt	5837
Arg	Thr	Leu	Arg	Glu	Ile	Leu	Pro	Thr	Leu	Phe	Gly	Leu	Leu	Leu	Gly	
1719					1724					1729					1734	
ttc	ctg	gcc	agc	acg	tgt	gca	gat	aag	aga	acg	att	gca	gcg	aga	aca	5885
Phe	Leu	Ala	Ser	Thr	Cys	Ala	Asp	Lys	Arg	Thr	Ile	Ala	Ala	Arg	Thr	
1735					1740					1745					1750	
ttg	gga	gat	ctt	gtg	cgg	aag	tta	ggg	gag	aaa	atc	ctc	ccc	gag	atc	5933
Leu	Gly	Asp	Leu	Val	Arg	Lys	Leu	Gly	Glu	Lys	Ile	Leu	Pro	Glu	Ile	
1751					1756					1761					1766	
atc	ccc	atc	ctt	gag	gaa	ggc	ctg	agg	tct	cag	aag	agc	gat	gag	agg	5981
Ile	Pro	Ile	Leu	Glu	Glu	Gly	Leu	Arg	Ser	Gln	Lys	Ser	Asp	Glu	Arg	
1767					1772					1777					1782	
cag	ggt	gtg	tgc	att	ggc	cta	agt	gag	atc	atg	aag	tcc	acc	agc	cgg	6029
Gln	Gly	Val	Cys	Ile	Gly	Leu	Ser	Glu	Ile	Met	Lys	Ser	Thr	Ser	Arg	
1783					1788					1793					1798	
gat	gcc	gtg	ctg	tat	ttc	tct	gaa	tcc	ctc	gtg	ccc	acg	gca	agg	aag	6077
Asp	Ala	Val	Leu	Tyr	Phe	Ser	Glu	Ser	Leu	Val	Pro	Thr	Ala	Arg	Lys	
1799					1804					1809					1814	
gct	ttg	tgt	gac	cca	ctg	gag	gag	gtc	aga	gag	gcg	gca	gcc	aag	act	6125
Ala	Leu	Cys	Asp	Pro	Leu	Glu	Glu	Val	Arg	Glu	Ala	Ala	Ala	Lys	Thr	
1815					1820					1825					1830	
ttc	gag	cag	ctg	cat	tcc	acc	atc	ggc	cac	cag	gct	ctg	gag	gac	att	6173
Phe	Glu	Gln	Leu	His	Ser	Thr	Ile	Gly	His	Gln	Ala	Leu	Glu	Asp	Ile	
1831					1836					1841					1846	
ctc	cca	ttt	tta	cta	aag	cag	ctg	gat	gac	gag	gag	gtg	tca	gag	ttt	6221
Leu	Pro	Phe	Leu	Leu	Lys	Gln	Leu	Asp	Asp	Glu	Glu	Val	Ser	Glu	Phe	
1847					1852					1857					1862	
gcc	ttg	gat	ggt	ctg	aag	caa	gtc	atg	gct	att	aag	agt	cgt	gtg	gtg	6269
Ala	Leu	Asp	Gly	Leu	Lys	Gln	Val	Met	Ala	Ile	Lys	Ser	Arg	Val	Val	

1863	1868	1873	1878	
ctg ccc tac ctt gtg ccc aag ctg aca acg cca cct gtc aac acc cgg				6317
Leu Pro Tyr Leu Val Pro Lys Leu Thr Thr Pro Pro Val Asn Thr Arg				
1879	1884	1889	1894	
gtg ctg gct ttc ctt tcg tca gtg gct ggt gat gcc ctc acc cgt cat				6365
Val Leu Ala Phe Leu Ser Ser Val Ala Gly Asp Ala Leu Thr Arg His				
1895	1900	1905	1910	
ctt ggc gtg atc ctc cca gcg gtc atg ctg gcc ctg aag gaa aag ctt				6413
Leu Gly Val Ile Leu Pro Ala Val Met Leu Ala Leu Lys Glu Lys Leu				
1911	1916	1921	1926	
ggg acc cca gat gag cag ctg gag atg gcc aat tgt cag gct gtg atc				6461
Gly Thr Pro Asp Glu Gln Leu Glu Met Ala Asn Cys Gln Ala Val Ile				
1927	1932	1937	1942	
ctc tcc gta gag gat gac aca ggg cac cgg atc atc atc gag gat ctg				6509
Leu Ser Val Glu Asp Asp Thr Gly His Arg Ile Ile Ile Glu Asp Leu				
1943	1948	1953	1958	
ctg gag gcc acc cgc agc cct gag gtg ggc atg agg caa gct gct gcc				6557
Leu Glu Ala Thr Arg Ser Pro Glu Val Gly Met Arg Gln Ala Ala Ala				
1959	1964	1969	1974	
atc atc ctc aac atc tac tgt tcc cgc tca aag gct gac tac acc agc				6605
Ile Ile Leu Asn Ile Tyr Cys Ser Arg Ser Lys Ala Asp Tyr Thr Ser				
1975	1980	1985	1990	
cac ctg cgg agc ctg gtc tcg ggc ctg atc cgc ctc ttc aat gac tcc				6653
His Leu Arg Ser Leu Val Ser Gly Leu Ile Arg Leu Phe Asn Asp Ser				
1991	1996	2001	2006	
agc cct gtg gtt ctg gag gag agc tgg gat gcc cta aat gcc atc act				6701
Ser Pro Val Val Leu Glu Glu Ser Trp Asp Ala Leu Asn Ala Ile Thr				
2007	2012	2017	2022	
aag aag ctg gat gct ggc aac cag ttg gca ctc att gaa gag ctg cac				6749
Lys Lys Leu Asp Ala Gly Asn Gln Leu Ala Leu Ile Glu Glu Leu His				
2023	2028	2033	2038	
aag gaa atc cgg ctc ata ggg aac gag agc aaa ggc gag cat gtg cca				6797
Lys Glu Ile Arg Leu Ile Gly Asn Glu Ser Lys Gly Glu His Val Pro				
2039	2044	2049	2054	
gga ttc tgc ctc ccg aag aag gga gtg acc tcc atc ctt cca gtg ttg				6845
Gly Phe Cys Leu Pro Lys Lys Gly Val Thr Ser Ile Leu Pro Val Leu				
2055	2060	2065	2070	
cgg gaa gga gtc ctg act ggc agc cct gag cag aag gag gag gca gcc				6893
Arg Glu Gly Val Leu Thr Gly Ser Pro Glu Gln Lys Glu Glu Ala Ala				
2071	2076	2081	2086	
aaa gcc tta ggc ttg gta atc cgc ctg acc tcg gct gac gcc ctg agg				6941
Lys Ala Leu Gly Leu Val Ile Arg Leu Thr Ser Ala Asp Ala Leu Arg				
2087	2092	2097	2102	

ccc tcc gtg gtc agc atc act ggc cct ctg atc cgc atc ctg ggg gac	6989
Pro Ser Val Val Ser Ile Thr Gly Pro Leu Ile Arg Ile Leu Gly Asp	
2103 2108 2113 2118	
agg ttc agc tgg aat gtg aag gcg gct ctg ctc gag aca ctc agc ctc	7037
Arg Phe Ser Trp Asn Val Lys Ala Ala Leu Leu Glu Thr Leu Ser Leu	
2119 2124 2129 2134	
ttg ttg gct aag gtt ggg att gcc ctg aag ccc ttc ctg ccc cag ctg	7085
Leu Leu Ala Lys Val Gly Ile Ala Leu Lys Pro Phe Leu Pro Gln Leu	
2135 2140 2145 2150	
cag acc act ttc acc aaa gcc ctg cag gac tcc aac cgg ggg gtg cgc	7133
Gln Thr Thr Phe Thr Lys Ala Leu Gln Asp Ser Asn Arg Gly Val Arg	
2151 2156 2161 2166	
ctg aag gcc gca gat gct ctg ggg aag ctc att tcc atc cac att aag	7181
Leu Lys Ala Ala Asp Ala Leu Gly Lys Leu Ile Ser Ile His Ile Lys	
2167 2172 2177 2182	
gtg gac ccc ctc ttc aca gag ctg ctc aat ggc atc cgc gcc atg gag	7229
Val Asp Pro Leu Phe Thr Glu Leu Leu Asn Gly Ile Arg Ala Met Glu	
2183 2188 2193 2198	
gac cca ggt gtc agg gac acc atg ctg cag gcc ctg agg ttt gtg att	7277
Asp Pro Gly Val Arg Asp Thr Met Leu Gln Ala Leu Arg Phe Val Ile	
2199 2204 2209 2214	
cag gga gca ggg gcc aaa gtg gat gcc gtc atc cgg aaa aac atc gtc	7325
Gln Gly Ala Gly Ala Lys Val Asp Ala Val Ile Arg Lys Asn Ile Val	
2215 2220 2225 2230	
tca ctc ctg ctg agc atg ctg gga cac gat gag gac aac act cgc atc	7373
Ser Leu Leu Leu Ser Met Leu Gly His Asp Glu Asp Asn Thr Arg Ile	
2231 2236 2241 2246	
tcc tca gcc ggg tgc cta ggg gaa ctg tgt gcc ttt ttg act gaa gag	7421
Ser Ser Ala Gly Cys Leu Gly Glu Leu Cys Ala Phe Leu Thr Glu Glu	
2247 2252 2257 2262	
gag ctt agt gcc gtt cta cag cag tgc ttg ctg gcg gac gtg tcc ggc	7469
Glu Leu Ser Ala Val Leu Gln Gln Cys Leu Leu Ala Asp Val Ser Gly	
2263 2268 2273 2278	
att gac tgg atg gtt cgg cac ggg cgg agc ctg gca ctt tcc gtg gct	7517
Ile Asp Trp Met Val Arg His Gly Arg Ser Leu Ala Leu Ser Val Ala	
2279 2284 2289 2294	
gtg aat gtg gct cct ggc aga ctt tgt gcc ggc aga tat agc agt gat	7565
Val Asn Val Ala Pro Gly Arg Leu Cys Ala Gly Arg Tyr Ser Ser Asp	
2295 2300 2305 2310	
gtt cag gaa atg atc ctg agc agt gcc acg gcg gac agg atc ccc att	7613
Val Gln Glu Met Ile Leu Ser Ser Ala Thr Ala Asp Arg Ile Pro Ile	
2311 2316 2321 2326	

aaaaaaaa

8649

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 <211> 2230
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (85)..(1152)

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 aagaatgccg tgtttcctgg atct atg gag gga atc cca gga ttt cct gga 111
 Met Glu Gly Ile Pro Gly Phe Pro Gly
 1 5

 aac cga gga tta atg ggc caa aag gga gaa att ggg cct cca gga cag 159
 Asn Arg Gly Leu Met Gly Gln Lys Gly Glu Ile Gly Pro Pro Gly Gln
 10 15 20 25

 caa gga aaa aaa gga gcc cca ggg atg cct ggt tta atg gga agc aat 207
 Gln Gly Lys Lys Gly Ala Pro Gly Met Pro Gly Leu Met Gly Ser Asn
 26 31 36 41

 ggc tca cca ggc cag cct gga aca ccg gga tct aag gga agc aaa ggt 255
 Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys Gly
 42 47 52 57

 gaa cct gga att caa ggg atg cct ggg gct tct ggg ctc aag gga gaa 303
 Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser Gly Leu Lys Gly Glu
 58 63 68 73

 cca gga gca acg ggt tcc cca gga gaa cca gga tac atg ggt tta ccc 351
 Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met Gly Leu Pro
 74 79 84 89

 ggg att caa gga aaa aag ggg gac aaa gga aat caa ggt gaa aaa ggt 399
 Gly Ile Gln Gly Lys Lys Gly Asp Lys Gly Asn Gln Gly Glu Lys Gly
 90 95 100 105

 att cag ggt caa aag gga gaa aat gga aga cag gga att cca ggg caa 447
 Ile Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln Gly Ile Pro Gly Gln
 106 111 116 121

 cag gga att caa ggc cat cat ggt gca aaa gga gag aga ggt gaa aag 495
 Gln Gly Ile Gln Gly His His Gly Ala Lys Gly Glu Arg Gly Glu Lys
 122 127 132 137

 gga gaa cct ggt gtc cga ggt gcc att gga tca aaa gga gaa tct ggg 543
 Gly Glu Pro Gly Val Arg Gly Ala Ile Gly Ser Lys Gly Glu Ser Gly
 138 143 148 153

gtg gat ggc ttg atg ggg ccc gca ggt cct aag ggg caa cct ggg gat	591
Val Asp Gly Leu Met Gly Pro Ala Gly Pro Lys Gly Gln Pro Gly Asp	
154 159 164 169	
cca ggt cct cag gga ccc cca ggt ttg gat ggg aag ccc gga aga gag	639
Pro Gly Pro Gln Gly Pro Pro Gly Leu Asp Gly Lys Pro Gly Arg Glu	
170 175 180 185	
ttt tca gaa caa ttt att cga caa gtt tgc aca gat gta ata aga gcc	687
Phe Ser Glu Gln Phe Ile Arg Gln Val Cys Thr Asp Val Ile Arg Ala	
186 191 196 201	
cag cta cca gtc tta ctt cag agt gga aga att aga aat tgt gat cat	735
Gln Leu Pro Val Leu Leu Gln Ser Gly Arg Ile Arg Asn Cys Asp His	
202 207 212 217	
tgc ctg tcc caa cat ggc tcc ccg ggt att cct ggg cca cct ggt ccg	783
Cys Leu Ser Gln His Gly Ser Pro Gly Ile Pro Gly Pro Pro Gly Pro	
218 223 228 233	
ata ggc cca gag ggt ccc aga gga tta cct ggt ttg cca gga aga gat	831
Ile Gly Pro Glu Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Arg Asp	
234 239 244 249	
ggg gtt cct gga tta gtg ggt gtc cct gga cgt cca ggt gtc aga gga	879
Gly Val Pro Gly Leu Val Gly Val Pro Gly Arg Pro Gly Val Arg Gly	
250 255 260 265	
tta aaa ggc cta cca gga aga aat ggg gaa aaa ggg agc caa ggg ttt	927
Leu Lys Gly Leu Pro Gly Arg Asn Gly Glu Lys Gly Ser Gln Gly Phe	
266 271 276 281	
ggg tat cct gga gaa caa ggt cct cct ggt ccc cca ggt cca gag ggc	975
Gly Tyr Pro Gly Glu Gln Gly Pro Pro Gly Pro Pro Gly Pro Glu Gly	
282 287 292 297	
cct cct gga ata agc aaa gaa ggt cct cca gga gac cca ggt ctc cct	1023
Pro Pro Gly Ile Ser Lys Glu Gly Pro Pro Gly Asp Pro Gly Leu Pro	
298 303 308 313	
ggc aaa gat gga gac cat gga aaa cct gga atc caa ggg caa cca ggc	1071
Gly Lys Asp Gly Asp His Gly Lys Pro Gly Ile Gln Gly Gln Pro Gly	
314 319 324 329	
ccc cca ggc atc tgc gac cca tca cta tgt ttt agt gta att gcc aga	1119
Pro Pro Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser Val Ile Ala Arg	
330 335 340 345	
aga gat ccg ttc aga aaa gga cca aac tat tag tgtctgat gcctcattca	1170
Arg Asp Pro Phe Arg Lys Gly Pro Asn Tyr *	
346 351 356	
gcagcctagg catggtgctt tttctgtggt cttttgcac tcaggaagat aaccaacagt	1230
aatcccttga aaagaaactt aagtacctcg gcgtttttat tttttttttc ttatggaaaa	1290

aaatataaaa gatcacatat actgatttta aaggctcctc agtcatttgg agcccttgga	1350
ttagcagcat taattaaatc tcaaggggtt cttgtaaagt ccatttatgt taatcaaagt	1410
tgaatataaa aatccaccat tgccgttag ccagtcagtt ttagtcactg tgaaatattt	1470
cacattcagc ctccatgcag tagagatttg agtttaattt catgtccatg tgactttcat	1530
gtttcctatc tcatagctca tgctactaca taagccaaaa catgtatctc atcattggaa	1590
gtaagatcag ggctgatatt cacctgggat agacagtatt ggtgaactac tcatttacta	1650
cagtgtctca gccttgataa ggggcagtggt attgcctgtt gttcgggtgtt gtgaatagca	1710
cctctgaata agattagagt gtttcttaat tcatttcaaa ctctaaaatt agattaatgg	1770
tggtgctaag aaagagtatt aattactttg ggaatggtca aaattaacat taaaaacatt	1830
ttagacaaaa agtttcattg tacattcaaa gaaaatgtaa gtttggaagt actaaaagac	1890
tattttatac ttgttgatta atcggaatgt ttgttgtagt ccttcatttt ccatttcact	1950
tatatgtgta tgtccatata tgtaatttt cattgtagca aagctaattg aaataaagct	2010
aatgctctag ttgaaagaaa aggaaaactc ctgaaatcct agaatgtctt gttattttta	2070
gctgactgta aaatattatg aacagtcttt gtgtattgtg cttaatgctt ttgtaagaaa	2130
cagaatttga aatatttcat ccttgatcat ctcaaaattt tgttacatgc ttgttattca	2190
gagtataata aagttttgta caggcctgaa aaaaaaaaaa	2230

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 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (266) .. (706)

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aatgtagggtg gagcaacttc cctgcaacac acgtcgaagc tgctgcagtg gctgttcttc	120
ccctccctt ggaaaggcac caaaagccag cctttggaag ggctgggtgga ctgtgccctt	180
ctttcccttc agagaaccag tgtccctgtg actccaccca ctcatctggc caccgttgcc	240
ctgacctgcc aggagcctgg agaag atg aag gca tcc gtg gtt ctc tcc ctc	292
Met Lys Ala Ser Val Val Leu Ser Leu	
1 5	

ctt ggc tac ctg gtg gtt cca agt ggt gct tac atc ttg ggg cgt tgc	340
Leu Gly Tyr Leu Val Val Pro Ser Gly Ala Tyr Ile Leu Gly Arg Cys	
10 15 20 25	
aca gtg gct aag aaa ctc cac gat gga ggc ctg gat tat ttt gag ggc	388
Thr Val Ala Lys Lys Leu His Asp Gly Gly Leu Asp Tyr Phe Glu Gly	
26 31 36 41	
tat agc ctt gag aac tgg gtg tgc ctg gcc tac ttc gag agc aag ttc	436
Tyr Ser Leu Glu Asn Trp Val Cys Leu Ala Tyr Phe Glu Ser Lys Phe	
42 47 52 57	
aac ccc atg gcc atc tac gag aac aca cgt gag ggc tac act ggc ttt	484
Asn Pro Met Ala Ile Tyr Glu Asn Thr Arg Glu Gly Tyr Thr Gly Phe	
58 63 68 73	
ggc ctc ttt cag atg cgt ggc agt gac tgg tgt ggc gac cat ggc agg	532
Gly Leu Phe Gln Met Arg Gly Ser Asp Trp Cys Gly Asp His Gly Arg	
74 79 84 89	
aac cgc tgc cat atg tca tgt tcc gct tta ctg aat cct aat tta gag	580
Asn Arg Cys His Met Ser Cys Ser Ala Leu Leu Asn Pro Asn Leu Glu	
90 95 100 105	
aag aca att aaa tgt gcc aag acc att gta aaa gga aaa gaa ggg atg	628
Lys Thr Ile Lys Cys Ala Lys Thr Ile Val Lys Gly Lys Glu Gly Met	
106 111 116 121	
gga gca tgg ccc acc tgg tcc cgg tac tgc cag tac tcc gat acc ctg	676
Gly Ala Trp Pro Thr Trp Ser Arg Tyr Cys Gln Tyr Ser Asp Thr Leu	
122 127 132 137	
gca cgg tgg ctg gat ggt tgc aag ctg tag c cgccctgcatg gccccctgcag	727
Ala Arg Trp Leu Asp Gly Cys Lys Leu *	
138 143	
cactcaccag ttgcatcttg tgaatgaagg tgctttttctg cttgctgctt cagtcaatcc	787
ttttgatgat ctcaccactt taagagttcc agatggaaaa agacaaaagt ttgcttcac	847
cggggatgca ggatgcagaa taaaccaaac tagttactca aaaaaaaaaa	897

<210> 242
 <211> 2817
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (96) .. (1232)

<400> 242	
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tggtctcagtg gcttctgcgg gcttcgagga gcggg	atg ttg cgg gct ggg tgg	113
	Met Leu Arg Ala Gly Trp	
	1	
ctc cgg ggc gcg gcg gcg ctg gcg ctg ctg ctg gcg gcc cga gtg gtg		161
Leu Arg Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala Ala Arg Val Val		
7 12 17 22		
gcg gcg ttc gag ccc atc acc gtg ggc cta gcc atc ggg gcc gcg tcg		209
Ala Ala Phe Glu Pro Ile Thr Val Gly Leu Ala Ile Gly Ala Ala Ser		
23 28 33 38		
gcc atc acc ggc tac ctg tcc tac aat gac atc tac tgc cgc ttc gcc		257
Ala Ile Thr Gly Tyr Leu Ser Tyr Asn Asp Ile Tyr Cys Arg Phe Ala		
39 44 49 54		
gag tgc tgc cgc gag gag cgg ccg ctc aac gct tcg gct ctc aag ctg		305
Glu Cys Cys Arg Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys Leu		
55 60 65 70		
gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg att		353
Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile		
71 76 81 86		
ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa cca		401
Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro		
87 92 97 102		
ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt gtc		449
Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val		
103 108 113 118		
agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac		497
Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn		
119 124 129 134		
ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag aag		545
Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys		
135 140 145 150		
ata aaa ctg tac ccg gac cag tta cag aag tgg atc cgc ggt aat gtg		593
Ile Lys Leu Tyr Pro Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val		
151 156 161 166		
agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa ttg		641
Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu		
167 172 177 182		
cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag		689
His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu		
183 188 193 198		
cag gtt gac gga gtg tat tac cgc aaa gcc atc ttc atc ttt ctc agc		737
Gln Val Asp Gly Val Tyr Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser		
199 204 209 214		
aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cgg		785

Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg	
215 220 225 230	
gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	833
Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val	
231 236 241 246	
ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	881
Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser	
247 252 257 262	
gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	929
Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro	
263 268 273 278	
ttg gag tac aga cat gtg aaa atg tgt gtg atg gcc gag atg agg gcc	977
Leu Glu Tyr Arg His Val Lys Met Cys Val Met Ala Glu Met Arg Ala	
279 284 289 294	
cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	1025
Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu	
295 300 305 310	
atg acg ttt ttt ccc cag aga cga gaa aat cta ctc aga caa ggg ctg	1073
Met Thr Phe Phe Pro Gln Arg Arg Glu Asn Leu Leu Arg Gln Gly Leu	
311 316 321 326	
caa gac tgt gca gtc gcg gct gga ttt cca ctg agc tcc tat cca gat	1121
Gln Asp Cys Ala Val Ala Ala Gly Phe Pro Leu Ser Ser Tyr Pro Asp	
327 332 337 342	
ggg gta gga gac agc tgg gag gct ccg cac gcc aga ggc ctt gcc ttt	1169
Gly Val Gly Asp Ser Trp Glu Ala Pro His Ala Arg Gly Leu Ala Phe	
343 348 353 358	
cag aag aac cct gaa gac cgc ttt ggg gtt ttg cct gtt tgc acc tta	1217
Gln Lys Asn Pro Glu Asp Arg Phe Gly Val Leu Pro Val Cys Thr Leu	
359 364 369 374	
gac ttt tgg gta tag aatctttttt ttgagaagag gtctcactcc gtcaccaag	1272
Asp Phe Trp Val *	
375	
ctggagtgcg gtggtgcaat cctcaactca ctgcaacctc cgctcccggt ttgagtgatt	1332
ctcatgcctc agcctcccga gtagctggga ttacaggcat gagccactgt gccagctgg	1392
gatatagaat ctaagagttg attgtggaaa acacgtgaat ctattgcgcg catttgcat	1452
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ccttcacact taatgtactg accgagacag aagtacctga aaacagctgt gcatggcagg	1572
cccggcaata gcttctgacc cacagcaccg gcgcctcaga agctacggtc acaactaaag	1632
gagtcagggt acttgctgca ggctgggggg cactgggtgg ttctcaccag caggctgcgg	1692

ggcactgtgt	tctcattggc	caaaaacatc	cttttgctct	gtctcgttct	ttacacagag	1752
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cggaggatgt	ggccgtgccc	gccgagcact	cttgatctga	gctgacctgt	gtgtgtgtgt	1872
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ccgcctgtcc	atcgctctag	ctgctaatac	agcgctggct	gtggaatcct	tcaccgtctc	1992
agctggatc	agccccagcc	tgccttgtgc	catatctcag	cttggatctc	tgctagagtc	2052
cccccaacca	tatatcatag	agttgaatca	caatgagacc	gttggctttg	aatttgagtc	2112
gttggttccc	atggtgagat	gcttggttaag	actttatact	tgggtcaatc	tctcacttta	2172
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gactgaacaa	gtcagcttga	tgatcttaaa	tgatggaagt	ataggacgtt	gcttatttta	2292
aaacaaggga	aggacacaaa	atggaatgac	tgcttagtcc	tttctcagat	actcttaaaa	2352
caatttttta	ttgttaaatt	tgtggaata	catggtcaca	accgtggatc	aaacaaggtc	2412
agtctaaagt	ggcaggctct	aggtgtgacc	tgataccacc	accctttgtg	gcagcacccg	2472
gctggactgc	cctgatccct	gggacgtgag	acttagcttc	cagccagtgt	gaatcattgt	2532
atctgtctca	taatcacagc	acagctgcag	acacaacaac	gtgcagcatt	ttttacataa	2592
aaatatggta	gaattaattt	atgacatgga	aatgccttac	gtggtatcac	acttagtctt	2652
gaaaaaaa	ccaaggtgac	gtttaaaatt	tttagtacat	atcctcaa	atgaggctaag	2712
ttatacttct	tttataacct	tttgggcata	tggtcgagag	aagacaagat	tttctctatt	2772
tacagtgagg	caataaatat	gtttgccacc	tttaaaaaaa	aaaaa		2817

<210> 243

<211> 1015

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (88) .. (351)

<400> 243

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acgcgtccgg	attgggaaaa	caacgat	atg gca gga gcc agt ctt ggg gcc	111
			Met Ala Gly Ala Ser Leu Gly Ala	
			1 5	

cgc ttc tac cgg cag atc aaa aga cat ccg ggg atc atc ccg atg atc	159
Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile Ile Pro Met Ile	
9 14 19 24	
ggc tta atc tgc ctg ggc atg ggc agc gct gcg ctt tac ttg ctg cga	207
Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu Tyr Leu Leu Arg	
25 30 35 40	
ctc gcc ctt cgc agc ccc gac gtc tgc tgg gac aga aag aac aac ccg	255
Leu Ala Leu Arg Ser Pro Asp Val Cys Trp Asp Arg Lys Asn Asn Pro	
41 46 51 56	
gag ccc tgg aac cgc ctg agc ccc aat gac caa tac aag ttc ctt gca	303
Glu Pro Trp Asn Arg Leu Ser Pro Asn Asp Gln Tyr Lys Phe Leu Ala	
57 62 67 72	
gtt tcc act gac tat aag aag ctg aag aag gac cgg cca gac ttc taa	351
Val Ser Thr Asp Tyr Lys Lys Leu Lys Lys Asp Arg Pro Asp Phe *	
73 78 83 88	
gccaggctgg gctgccagtg ccatgcaagc cacagccagc cagcccatcc acttcttcca	411
ctctctccccg caggccccaa ggcatactc cggccaccct gtcccgctac tgcttacaca	471
ggccgggttc ccacgcagag gggaggctgc tccacccta ctctctccc ttgctccag	531
cagcgggaagc gcctctgacc cttggcttga gtcccacgtg ggggaggagg aggcaggcag	591
caccagcagg ggtccaccaa gagcccagac cagccctct gccctctac ccgggcctcg	651
aagggtgtgg cacaggctac gtgttgagcg tggcctacgt gagccaacaa gaagcagggg	711
cctctgagt ccaagcgacg tggcgggctc cacgttagcc caggctctga gagccagccc	771
aggggcgggc ctgctcagct tgggctggtc cagggcctgc ccaggctggg gcacctttgc	831
ctcctgaggc gcagcgact cctcccctgc ccaagcctac tgccctccgc tgccgccagt	891
acccctcca gccccacacc tgggcctccc cctgccactc cctcccttg ctcccctctg	951
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aaaa	1015

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ctctctacag agacgcggac cccagac      atg agg agg ctc ctc ctg gtc acc      111
                                   Met Arg Arg Leu Leu Leu Val Thr
                                   1                               5

agc ctg gtg gtt gtg ctg ctg tgg gag gca ggt gca gtc cca gca ccc      159
Ser Leu Val Val Val Leu Leu Trp Glu Ala Gly Ala Val Pro Ala Pro
  9                               14                               19                               24

aag gtc cct atc aag atg caa gtc aaa cac tgg ccc tca gag cag gac      207
Lys Val Pro Ile Lys Met Gln Val Lys His Trp Pro Ser Glu Gln Asp
 25                               30                               35                               40

cca gag aag gcc tgg ggc gcc cgt gtg gtg gag cct ccg gag aag gac      255
Pro Glu Lys Ala Trp Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp
 41                               46                               51                               56

gac cag ctg gtg gtg ctg ttc cct gtc cag aag ccg aaa ctc ttg acc      303
Asp Gln Leu Val Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr
 57                               62                               67                               72

acc gag gag aag cca cga ggc acc aag gcc tgg atg gag acc gag gac      351
Thr Glu Glu Lys Pro Arg Gly Thr Lys Ala Trp Met Glu Thr Glu Asp
 73                               78                               83                               88

acc ctg ggc cgt gtc ctg agt ccc gag ccc gac cat gac agc ctg tac      399
Thr Leu Gly Arg Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu Tyr
 89                               94                               99                               104

cac cct ccg cct gag gag gac cag ggc gag gag agg ccc ccg ttg tgg      447
His Pro Pro Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu Trp
105                               110                               115                               120

gtg atg cca aat cac cag gtg ctc ctg gga ccg gag gaa gac caa gac      495
Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln Asp
121                               126                               131                               136

cac atc tac cac ccc cag tag gg ctccaggggc catcactgcc cccgccctgt      548
His Ile Tyr His Pro Gln *
137                               142

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Met Arg Arg Leu Leu Leu Val Thr
1 5
agc ctg gtg gtt gtg ctg ctg tgg gag gca ggt gca gtc cca gca ccc 159
Ser Leu Val Val Val Leu Leu Trp Glu Ala Gly Ala Val Pro Ala Pro
9 14 19 24
aag gtc cct atc aag atg caa gtc aaa cac tgg ccc tca gag cag gac 207
Lys Val Pro Ile Lys Met Gln Val Lys His Trp Pro Ser Glu Gln Asp
25 30 35 40
cca gag aag gcc tgg ggc gcc cgt gtg gtg gag cct ccg gag aag gac 255
Pro Glu Lys Ala Trp Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp
41 46 51 56
gac cag ctg gtg gtg ctg ttc cct gtc cag aag ccg aaa ctc ttg acc 303
Asp Gln Leu Val Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr
57 62 67 72
acc gag gag aag cca cga ggt cag ggc agg ggc ccc atc ctt cca ggc 351
Thr Glu Glu Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly
73 78 83 88
acc aag gcc tgg atg gag acc gag gac acc ctg ggc cgt gtc ctg agt 399
Thr Lys Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser
89 94 99 104
ccc gag ccc gac cat gac agc ctg tac cac cct ccg cct gag gag gac 447
Pro Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
105 110 115 120
cag ggc gag gag agg ccc cgg ttg tgg gtg atg cca aat cac cag gtg 495
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln Val
121 126 131 136
ctc ctg gga ccg gag gaa gac caa gac cac atc tac cac ccc cag tag 543
Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro Gln *
137 142 147 152
ggctccaggg gccatcactg cccccgcct gtcccaaggc ccaggetggt gggactggga 603
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tcc gtc gac ggc ctc acg ctc agc ccg gac ccg gag gag cgg cct ggg	96	
Ser Val Asp Gly Leu Thr Leu Ser Pro Asp Pro Glu Glu Arg Pro Gly		
13 18 23 28		
gcg gag ggc gcc ccg ctg ctg ccg cca ccg ctg cca ccg ccc tcg cca	144	
Ala Glu Gly Ala Pro Leu Leu Pro Pro Pro Leu Pro Pro Pro Ser Pro		
29 34 39 44		
cct gga tcc ggt cgc ggc ccg ggc gcc tca ggg gag cag ccc gag ccc	192	
Pro Gly Ser Gly Arg Gly Pro Gly Ala Ser Gly Glu Gln Pro Glu Pro		
45 50 55 60		
ggg gag gcg gcg gct ggg ggc gcg gcg gag gag gcg cgg cgg ctg gag	240	
Gly Glu Ala Ala Ala Gly Gly Ala Ala Glu Glu Ala Arg Arg Leu Glu		
61 66 71 76		
cag cgc tgg ggt ttc ggc ctg gag gag ttg tac ggc ctg gca ctg cgc	288	
Gln Arg Trp Gly Phe Gly Leu Glu Glu Leu Tyr Gly Leu Ala Leu Arg		
77 82 87 92		
ttc ttc aaa gaa aaa gat ggc aaa gca ttt cat cca act tat gaa gaa	336	
Phe Phe Lys Glu Lys Asp Gly Lys Ala Phe His Pro Thr Tyr Glu Glu		
93 98 103 108		
aaa ttg aag ctt gtg gca ctg cat aag caa gtt ctt atg ggc cca tat	384	
Lys Leu Lys Leu Val Ala Leu His Lys Gln Val Leu Met Gly Pro Tyr		
109 114 119 124		
aat cca gac act tgt cct gag gtt gga ttc ttt gat gtg ttg ggg aat	432	
Asn Pro Asp Thr Cys Pro Glu Val Gly Phe Phe Asp Val Leu Gly Asn		
125 130 135 140		
gac agg agg aga gaa tgg gca gcc ctg gga aac atg tct aaa gag gat	480	
Asp Arg Arg Arg Glu Trp Ala Ala Leu Gly Asn Met Ser Lys Glu Asp		
141 146 151 156		
gcc atg gtg gag ttt gtc aag ctc tta aat agg tgt tgc cat ctc ttt	528	
Ala Met Val Glu Phe Val Lys Leu Leu Asn Arg Cys Cys His Leu Phe		
157 162 167 172		
tca aca tat gtt gcg tcc cac aaa ata gag aag gaa gag caa gac aaa	576	
Ser Thr Tyr Val Ala Ser His Lys Ile Glu Lys Glu Glu Gln Asp Lys		
173 178 183 188		
aaa agg aag gag gaa gag gag cga agg cat cgt gaa gag gaa gaa aga	624	
Lys Arg Lys Glu Glu Glu Glu Arg Arg His Arg Glu Glu Glu Glu Arg		
189 194 199 204		
gaa cgt ctg caa aag gag gaa gag aaa cgt agg aga gaa gaa gag gaa	672	

Glu Arg Leu Gln Lys	Glu Glu Glu Lys Arg	Arg Arg Glu Glu Glu Glu	205	210	215	220	
agg ctt cga cgg gag	gaa gag gaa agg aga	cgg ata gaa gaa gaa agg	720				
Arg Leu Arg Arg Glu	Glu Glu Glu Arg Arg	Arg Ile Glu Glu Glu Arg	221	226	231	236	
ctt cgg ttg gag cag	caa aag cag cag ata	atg gca gct tta aac tcc	768				
Leu Arg Leu Glu Gln	Gln Lys Gln Gln Ile	Met Ala Ala Leu Asn Ser	237	242	247	252	
cag act gcc gtg cag	ttc cag cag tat gca	gcc caa cag tat cca ggg	816				
Gln Thr Ala Val Gln	Phe Gln Gln Tyr Ala	Ala Gln Gln Tyr Pro Gly	253	258	263	268	
aac tac gaa cag cag	caa att ctc atc cgc	cag ttg cag gag caa cac	864				
Asn Tyr Glu Gln Gln	Gln Ile Leu Ile Arg	Gln Leu Gln Glu Gln His	269	274	279	284	
tat cag cag tac atg	cag cag ttg tat caa	gtc cag ctt gca cag caa	912				
Tyr Gln Gln Tyr Met	Gln Gln Leu Tyr Gln	Val Gln Leu Ala Gln Gln	285	290	295	300	
cag gca gca tta cag	aaa caa cag gaa gta	gta gtg gct ggg tct tcc	960				
Gln Ala Ala Leu Gln	Lys Gln Gln Glu Val	Val Val Ala Gly Ser Ser	301	306	311	316	
ttg cct aca tca tca	aaa gtg aat gca act	gta cca agt aat atg atg	1008				
Leu Pro Thr Ser Ser	Lys Val Asn Ala Thr	Val Pro Ser Asn Met Met	317	322	327	332	
tca gtt aat gga cag	gcc aaa aca cac act	gac agc tcc gaa aaa gaa	1056				
Ser Val Asn Gly Gln	Ala Lys Thr His Thr	Asp Ser Ser Glu Lys Glu	333	338	343	348	
ctg gaa cca gaa gct	gca gaa gaa gcc ctg	gag aat gga cca aaa gaa	1104				
Leu Glu Pro Glu Ala	Ala Glu Glu Ala Leu	Glu Asn Gly Pro Lys Glu	349	354	359	364	
tct ctt cca gta ata	gca gct cca tcc atg	tgg aca cga cct cag atc	1152				
Ser Leu Pro Val Ile	Ala Ala Pro Ser Met	Trp Thr Arg Pro Gln Ile	365	370	375	380	
aaa gac ttc aaa gag	aag att cag cag gat	gca gat tcc gtg att aca	1200				
Lys Asp Phe Lys Glu	Lys Ile Gln Gln Asp	Ala Asp Ser Val Ile Thr	381	386	391	396	
gtg ggc cga gga gaa	gtg gtc act gtt cga	gta ccc acc cat gaa gaa	1248				
Val Gly Arg Gly Glu	Val Val Thr Val Arg	Val Pro Thr His Glu Glu	397	402	407	412	
gga tca tat ctc ttt	tgg gaa ttt gcc aca	gac aat tat gac att ggg	1296				
Gly Ser Tyr Leu Phe	Trp Glu Phe Ala Thr	Asp Asn Tyr Asp Ile Gly	413	418	423	428	
ttt ggg gtg tat ttt	gaa tgg aca gac tct	cca aac act gct gtc agc	1344				
Phe Gly Val Tyr Phe	Glu Trp Thr Asp Ser	Pro Asn Thr Ala Val Ser					

429	434	439	444	
gtg cat gtc agt gag tcc agc gat gac gac	gag gag gaa gaa gaa aac	1392		
Val His Val Ser Glu Ser Ser Asp Asp Asp	Glu Glu Glu Glu Glu Asn			
445	450	455	460	
atc ggt tgt gaa gag aaa gcc aaa aag aat	gcc aac aag cct ttg ctg	1440		
Ile Gly Cys Glu Glu Lys Ala Lys Lys Asn	Ala Asn Lys Pro Leu Leu			
461	466	471	476	
gat gag att gtg cct gtg tac cga cgg gac	tgt cat gag gag gtg tat	1488		
Asp Glu Ile Val Pro Val Tyr Arg Arg Asp	Cys His Glu Glu Val Tyr			
477	482	487	492	
gct ggc agc cat caa tat cca ggg aga gga	gtc tat ctc ctc aag ttt	1536		
Ala Gly Ser His Gln Tyr Pro Gly Arg Gly	Val Tyr Leu Leu Lys Phe			
493	498	503	508	
gac aac tcc tac tct ttg tgg cgg tca aaa	tca gtc tac tac aga gtc	1584		
Asp Asn Ser Tyr Ser Leu Trp Arg Ser Lys	Ser Val Tyr Tyr Arg Val			
509	514	519	524	
tat tat act aga taa aaatgttggt acaaagtctg	gagtctaggg ttgggcagaa	1639		
Tyr Tyr Thr Arg *				
525				
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 gttctctctt gcacagccta aaatgaccaa tgtgtgattt cagtgaata a atg gcg 177
 Met Ala
 1
 tcc aaa gtc aca gat gct ata gtc tgg tat caa aag aag att gga gca 225
 Ser Lys Val Thr Asp Ala Ile Val Trp Tyr Gln Lys Lys Ile Gly Ala
 3 8 13 18
 tat gaa caa caa ata tgg gaa aaa tct gtt gaa cag aga gaa atc aag 273
 Tyr Glu Gln Gln Ile Trp Glu Lys Ser Val Glu Gln Arg Glu Ile Lys
 19 24 29 34

ttt att aaa ctg ggg cta agg aat aaa cca aag aaa aca gca cat gtg	321
Phe Ile Lys Leu Gly Leu Arg Asn Lys Pro Lys Lys Thr Ala His Val	
35 40 45 50	
aaa cca gac ctc ata gat gtt gat ctt gta aga ggg tct gca ttt gca	369
Lys Pro Asp Leu Ile Asp Val Asp Leu Val Arg Gly Ser Ala Phe Ala	
51 56 61 66	
aag gca aag cct gaa agt cct tgg act tct cta cca aga aag gga att	417
Lys Ala Lys Pro Glu Ser Pro Trp Thr Ser Leu Pro Arg Lys Gly Ile	
67 72 77 82	
gtt cga gtt gta ttt ttc ccc ttt ttc ttc cgg tgg tgg tta caa gta	465
Val Arg Val Val Phe Phe Pro Phe Phe Phe Arg Trp Trp Leu Gln Val	
83 88 93 98	
aca tca aag gtc atc ttt ttc tgg ctt ctt gtc ctt tat ctt ctt caa	513
Thr Ser Lys Val Ile Phe Phe Trp Leu Leu Val Leu Tyr Leu Leu Gln	
99 104 109 114	
gtt gct gca ata gta tta ttc tgc tcc act tct agc cca cac agc ata	561
Val Ala Ala Ile Val Leu Phe Cys Ser Thr Ser Ser Pro His Ser Ile	
115 120 125 130	
cct ctg aca gag gtg att ggg ccg ata tgg ctg atg ctg ctc ctg gga	609
Pro Leu Thr Glu Val Ile Gly Pro Ile Trp Leu Met Leu Leu Leu Gly	
131 136 141 146	
act gtg cat tgc cag att gtt tcc aca aga aca ccc aaa cct cct cta	657
Thr Val His Cys Gln Ile Val Ser Thr Arg Thr Pro Lys Pro Pro Leu	
147 152 157 162	
agt aca ggg ggt aaa aga aga agg aaa tta aga aaa gca gcc cat ttg	705
Ser Thr Gly Gly Lys Arg Arg Arg Lys Leu Arg Lys Ala Ala His Leu	
163 168 173 178	
gaa gta cat agg gaa gga gat ggt tct agt acc aca gat aac aca caa	753
Glu Val His Arg Glu Gly Asp Gly Ser Ser Thr Thr Asp Asn Thr Gln	
179 184 189 194	
gag gga gca gtt cag aac cac ggt aca agc acc tct cac agc gtt ggc	801
Glu Gly Ala Val Gln Asn His Gly Thr Ser Thr Ser His Ser Val Gly	
195 200 205 210	
act gtc ttc aga gat ctc tgg cat gct gct ttc ttt tta tca gga tca	849
Thr Val Phe Arg Asp Leu Trp His Ala Ala Phe Phe Leu Ser Gly Ser	
211 216 221 226	
aag aaa gca aag aat tca att gat aaa tca act gaa act gac aat ggc	897
Lys Lys Ala Lys Asn Ser Ile Asp Lys Ser Thr Glu Thr Asp Asn Gly	
227 232 237 242	
tat gta tcc ctt gat ggg aag aag act gtt aaa agc ggt gaa gat gga	945
Tyr Val Ser Leu Asp Gly Lys Lys Thr Val Lys Ser Gly Glu Asp Gly	
243 248 253 258	

ata caa aac cat gaa cct cag tgt gaa act att cga cca gaa gag aca	993
Ile Gln Asn His Glu Pro Gln Cys Glu Thr Ile Arg Pro Glu Glu Thr	
259 264 269 274	
gcc tgg aac aca gga aca ctg agg aat ggt cct agc aaa gat acc caa	1041
Ala Trp Asn Thr Gly Thr Leu Arg Asn Gly Pro Ser Lys Asp Thr Gln	
275 280 285 290	
agg aca ata aca aat gtc tct gat gaa gtc tcc agt gag gaa ggt cct	1089
Arg Thr Ile Thr Asn Val Ser Asp Glu Val Ser Ser Glu Glu Gly Pro	
291 296 301 306	
gaa aca gga tac tca tta cgt cgt cat gtg gac agg act tct gaa ggt	1137
Glu Thr Gly Tyr Ser Leu Arg Arg His Val Asp Arg Thr Ser Glu Gly	
307 312 317 322	
gtt ctt cgg aat aga aag tca cac cat tat aag aaa cat tac cct aat	1185
Val Leu Arg Asn Arg Lys Ser His His Tyr Lys Lys His Tyr Pro Asn	
323 328 333 338	
gag gac gcc cct aaa tcg ggt act agt tgc agc tct cgc tgt tca agt	1233
Glu Asp Ala Pro Lys Ser Gly Thr Ser Cys Ser Ser Arg Cys Ser Ser	
339 344 349 354	
tcc aga cag gat tct gag agt gca agg cca gaa tct gaa aca gaa gat	1281
Ser Arg Gln Asp Ser Glu Ser Ala Arg Pro Glu Ser Glu Thr Glu Asp	
355 360 365 370	
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Val Leu Trp Glu Asp Leu Leu His Cys Ala Glu Cys His Ser Ser Cys	
371 376 381 386	
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Thr Ser Glu Thr Asp Val Glu Asn His Gln Ile Asn Pro Cys Val Lys	
387 392 397 402	
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Lys Glu Tyr Arg Asp Asp Pro Phe His Gln Ser His Leu Pro Trp Leu	
403 408 413 418	
cat agt tcc cac cca gga tta gaa aaa ata agt gct ata gta tgg gaa	1473
His Ser Ser His Pro Gly Leu Glu Lys Ile Ser Ala Ile Val Trp Glu	
419 424 429 434	
ggg aat gat tgt aag aaa gca gac atg tct gta ctt gaa atc agt gga	1521
Gly Asn Asp Cys Lys Lys Ala Asp Met Ser Val Leu Glu Ile Ser Gly	
435 440 445 450	
atg ata atg aac aga gtg aac agc cat ata cca gga ata gga tac cag	1569
Met Ile Met Asn Arg Val Asn Ser His Ile Pro Gly Ile Gly Tyr Gln	
451 456 461 466	
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Ile Phe Gly Asn Ala Val Ser Leu Ile Leu Gly Leu Thr Pro Phe Val	
467 472 477 482	
ttc cga ctt tct caa gct aca gac ttg gaa caa ctc aca gca cat tct	1665

Arg	Ala	Asp	Cys	Thr	Met	Pro	Asp	Glu	Asp	Leu	Phe	Asn	Pro	Asp	Tyr		
56					61					66					71		
gta	gaa	gtt	gat	cgc	atc	ttg	gag	gtg	gcc	cac	acc	aag	gat	gca	gaa	411	
Val	Glu	Val	Asp	Arg	Ile	Leu	Glu	Val	Ala	His	Thr	Lys	Asp	Ala	Glu		
72					77					82					87		
aca	ggg	gag	gag	gta	aca	cat	tac	ctg	gtg	aag	tgg	tgc	tca	cta	cca	459	
Thr	Gly	Glu	Glu	Val	Thr	His	Tyr	Leu	Val	Lys	Trp	Cys	Ser	Leu	Pro		
88					93					98					103		
tat	gaa	gaa	agc	acg	tgg	gag	cta	gag	gaa	gat	gta	gat	cct	gca	aaa	507	
Tyr	Glu	Glu	Ser	Thr	Trp	Glu	Leu	Glu	Glu	Asp	Val	Asp	Pro	Ala	Lys		
104					109					114					119		
gtt	aaa	gaa	ttt	gaa	tct	ctt	caa	gtt	ctc	cct	gaa	att	aag	cat	gtg	555	
Val	Lys	Glu	Phe	Glu	Ser	Leu	Gln	Val	Leu	Pro	Glu	Ile	Lys	His	Val		
120					125					130					135		
gag	cgg	cct	gct	tca	gac	tcc	tgg	cag	aaa	ctt	gag	aag	tct	cgc	gag	603	
Glu	Arg	Pro	Ala	Ser	Asp	Ser	Trp	Gln	Lys	Leu	Glu	Lys	Ser	Arg	Glu		
136					141					146					151		
tat	aag	aac	agt	aac	cag	ctc	cgg	gag	tac	cag	ctg	gaa	ggg	atg	aac	651	
Tyr	Lys	Asn	Ser	Asn	Gln	Leu	Arg	Glu	Tyr	Gln	Leu	Glu	Gly	Met	Asn		
152					157					162					167		
tgg	ctt	ctt	ttt	aac	tgg	tat	aac	aga	aaa	aac	tgt	att	ttg	gct	gat	699	
Trp	Leu	Leu	Phe	Asn	Trp	Tyr	Asn	Arg	Lys	Asn	Cys	Ile	Leu	Ala	Asp		
168					173					178					183		
gag	atg	ggc	cta	ggg	aaa	acc	atc	cag	tcc	atc	aca	ttc	ctt	tca	gaa	747	
Glu	Met	Gly	Leu	Gly	Lys	Thr	Ile	Gln	Ser	Ile	Thr	Phe	Leu	Ser	Glu		
184					189					194					199		
ata	ttt	ctg	aga	gga	atc	cac	ggc	cct	ttt	ctc	att	atc	gcc	cct	ctc	795	
Ile	Phe	Leu	Arg	Gly	Ile	His	Gly	Pro	Phe	Leu	Ile	Ile	Ala	Pro	Leu		
200					205					210					215		
tcc	acc	atc	act	aac	tgg	gag	cgg	gag	ttc	cgg	aca	tgg	aca	gag	atg	843	
Ser	Thr	Ile	Thr	Asn	Trp	Glu	Arg	Glu	Phe	Arg	Thr	Trp	Thr	Glu	Met		
216					221					226					231		
aat	gcc	att	gtg	tac	cac	ggc	agc	cag	atc	agc	agg	cag	atg	atc	cag	891	
Asn	Ala	Ile	Val	Tyr	His	Gly	Ser	Gln	Ile	Ser	Arg	Gln	Met	Ile	Gln		
232					237					242					247		
cag	tat	gaa	atg	gtg	tac	aga	gac	gcc	cag	gga	aac	ccc	ctt	tca	gga	939	
Gln	Tyr	Glu	Met	Val	Tyr	Arg	Asp	Ala	Gln	Gly	Asn	Pro	Leu	Ser	Gly		
248					253					258					263		
gtc	ttc	aag	ttc	cac	gtc	gtc	atc	aca	aca	ttt	gaa	atg	atc	cta	gca	987	
Val	Phe	Lys	Phe	His	Val	Val	Ile	Thr	Thr	Phe	Glu	Met	Ile	Leu	Ala		
264					269					274					279		
gac	tgc	cca	gag	ttg	aag	aag	att	cac	tgg	agc	tgt	gtg	ata	att	gat	1035	
Asp	Cys	Pro	Glu	Leu	Lys	Lys	Ile	His	Trp	Ser	Cys	Val	Ile	Ile	Asp		

280	285	290	295	
gaa gcc cac aga ctg	aag aat agg aac tgc	aaa ctt ctg gag ggt cta		1083
Glu Ala His Arg Leu	Lys Asn Arg Asn Cys	Lys Leu Leu Glu Gly Leu		
296	301	306	311	
aag ctt atg gcc ctg	gaa cat aaa gtg ctt ctc	act gga aca ccc ttg		1131
Lys Leu Met Ala Leu	Glu His Lys Val Leu	Leu Thr Gly Thr Pro Leu		
312	317	322	327	
cag aac tct gtg gag	gag ctc ttc agt ttg tta	aat ttt ctg gag cca		1179
Gln Asn Ser Val Glu	Glu Leu Phe Ser Leu	Leu Asn Phe Leu Glu Pro		
328	333	338	343	
tca cag ttt cct tca	gag acc gct ttc ttg	gag gaa ttt gga gat ctg		1227
Ser Gln Phe Pro Ser	Glu Thr Ala Phe Leu	Glu Glu Phe Gly Asp Leu		
344	349	354	359	
aaa aca gag gag cag	gta aag aaa ctg cag	tct atc cta aaa cca atg		1275
Lys Thr Glu Glu Gln	Val Lys Lys Leu Gln	Ser Ile Leu Lys Pro Met		
360	365	370	375	
atg ctt cgg cgg ctg	aaa gat gat gtg gaa	aag aac ctt gct ccc aaa		1323
Met Leu Arg Arg Leu	Lys Asp Asp Val Glu	Lys Asn Leu Ala Pro Lys		
376	381	386	391	
caa gag acg atc att	gag gtg gaa ctg acc	aat atc cag aaa aag tac		1371
Gln Glu Thr Ile Ile	Glu Val Glu Leu Thr	Asn Ile Gln Lys Lys Tyr		
392	397	402	407	
tac cgt gcc atc ctc	gag aag aac ttt tcc	ttc ctg acc aag ggg gca		1419
Tyr Arg Ala Ile Leu	Glu Lys Asn Phe Ser	Phe Leu Thr Lys Gly Ala		
408	413	418	423	
aat cag cac aac atg	ccc aat ctc atc aac	acc atg atg gag ctg agg		1467
Asn Gln His Asn Met	Pro Asn Leu Ile Asn	Thr Met Met Glu Leu Arg		
424	429	434	439	
aag tgc tgt aac cat	ccc tac ctg atc aat	gga gca gag gag aaa att		1515
Lys Cys Cys Asn His	Pro Tyr Leu Ile Asn	Gly Ala Glu Glu Lys Ile		
440	445	450	455	
cta gaa gat ttc cga	aaa acc cac agc cct	gat gcc cct gac ttt cag		1563
Leu Glu Asp Phe Arg	Lys Thr His Ser Pro	Asp Ala Pro Asp Phe Gln		
456	461	466	471	
ctg cag gcc atg att	cag gca gca gga aag	ctt gtg ttg att gat aaa		1611
Leu Gln Ala Met Ile	Gln Ala Ala Gly Lys	Leu Val Leu Ile Asp Lys		
472	477	482	487	
cta ctc cct aag ctg	att gca ggt ggc cac	aaa gta ctc atc ttc tcc		1659
Leu Leu Pro Lys Leu	Ile Ala Gly Gly His	Lys Val Leu Ile Phe Ser		
488	493	498	503	
cag atg gtg cgc tgc	ctc gac atc cta gaa	gat tac ctc atc cag aga		1707
Gln Met Val Arg Cys	Leu Asp Ile Leu Glu	Asp Tyr Leu Ile Gln Arg		
504	509	514	519	

aga tac acc tat gag cga att gat ggg cga gta cgg gga aac ctg cgc	1755
Arg Tyr Thr Tyr Glu Arg Ile Asp Gly Arg Val Arg Gly Asn Leu Arg	
520 525 530 535	
cag gca gcc atc gac cgg ttc tgt aag cca gat tca gac cgc ttt gtc	1803
Gln Ala Ala Ile Asp Arg Phe Cys Lys Pro Asp Ser Asp Arg Phe Val	
536 541 546 551	
ttt ctt ctg tgc acc aga gcg gga ggc ctg ggg atc aat ctc aca gct	1851
Phe Leu Leu Cys Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala	
552 557 562 567	
gct gat acc tgc atc ata ttt gat tct gac tgg aac cca caa aat gac	1899
Ala Asp Thr Cys Ile Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp	
568 573 578 583	
ttg cag gtc cct gaa ggc aga att cag aaa gtg tgg gag cag atg tcc	1947
Leu Gln Val Pro Glu Gly Arg Ile Gln Lys Val Trp Glu Gln Met Ser	
584 589 594 599	
tgg cca aga gca cag cca caa gat aat gca gct gct gca tgt ctg cag	1995
Trp Pro Arg Ala Gln Pro Gln Asp Asn Ala Ala Ala Cys Leu Gln	
600 605 610 615	
gat ttt gga agt cag ttg gga gtc cag agt gag gag aca ggc cct ttc	2043
Asp Phe Gly Ser Gln Leu Gly Val Gln Ser Glu Glu Thr Gly Pro Phe	
616 621 626 631	
cac aat cgc cag aag cag gac tca gga aac tcc cac act gct ccg agg	2091
His Asn Arg Gln Lys Gln Asp Ser Gly Asn Ser His Thr Ala Pro Arg	
632 637 642 647	
gga aga gta ctt act ggg ctt ctt agt gtt tgg gcc gct tta gta cta	2139
Gly Arg Val Leu Thr Gly Leu Leu Ser Val Trp Ala Ala Leu Val Leu	
648 653 658 663	
agt ata gga att ctg gtg tca ttt tca gcc atg agg tta ggg gaa gaa	2187
Ser Ile Gly Ile Leu Val Ser Phe Ser Ala Met Arg Leu Gly Glu Glu	
664 669 674 679	
tgt ggg cag ggc atg ggt ggg ggc ttc cat atc cag gga ttc tgg cac	2235
Cys Gly Gln Gly Met Gly Gly Gly Phe His Ile Gln Gly Phe Trp His	
680 685 690 695	
tgg gct cag gcc cga tgt cac cgc ata ggc cag agc aaa gct gtg aag	2283
Trp Ala Gln Ala Arg Cys His Arg Ile Gly Gln Ser Lys Ala Val Lys	
696 701 706 711	
gtg tat cgc ctc atc act cga aat tcc tac gag cgc gag atg ttt gac	2331
Val Tyr Arg Leu Ile Thr Arg Asn Ser Tyr Glu Arg Glu Met Phe Asp	
712 717 722 727	
aag gcc agc cta aag ctg ggg ctg gac aag gct gtt ctt cag gac atc	2379
Lys Ala Ser Leu Lys Leu Gly Leu Asp Lys Ala Val Leu Gln Asp Ile	
728 733 738 743	

aac cga aag ggc ggc acc aat ggg gta cag cag ctc tca aaa atg gag	2427
Asn Arg Lys Gly Gly Thr Asn Gly Val Gln Gln Leu Ser Lys Met Glu	
744 749 754 759	
gtg gag gac cta ctc cgg aaa ggt gct tat gga gcc tta atg gat gaa	2475
Val Glu Asp Leu Leu Arg Lys Gly Ala Tyr Gly Ala Leu Met Asp Glu	
760 765 770 775	
gaa gat gaa ggc tcc aag ttc tgt gaa gaa gac ata gac cag att ctg	2523
Glu Asp Glu Gly Ser Lys Phe Cys Glu Glu Asp Ile Asp Gln Ile Leu	
776 781 786 791	
cag agg cga acg cac acc atc acc atc cag tct gag ggg aaa ggg tcc	2571
Gln Arg Arg Thr His Thr Ile Thr Ile Gln Ser Glu Gly Lys Gly Ser	
792 797 802 807	
act ttt gcc aag gct agc ttt gtg gct tca gga aac aga aca gat att	2619
Thr Phe Ala Lys Ala Ser Phe Val Ala Ser Gly Asn Arg Thr Asp Ile	
808 813 818 823	
tcc tta gat gat cct aac ttt tgg cag aaa tgg gct aaa ata gct gaa	2667
Ser Leu Asp Asp Pro Asn Phe Trp Gln Lys Trp Ala Lys Ile Ala Glu	
824 829 834 839	
cta gac act gaa gca aag aat gaa aag gaa agc tta gtg atc gac cga	2715
Leu Asp Thr Glu Ala Lys Asn Glu Lys Glu Ser Leu Val Ile Asp Arg	
840 845 850 855	
cct cgc gtg aga aag cag acc aaa cac tac aac tcg ttt gag gaa gac	2763
Pro Arg Val Arg Lys Gln Thr Lys His Tyr Asn Ser Phe Glu Glu Asp	
856 861 866 871	
gag ctc atg gag ttt tca gag tta gac agc gac tca gac gaa agg ccc	2811
Glu Leu Met Glu Phe Ser Glu Leu Asp Ser Asp Ser Asp Glu Arg Pro	
872 877 882 887	
acg aga tcc agg cgc ctc aat gac aaa gcc agg cgc tac ctc cga gcg	2859
Thr Arg Ser Arg Arg Leu Asn Asp Lys Ala Arg Arg Tyr Leu Arg Ala	
888 893 898 903	
gag tgc ttc cgg gta gag aag aac ctg ctc atc ttt ggc tgg ggc cgg	2907
Glu Cys Phe Arg Val Glu Lys Asn Leu Leu Ile Phe Gly Trp Gly Arg	
904 909 914 919	
tgg aag gac atc ctg act cat ggc cga ttc aag tgg cat ctg aac gag	2955
Trp Lys Asp Ile Leu Thr His Gly Arg Phe Lys Trp His Leu Asn Glu	
920 925 930 935	
aag gac atg gag atg att tgc cgt gcc ctc ctg gtg tac tgt gtc aag	3003
Lys Asp Met Glu Met Ile Cys Arg Ala Leu Leu Val Tyr Cys Val Lys	
936 941 946 951	
cat tat aag ggg gac gag aag atc aag agt ttc att tgg gaa ctg atc	3051
His Tyr Lys Gly Asp Glu Lys Ile Lys Ser Phe Ile Trp Glu Leu Ile	
952 957 962 967	
aca cct acc aaa gat ggg caa gcc cag acc ctc cag aac cac tca ggc	3099

Thr	Pro	Thr	Lys	Asp	Gly	Gln	Ala	Gln	Thr	Leu	Gln	Asn	His	Ser	Gly	
968					973					978					983	
tta	tct	gcc	cca	gtc	ccc	aga	ggg	agg	aag	ggg	aag	aag	acg	aag	aac	3147
Leu	Ser	Ala	Pro	Val	Pro	Arg	Gly	Arg	Lys	Gly	Lys	Lys	Thr	Lys	Asn	
984					989					994					999	
cag	ttg	cta	atc	cca	gag	cta	aag	gat	gca	gat	tgg	cta	gcc	acc	tgc	3195
Gln	Leu	Leu	Ile	Pro	Glu	Leu	Lys	Asp	Ala	Asp	Trp	Leu	Ala	Thr	Cys	
1000					1005					1010					1015	
aac	ccc	gag	gtg	gtc	ttg	cat	gat	gat	ggc	tat	aag	aaa	cac	ctc	aaa	3243
Asn	Pro	Glu	Val	Val	Leu	His	Asp	Asp	Gly	Tyr	Lys	Lys	His	Leu	Lys	
1016					1021					1026					1031	
cag	cac	tgc	aac	aaa	gta	ctt	ttg	cga	gtc	cgg	atg	ctg	tac	tac	cta	3291
Gln	His	Cys	Asn	Lys	Val	Leu	Leu	Arg	Val	Arg	Met	Leu	Tyr	Tyr	Leu	
1032					1037					1042					1047	
aaa	gct	gaa	ata	ctg	gga	gaa	gca	gct	gag	aaa	gca	ttt	gaa	gga	tct	3339
Lys	Ala	Glu	Ile	Leu	Gly	Glu	Ala	Ala	Glu	Lys	Ala	Phe	Glu	Gly	Ser	
1048					1053					1058					1063	
cct	gcc	agg	gag	ctg	gat	gta	cct	ctg	cct	gac	atc	gac	tac	atg	gag	3387
Pro	Ala	Arg	Glu	Leu	Asp	Val	Pro	Leu	Pro	Asp	Ile	Asp	Tyr	Met	Glu	
1064					1069					1074					1079	
atc	cca	gtg	gac	tgg	tgg	gat	gct	gaa	gcc	gat	aag	tca	ctt	ctc	att	3435
Ile	Pro	Val	Asp	Trp	Trp	Asp	Ala	Glu	Ala	Asp	Lys	Ser	Leu	Leu	Ile	
1080					1085					1090					1095	
ggc	gtg	ttc	aag	cat	ggt	tat	gaa	agg	tac	aat	gcc	atg	cga	gca	gac	3483
Gly	Val	Phe	Lys	His	Gly	Tyr	Glu	Arg	Tyr	Asn	Ala	Met	Arg	Ala	Asp	
1096					1101					1106					1111	
cca	gca	ctt	tgc	ttc	ctg	gag	aaa	gtt	ggg	atg	ccc	gat	gag	aag	tcc	3531
Pro	Ala	Leu	Cys	Phe	Leu	Glu	Lys	Val	Gly	Met	Pro	Asp	Glu	Lys	Ser	
1112					1117					1122					1127	
ctt	tct	gca	gaa	cag	ggt	gtt	aca	gat	ggg	acc	tca	gac	att	cct	gaa	3579
Leu	Ser	Ala	Glu	Gln	Gly	Val	Thr	Asp	Gly	Thr	Ser	Asp	Ile	Pro	Glu	
1128					1133					1138					1143	
aga	ggc	aac	aca	gat	aaa	gaa	gac	aat	gct	gag	gac	aaa	gta	gat	ggc	3627
Arg	Gly	Asn	Thr	Asp	Lys	Glu	Asp	Asn	Ala	Glu	Asp	Lys	Val	Asp	Gly	
1144					1149					1154					1159	
ctc	cag	aaa	caa	acg	gag	agt	tcc	agt	gat	gga	ggt	gat	ggc	gtt	ttt	3675
Leu	Gln	Lys	Gln	Thr	Glu	Ser	Ser	Ser	Asp	Gly	Gly	Asp	Gly	Val	Phe	
1160					1165					1170					1175	
agc	gaa	aag	aag	gat	gac	agc	cgg	gca	gct	cgt	ctc	aga	cgt	ctg	gtc	3723
Ser	Glu	Lys	Lys	Asp	Asp	Ser	Arg	Ala	Ala	Arg	Leu	Arg	Arg	Leu	Val	
1176					1181					1186					1191	
act	gtt	tac	cag	cgc	tgc	aac	cgc	aag	gaa	ctg	tgc	cgg	cct	gaa	att	3771
Thr	Val	Tyr	Gln	Arg	Cys	Asn	Arg	Lys	Glu	Leu	Cys	Arg	Pro	Glu	Ile	

1192	1197	1202	1207	
ctg gga cca ggt aac caa gga tat tgg gtt cag gaa gag atg ttc agg				3819
Leu Gly Pro Gly Asn Gln Gly Tyr Trp Val Gln Glu Glu Met Phe Arg				
1208	1213	1218	1223	
aga acc tca gaa atg gac ctc atc aac aag gaa gcc caa aag agg tgg				3867
Arg Thr Ser Glu Met Asp Leu Ile Asn Lys Glu Ala Gln Lys Arg Trp				
1224	1229	1234	1239	
act agg aga gaa caa gca gac ttc tat aga aca gtg tct tcc ttt ggt				3915
Thr Arg Arg Glu Gln Ala Asp Phe Tyr Arg Thr Val Ser Ser Phe Gly				
1240	1245	1250	1255	
gtt gtt tac gat caa gaa aag aaa acc ttt gac tgg aca cag ttc cgc				3963
Val Val Tyr Asp Gln Glu Lys Lys Thr Phe Asp Trp Thr Gln Phe Arg				
1256	1261	1266	1271	
atc att tcc cgt ttg gac aag aag tgc gat gag agc ctg gaa cag tat				4011
Ile Ile Ser Arg Leu Asp Lys Lys Ser Asp Glu Ser Leu Glu Gln Tyr				
1272	1277	1282	1287	
ttt tat agt ttt gtg gcc atg tgc cgg aat gtc tgt cgt cta ccc aca				4059
Phe Tyr Ser Phe Val Ala Met Cys Arg Asn Val Cys Arg Leu Pro Thr				
1288	1293	1298	1303	
tgg aaa gat ggc ggt ccc cca gat acc acc atc tac gtt gaa ccc atc				4107
Trp Lys Asp Gly Gly Pro Pro Asp Thr Thr Ile Tyr Val Glu Pro Ile				
1304	1309	1314	1319	
act gag gaa cgt gct gca aga act ctg tac cgc att gaa ctg tta cgg				4155
Thr Glu Glu Arg Ala Ala Arg Thr Leu Tyr Arg Ile Glu Leu Leu Arg				
1320	1325	1330	1335	
aaa gtc cga gag caa gtg ctc aag tgc cct cag ctg cat gaa cgc ctc				4203
Lys Val Arg Glu Gln Val Leu Lys Cys Pro Gln Leu His Glu Arg Leu				
1336	1341	1346	1351	
cag ctg tgc agg ccc agc ctc tac ctc cca gtc tgg tgg gag tgt ggg				4251
Gln Leu Cys Arg Pro Ser Leu Tyr Leu Pro Val Trp Trp Glu Cys Gly				
1352	1357	1362	1367	
aag cat gat cga gac ctg ctc atc ggc act gcc aaa cat ggg ctg aac				4299
Lys His Asp Arg Asp Leu Leu Ile Gly Thr Ala Lys His Gly Leu Asn				
1368	1373	1378	1383	
cgc act gac tgt tac atc atg aac gac ccc cag ctg tcc ttc ctg gat				4347
Arg Thr Asp Cys Tyr Ile Met Asn Asp Pro Gln Leu Ser Phe Leu Asp				
1384	1389	1394	1399	
gcc tat aga aac tat gcc cag cat aaa aga tct ggc acc cag gca cca				4395
Ala Tyr Arg Asn Tyr Ala Gln His Lys Arg Ser Gly Thr Gln Ala Pro				
1400	1405	1410	1415	
gga aat ctc tgt tgc ctt tac cag acc aac tcc aag tta tat gaa tct				4443
Gly Asn Leu Cys Cys Leu Tyr Gln Thr Asn Ser Lys Leu Tyr Glu Ser				
1416	1421	1426	1431	

gag gaa gaa gag gag gaa aac gag gag gaa aac tta gcc atg gca gta	5163
Glu Glu Glu Glu Glu Glu Asn Glu Glu Glu Asn Leu Ala Met Ala Val	
1656 1661 1666 1671	
ggc atg ggg gaa agg cca gag gta ttg cat ctc acg gag ccc act act	5211
Gly Met Gly Glu Arg Pro Glu Val Leu His Leu Thr Glu Pro Thr Thr	
1672 1677 1682 1687	
aac atc tca agg gaa aag aac caa ggc ttc caa gat gaa acc aag aaa	5259
Asn Ile Ser Arg Glu Lys Asn Gln Gly Phe Gln Asp Glu Thr Lys Lys	
1688 1693 1698 1703	
gga agc tta gag gtg gca aac cag act cct ggg cta cag agg gct ttc	5307
Gly Ser Leu Glu Val Ala Asn Gln Thr Pro Gly Leu Gln Arg Ala Phe	
1704 1709 1714 1719	
ccc gct cca gca gcc tgt cag tgc cac tgc aaa cac atg gag agg tgg	5355
Pro Ala Pro Ala Ala Cys Gln Cys His Cys Lys His Met Glu Arg Trp	
1720 1725 1730 1735	
atg cat ggc ctc gag aat gat gaa ttt gaa atc gag aaa ccc aag gct	5403
Met His Gly Leu Glu Asn Asp Glu Phe Glu Ile Glu Lys Pro Lys Ala	
1736 1741 1746 1751	
tat atc cca gat ctg ttc aaa agt aaa acc aat act atc gcc atg gag	5451
Tyr Ile Pro Asp Leu Phe Lys Ser Lys Thr Asn Thr Ile Ala Met Glu	
1752 1757 1762 1767	
ggg gaa ccc act gct att cca tca cag ccg ttt aaa gtg aag cat gag	5499
Gly Glu Pro Thr Ala Ile Pro Ser Gln Pro Phe Lys Val Lys His Glu	
1768 1773 1778 1783	
ctt tta aaa gaa cct tgg aaa gaa agt gca gag ggg caa aac gtt ttc	5547
Leu Leu Lys Glu Pro Trp Lys Glu Ser Ala Glu Gly Gln Asn Val Phe	
1784 1789 1794 1799	
ccc aca tat cct ctt gaa gga agt gag ctc aaa tca gaa gac atg gat	5595
Pro Thr Tyr Pro Leu Glu Gly Ser Glu Leu Lys Ser Glu Asp Met Asp	
1800 1805 1810 1815	
ttt gag aat aaa gat gat tat gat aga gac gga aac tgc cat agt caa	5643
Phe Glu Asn Lys Asp Asp Tyr Asp Arg Asp Gly Asn Cys His Ser Gln	
1816 1821 1826 1831	
gat tat cca ggg aag tac tct gaa gag gag agc aag agc tca aca tcg	5691
Asp Tyr Pro Gly Lys Tyr Ser Glu Glu Glu Ser Lys Ser Ser Thr Ser	
1832 1837 1842 1847	
ggc atc aca gga gac att ggg gat gag cta cag gag gct cga gct ccc	5739
Gly Ile Thr Gly Asp Ile Gly Asp Glu Leu Gln Glu Ala Arg Ala Pro	
1848 1853 1858 1863	
act att gct cag ctg cta cag gag aaa act ctc tat tcc ttc tct gag	5787
Thr Ile Ala Gln Leu Leu Gln Glu Lys Thr Leu Tyr Ser Phe Ser Glu	
1864 1869 1874 1879	
tgg cca aag gac cgc gtg ata att aac cgc cta gat aat atc tgc cac	5835

Trp	Pro	Lys	Asp	Arg	Val	Ile	Ile	Asn	Arg	Leu	Asp	Asn	Ile	Cys	His	
1880					1885					1890					1895	
gtg	gtg	tta	aag	ggg	aag	tgg	ccc	tct	agc	cag	cag	tat	gag	ccc	tca	5883
Val	Val	Leu	Lys	Gly	Lys	Trp	Pro	Ser	Ser	Gln	Gln	Tyr	Glu	Pro	Ser	
1896					1901					1906					1911	
ggc	aca	ctg	ccc	acc	ccg	gta	tta	acc	agc	agt	gct	ggg	tct	cga	acc	5931
Gly	Thr	Leu	Pro	Thr	Pro	Val	Leu	Thr	Ser	Ser	Ala	Gly	Ser	Arg	Thr	
1912					1917					1922					1927	
agc	ctc	tca	gag	ccg	gaa	gca	gca	gaa	cac	agc	ttc	agc	aac	ggc	gca	5979
Ser	Leu	Ser	Glu	Pro	Glu	Ala	Ala	Glu	His	Ser	Phe	Ser	Asn	Gly	Ala	
1928					1933					1938					1943	
gca	ttg	gcg	gcc	cag	atc	cac	aag	gag	agc	ttc	tta	gct	cca	gta	ttc	6027
Ala	Leu	Ala	Ala	Gln	Ile	His	Lys	Glu	Ser	Phe	Leu	Ala	Pro	Val	Phe	
1944					1949					1954					1959	
aca	aag	gat	gaa	caa	aag	cac	agg	cgt	ccc	tat	gag	ttt	gag	gtg	gag	6075
Thr	Lys	Asp	Glu	Gln	Lys	His	Arg	Arg	Pro	Tyr	Glu	Phe	Glu	Val	Glu	
1960					1965					1970					1975	
agg	gat	gca	aag	gct	cgg	ggc	ctg	gag	cag	ttc	tct	gcc	acc	cac	ggg	6123
Arg	Asp	Ala	Lys	Ala	Arg	Gly	Leu	Glu	Gln	Phe	Ser	Ala	Thr	His	Gly	
1976					1981					1986					1991	
cac	acc	cct	atc	atc	ctc	aat	ggc	tgg	cat	ggg	gag	tca	gct	atg	gac	6171
His	Thr	Pro	Ile	Ile	Leu	Asn	Gly	Trp	His	Gly	Glu	Ser	Ala	Met	Asp	
1992					1997					2002					2007	
ctc	tcc	tgc	tca	tca	gag	ggg	tcc	cca	gga	gcc	aca	tcc	cct	ttc	cca	6219
Leu	Ser	Cys	Ser	Ser	Glu	Gly	Ser	Pro	Gly	Ala	Thr	Ser	Pro	Phe	Pro	
2008					2013					2018					2023	
gtg	agc	gcc	agc	acc	cct	aag	att	ggg	gct	atc	agt	tca	ctt	cag	gga	6267
Val	Ser	Ala	Ser	Thr	Pro	Lys	Ile	Gly	Ala	Ile	Ser	Ser	Leu	Gln	Gly	
2024					2029					2034					2039	
gcc	ctt	ggc	atg	gac	ttg	tct	ggg	att	ctg	caa	gct	ggc	ctg	atc	cat	6315
Ala	Leu	Gly	Met	Asp	Leu	Ser	Gly	Ile	Leu	Gln	Ala	Gly	Leu	Ile	His	
2040					2045					2050					2055	
cct	gtg	act	gga	cag	att	gtc	aat	gga	agc	ctc	aga	aga	gat	gat	gca	6363
Pro	Val	Thr	Gly	Gln	Ile	Val	Asn	Gly	Ser	Leu	Arg	Arg	Asp	Asp	Ala	
2056					2061					2066					2071	
gcc	acg	agg	agg	cgg	aga	ggg	agg	cgg	aaa	cat	gtt	gaa	gga	ggg	atg	6411
Ala	Thr	Arg	Arg	Arg	Arg	Gly	Arg	Arg	Lys	His	Val	Glu	Gly	Gly	Met	
2072					2077					2082					2087	
gac	ctc	atc	ttt	ttg	aag	gag	cag	aca	ctt	cag	gcg	gga	atc	ttg	gaa	6459
Asp	Leu	Ile	Phe	Leu	Lys	Glu	Gln	Thr	Leu	Gln	Ala	Gly	Ile	Leu	Glu	
2088					2093					2098					2103	
gtc	cat	gaa	gac	cca	ggg	cag	gcc	acc	ttg	agc	acc	aca	cac	cct	gag	6507
Val	His	Glu	Asp	Pro	Gly	Gln	Ala	Thr	Leu	Ser	Thr	Thr	His	Pro	Glu	

2104	2109	2114	2119	
ggg cca ggg cct gcc acc tcg gct cct gag cca gct acg gca gcc agc				6555
Gly Pro Gly Pro Ala Thr Ser Ala Pro Glu Pro Ala Thr Ala Ala Ser				
2120	2125	2130	2135	
agc caa gcc gag aaa tcc att ccc agc aag agt ctg ctt gac tgg cta				6603
Ser Gln Ala Glu Lys Ser Ile Pro Ser Lys Ser Leu Leu Asp Trp Leu				
2136	2141	2146	2151	
agg cag cag gct gac tac tcc tta gaa gtt cct ggc ttt ggg gca ggg				6651
Arg Gln Gln Ala Asp Tyr Ser Leu Glu Val Pro Gly Phe Gly Ala Gly				
2152	2157	2162	2167	
ttt ctt cca gaa aac aag ttc aat cac act ctg gct gag cct att ctt				6699
Phe Leu Pro Glu Asn Lys Phe Asn His Thr Leu Ala Glu Pro Ile Leu				
2168	2173	2178	2183	
cga gat acg ggc ccc cgc agg agg ggg agg cgg cct cgg agc gaa ctc				6747
Arg Asp Thr Gly Pro Arg Arg Arg Gly Arg Arg Pro Arg Ser Glu Leu				
2184	2189	2194	2199	
ctg aag gct cct tcc att gtg gca gac tct ccc tct gga atg ggg cca				6795
Leu Lys Ala Pro Ser Ile Val Ala Asp Ser Pro Ser Gly Met Gly Pro				
2200	2205	2210	2215	
ctg ttc atg aat gga ctg att gct ggg atg gac ctg gta gga ctt cag				6843
Leu Phe Met Asn Gly Leu Ile Ala Gly Met Asp Leu Val Gly Leu Gln				
2216	2221	2226	2231	
aac atg aga aat atg cca ggc atc ccc ctc acc ggg ctg gtg ggg ttt				6891
Asn Met Arg Asn Met Pro Gly Ile Pro Leu Thr Gly Leu Val Gly Phe				
2232	2237	2242	2247	
cca gct ggc ttt gcc acg atg cca aca ggt gaa gag gtc aaa agt acc				6939
Pro Ala Gly Phe Ala Thr Met Pro Thr Gly Glu Glu Val Lys Ser Thr				
2248	2253	2258	2263	
ctg agc atg ctg ccc atg atg ctg cca ggc atg gct gct gtg ccc cag				6987
Leu Ser Met Leu Pro Met Met Leu Pro Gly Met Ala Ala Val Pro Gln				
2264	2269	2274	2279	
atg ttt ggt gtt ggg gga ctc ctc agt cca ccc atg gca acc acc tgc				7035
Met Phe Gly Val Gly Gly Leu Leu Ser Pro Pro Met Ala Thr Thr Cys				
2280	2285	2290	2295	
act tcc act gcc ccg gcg tct cta tca agc aca acg aaa agt ggt acg				7083
Thr Ser Thr Ala Pro Ala Ser Leu Ser Ser Thr Thr Lys Ser Gly Thr				
2296	2301	2306	2311	
gca gtg act gaa aag act gcg gaa gac aag ccg agt agc cat gat gtg				7131
Ala Val Thr Glu Lys Thr Ala Glu Asp Lys Pro Ser Ser His Asp Val				
2312	2317	2322	2327	
aaa aca gac act tta gct gag gac aag cct ggt cca ggt cca ttt tct				7179
Lys Thr Asp Thr Leu Ala Glu Asp Lys Pro Gly Pro Gly Pro Phe Ser				
2328	2333	2338	2343	

gat cag tct gaa cct gca ata act act agt agt cct gtg gct ttt aac	7227
Asp Gln Ser Glu Pro Ala Ile Thr Thr Ser Ser Pro Val Ala Phe Asn	
2344 2349 2354 2359	
cca ttt ctc atc cca gga gta tct cct gga ctc att tac cca tcc atg	7275
Pro Phe Leu Ile Pro Gly Val Ser Pro Gly Leu Ile Tyr Pro Ser Met	
2360 2365 2370 2375	
ttc ctc tcc cct ggt atg ggc atg gct ctg cca gcc atg cag cag gcc	7323
Phe Leu Ser Pro Gly Met Gly Met Ala Leu Pro Ala Met Gln Gln Ala	
2376 2381 2386 2391	
aga cac tcg gaa ata gta ggt ctg gag agc cag aag agg aag aag aag	7371
Arg His Ser Glu Ile Val Gly Leu Glu Ser Gln Lys Arg Lys Lys Lys	
2392 2397 2402 2407	
aag aca aag ggg gac aac ccc aac tcc cac cca gag cct gct ccc agc	7419
Lys Thr Lys Gly Asp Asn Pro Asn Ser His Pro Glu Pro Ala Pro Ser	
2408 2413 2418 2423	
tgt gaa agg gag ccc agc ggt gat gag aac tgt gcc gaa ccc agt gcc	7467
Cys Glu Arg Glu Pro Ser Gly Asp Glu Asn Cys Ala Glu Pro Ser Ala	
2424 2429 2434 2439	
cct ttg ccc gca gag aga gaa cat ggg gca cag gct ggg gag ggg gca	7515
Pro Leu Pro Ala Glu Arg Glu His Gly Ala Gln Ala Gly Glu Gly Ala	
2440 2445 2450 2455	
ctc aaa gac tcc aac aac gac acc aat tag a acttttttca tttaagaaat	7566
Leu Lys Asp Ser Asn Asn Asp Thr Asn *	
2456 2461	
tattgtgact tgtaagtttc ttatcccata aaggtttggt acttccttca cttcacctcc	7626
ataagaacct gtgtttccat aagtaagatt acgtacctga tttcctgtct gagaactatg	7686
gtaacagatg ttaatagttg caggggtctca ccacttcatt agataagtgt tgtctaccta	7746
gtctaggagg cacagaattc tcattctggt atccagttca ttccagcaat catagttaat	7806
acagtacttg gtgacacgcc ctacccccctt ctcttccaag tttcccactc acttgaggag	7866
gaaaaatggc aaaagaaagc tgtctagggt ttaccattg aagggtggaa gaacagagac	7926
aaagaggagc tctttttctg tgagctgggt tgcacaggaa gaatgtcaca gggaacccaa	7986
aagcacagaa aaaggaagtg ctggtgcata tttttgagtt aaaatatttc cctattttat	8046
catgattact aagtgagtag tatagacaga agtatataac taatggttga aaatacatat	8106
attcatttct ttataaaaaa caaaaacctt accggtagta atataatttc ccccttggtg	8166
gtttttcaga cacctgcagc aagaagaaat actgactgac taggcattat tttctataca	8226
tcctctcac cagtgaaaag attcctcttg ctgcgagaaa gctttaccca ccatgagtta	8286

108	113	118	123	
aca ttc gaa ggc ctg	caa caa caa ttt tta	gga gct aat gag aac tct		613
Thr Phe Glu Gly Leu	Gln Gln Gln Phe Leu	Gly Ala Asn Glu Asn Ser		
124	129	134	139	
gca gaa aat atg cag att att caa ctt cag gtt ctt aac aaa gca aaa				661
Ala Glu Asn Met Gln Ile Ile Gln Leu Gln Val Leu Asn Lys Ala Lys				
140	145	150	155	
gag aga caa ctg gag aac tta att gaa aag tta aat gaa agt gaa cgt				709
Glu Arg Gln Leu Glu Asn Leu Ile Glu Lys Leu Asn Glu Ser Glu Arg				
156	161	166	171	
caa att cga tat ctg aat cac cag ctt gta ata ata aaa gat gaa aag				757
Gln Ile Arg Tyr Leu Asn His Gln Leu Val Ile Ile Lys Asp Glu Lys				
172	177	182	187	
gat ggt ttg act ctc agc ctt cga gaa tca cag aaa ctc ttt cag aat				805
Asp Gly Leu Thr Leu Ser Leu Arg Glu Ser Gln Lys Leu Phe Gln Asn				
188	193	198	203	
gga aaa gaa aga gag ata cag ctt gaa gct caa ata aaa gca ctg gag				853
Gly Lys Glu Arg Glu Ile Gln Leu Glu Ala Gln Ile Lys Ala Leu Glu				
204	209	214	219	
act cag ata caa gca tta aaa gtc aat gaa gaa cag atg atc aag aag				901
Thr Gln Ile Gln Ala Leu Lys Val Asn Glu Glu Gln Met Ile Lys Lys				
220	225	230	235	
tcc aga aca act gaa atg gct ctg gaa agc ttg aag cag cag ctg gtg				949
Ser Arg Thr Thr Glu Met Ala Leu Glu Ser Leu Lys Gln Gln Leu Val				
236	241	246	251	
gac ctt cat cat tct gaa tca ctt caa cga gct aga gaa cag cat gag				997
Asp Leu His His Ser Glu Ser Leu Gln Arg Ala Arg Glu Gln His Glu				
252	257	262	267	
agc att gtt atg ggc ctc aca aag aag tac gaa gag caa gta ttg tcc				1045
Ser Ile Val Met Gly Leu Thr Lys Lys Tyr Glu Glu Gln Val Leu Ser				
268	273	278	283	
tta caa aag aat ttg gat gcc aca gtc acc gca ctt aaa gaa cag gaa				1093
Leu Gln Lys Asn Leu Asp Ala Thr Val Thr Ala Leu Lys Glu Gln Glu				
284	289	294	299	
gac att tgc tct cgt ctg aaa gat cac gtg aaa caa ctg gaa agg aat				1141
Asp Ile Cys Ser Arg Leu Lys Asp His Val Lys Gln Leu Glu Arg Asn				
300	305	310	315	
caa gaa gca atc aag tta gaa aag act gag atc att aat aag ttg aca				1189
Gln Glu Ala Ile Lys Leu Glu Lys Thr Glu Ile Ile Asn Lys Leu Thr				
316	321	326	331	
aga agt cta gag gag agt caa aag cag tgt gcc cac ttg ttg cag tcc				1237
Arg Ser Leu Glu Glu Ser Gln Lys Gln Cys Ala His Leu Leu Gln Ser				
332	337	342	347	

ggg tca gta caa gag gtg gct cag cta cag ttc cag ctg cag caa gca	1285
Gly Ser Val Gln Glu Val Ala Gln Leu Gln Phe Gln Leu Gln Gln Ala	
348 353 358 363	
cag aag gca cat gct atg agt gca aac atg aac aag gct ttg caa gaa	1333
Gln Lys Ala His Ala Met Ser Ala Asn Met Asn Lys Ala Leu Gln Glu	
364 369 374 379	
gaa tta aca gaa cta aaa gat gaa att tct ctc tat gaa tct gct gca	1381
Glu Leu Thr Glu Leu Lys Asp Glu Ile Ser Leu Tyr Glu Ser Ala Ala	
380 385 390 395	
aaa cta gga ata cat cca agt gac tca gaa gga gaa tta aat ata gaa	1429
Lys Leu Gly Ile His Pro Ser Asp Ser Glu Gly Glu Leu Asn Ile Glu	
396 401 406 411	
ctc act gaa tcg tat gtg gat ttg ggt att aaa aag gtc aac tgg aaa	1477
Leu Thr Glu Ser Tyr Val Asp Leu Gly Ile Lys Lys Val Asn Trp Lys	
412 417 422 427	
aaa tcc aaa gtt acc agc att gta caa gaa gaa gac cca aat gaa gag	1525
Lys Ser Lys Val Thr Ser Ile Val Gln Glu Glu Asp Pro Asn Glu Glu	
428 433 438 443	
ctt tca aaa gat gag ttc att ctg aag tta aag gca gaa gta cag cgt	1573
Leu Ser Lys Asp Glu Phe Ile Leu Lys Leu Lys Ala Glu Val Gln Arg	
444 449 454 459	
ttg ctg ggt agc aac tca atg aag cgt cat ctg gtg tct cag tta caa	1621
Leu Leu Gly Ser Asn Ser Met Lys Arg His Leu Val Ser Gln Leu Gln	
460 465 470 475	
aat gac ctc aaa gac tgt cat aag aaa att gaa gat ctc cac caa gtg	1669
Asn Asp Leu Lys Asp Cys His Lys Lys Ile Glu Asp Leu His Gln Val	
476 481 486 491	
aag aag gat gaa aaa agc att gag gtt gag act aaa aca gat acc tca	1717
Lys Lys Asp Glu Lys Ser Ile Glu Val Glu Thr Lys Thr Asp Thr Ser	
492 497 502 507	
gaa aaa cca aag aat caa tta tgg cct gag tct tct act tct gat gtt	1765
Glu Lys Pro Lys Asn Gln Leu Trp Pro Glu Ser Ser Thr Ser Asp Val	
508 513 518 523	
gtc aga gat gat att ctg ctg ctt aaa aat gaa att caa gtt tta caa	1813
Val Arg Asp Asp Ile Leu Leu Leu Lys Asn Glu Ile Gln Val Leu Gln	
524 529 534 539	
caa caa aat cag gaa ctt aaa gaa act gaa gga aaa ctg aga aat aca	1861
Gln Gln Asn Gln Glu Leu Lys Glu Thr Glu Gly Lys Leu Arg Asn Thr	
540 545 550 555	
aat caa gac tta tgt aat caa atg aga caa atg gta caa gat ttt gac	1909
Asn Gln Asp Leu Cys Asn Gln Met Arg Gln Met Val Gln Asp Phe Asp	
556 561 566 571	

cat gac aaa caa gaa gct gtg gat agg tgt gaa agg act tat cag cag	1957
His Asp Lys Gln Glu Ala Val Asp Arg Cys Glu Arg Thr Tyr Gln Gln	
572 577 582 587	
cac cat gaa gcc atg aaa act caa ata cgt gaa agc cta tta gca aag	2005
His His Glu Ala Met Lys Thr Gln Ile Arg Glu Ser Leu Leu Ala Lys	
588 593 598 603	
cat gct ttg gag aag cag cag ctc ttt gag gct tat gag aga act cat	2053
His Ala Leu Glu Lys Gln Gln Leu Phe Glu Ala Tyr Glu Arg Thr His	
604 609 614 619	
ttg caa ctg agg tct gag ttg gat aag ttg aat aag gag gtg act gct	2101
Leu Gln Leu Arg Ser Glu Leu Asp Lys Leu Asn Lys Glu Val Thr Ala	
620 625 630 635	
gtg cag gaa tgt tac cta gaa gtg tgc aga gag aag gat aat cta gaa	2149
Val Gln Glu Cys Tyr Leu Glu Val Cys Arg Glu Lys Asp Asn Leu Glu	
636 641 646 651	
ttg act ctc agg aag acc act gaa aag gag caa cag act cag gag aag	2197
Leu Thr Leu Arg Lys Thr Thr Glu Lys Glu Gln Thr Gln Glu Lys	
652 657 662 667	
atc aaa gaa aaa ctc att caa cag ctt gaa aag gag tgg cag tct aag	2245
Ile Lys Glu Lys Leu Ile Gln Gln Leu Glu Lys Glu Trp Gln Ser Lys	
668 673 678 683	
ctg gat caa act ata aag gca atg aaa aag aag acc tta gat tgt ggc	2293
Leu Asp Gln Thr Ile Lys Ala Met Lys Lys Lys Thr Leu Asp Cys Gly	
684 689 694 699	
agc caa act gac caa gta acc acc agt gat gtt att tcc aag aaa gag	2341
Ser Gln Thr Asp Gln Val Thr Thr Ser Asp Val Ile Ser Lys Lys Glu	
700 705 710 715	
atg gca att atg ata gaa gag cag aag tgc aca atc cag caa aac tta	2389
Met Ala Ile Met Ile Glu Glu Gln Lys Cys Thr Ile Gln Gln Asn Leu	
716 721 726 731	
gaa caa gag aag gac ata gcc atc aag ggg gct atg aag aaa ctc gaa	2437
Glu Gln Glu Lys Asp Ile Ala Ile Lys Gly Ala Met Lys Lys Leu Glu	
732 737 742 747	
att gaa ttg gaa ctc aaa cat tgt gaa aat att acc aaa cag gta gaa	2485
Ile Glu Leu Glu Leu Lys His Cys Glu Asn Ile Thr Lys Gln Val Glu	
748 753 758 763	
ata gct gtg caa aat gct cat cag cga tgg ctg gga gaa cta cca gag	2533
Ile Ala Val Gln Asn Ala His Gln Arg Trp Leu Gly Glu Leu Pro Glu	
764 769 774 779	
ctg gca gag tat caa gca ctt gtg aag gca gaa cag aaa aag tgg gaa	2581
Leu Ala Glu Tyr Gln Ala Leu Val Lys Ala Glu Gln Lys Lys Trp Glu	
780 785 790 795	
gaa cag cat gag gtc tct gtg aac aaa agg ata tca ttt gct gtt tct	2629

Glu	Gln	His	Glu	Val	Ser	Val	Asn	Lys	Arg	Ile	Ser	Phe	Ala	Val	Ser		
796					801					806					811		
gaa	gct	aaa	gag	aaa	tgg	aag	agt	gag	ctt	gaa	aat	atg	agg	aaa	aat	2677	
Glu	Ala	Lys	Glu	Lys	Trp	Lys	Ser	Glu	Leu	Glu	Asn	Met	Arg	Lys	Asn		
812					817					822					827		
ata	ctt	cct	gga	aag	gaa	ttg	gaa	gag	aag	att	cat	tct	ctt	cag	aag	2725	
Ile	Leu	Pro	Gly	Lys	Glu	Leu	Glu	Glu	Lys	Ile	His	Ser	Leu	Gln	Lys		
828					833					838					843		
gaa	ctt	gag	tta	aag	aac	gaa	gaa	gtc	cct	gtg	gtc	atc	agg	gct	gag	2773	
Glu	Leu	Glu	Leu	Lys	Asn	Glu	Glu	Val	Pro	Val	Val	Ile	Arg	Ala	Glu		
844					849					854					859		
tta	gct	aag	gct	cgg	agt	gaa	tgg	aac	aaa	gaa	aag	caa	gaa	gaa	atc	2821	
Leu	Ala	Lys	Ala	Arg	Ser	Glu	Trp	Asn	Lys	Glu	Lys	Gln	Glu	Glu	Ile		
860					865					870					875		
cac	aga	atc	caa	gaa	caa	aat	gag	caa	gat	tac	cgg	caa	ttt	tta	gat	2869	
His	Arg	Ile	Gln	Glu	Gln	Asn	Glu	Gln	Asp	Tyr	Arg	Gln	Phe	Leu	Asp		
876					881					886					891		
gat	cac	cga	aat	aaa	att	aat	gag	gtg	ctt	gcg	gca	gct	aaa	gaa	gac	2917	
Asp	His	Arg	Asn	Lys	Ile	Asn	Glu	Val	Leu	Ala	Ala	Ala	Lys	Glu	Asp		
892					897					902					907		
ttt	atg	aaa	caa	aaa	act	gaa	cta	ctt	ctt	cag	aag	gag	aca	gaa	tta	2965	
Phe	Met	Lys	Gln	Lys	Thr	Glu	Leu	Leu	Leu	Gln	Lys	Glu	Thr	Glu	Leu		
908					913					918					923		
caa	act	tgt	cta	gac	cag	agt	cgt	aga	gaa	tgg	act	atg	cag	gaa	gcc	3013	
Gln	Thr	Cys	Leu	Asp	Gln	Ser	Arg	Arg	Glu	Trp	Thr	Met	Gln	Glu	Ala		
924					929					934					939		
aag	cgg	atc	caa	ctg	gaa	atc	tat	cag	tat	gag	gaa	gac	atc	ctg	act	3061	
Lys	Arg	Ile	Gln	Leu	Glu	Ile	Tyr	Gln	Tyr	Glu	Glu	Asp	Ile	Leu	Thr		
940					945					950					955		
gta	ctt	ggg	gtt	ctt	tta	agt	gat	acc	caa	aag	gag	cac	atc	agt	gat	3109	
Val	Leu	Gly	Val	Leu	Leu	Ser	Asp	Thr	Gln	Lys	Glu	His	Ile	Ser	Asp		
956					961					966					971		
tct	gag	gac	aag	cag	ctt	ttg	gaa	atc	atg	tgc	act	tgt	tct	tca	aaa	3157	
Ser	Glu	Asp	Lys	Gln	Leu	Leu	Glu	Ile	Met	Ser	Thr	Cys	Ser	Ser	Lys		
972					977					982					987		
tgg	atg	tct	gtg	caa	tat	ttt	gaa	aaa	cta	aag	ggc	tgc	ata	cag	aaa	3205	
Trp	Met	Ser	Val	Gln	Tyr	Phe	Glu	Lys	Leu	Lys	Gly	Cys	Ile	Gln	Lys		
988					993					998					1003		
gca	ttt	caa	gat	aca	ctt	cct	ctg	ctt	gta	gaa	aac	gct	gac	cca	gaa	3253	
Ala	Phe	Gln	Asp	Thr	Leu	Pro	Leu	Leu	Val	Glu	Asn	Ala	Asp	Pro	Glu		
1004					1009					1014					1019		
tgg	aaa	aag	aga	aat	atg	gcc	gag	ctc	tct	aag	gat	tct	gcc	agc	cag	3301	
Trp	Lys	Lys	Arg	Asn	Met	Ala	Glu	Leu	Ser	Lys	Asp	Ser	Ala	Ser	Gln		

1020	1025	1030	1035	
ggc act ggc caa gga gac cct gga cct gct gct gga cac cat gct cag				3349
Gly Thr Gly Gln Gly Asp Pro Gly Pro Ala Ala Gly His His Ala Gln				
1036	1041	1046	1051	
ccc ttg gcc tta caa gca aca gaa gca gaa gct gat aag aaa aag gtc				3397
Pro Leu Ala Leu Gln Ala Thr Glu Ala Glu Ala Asp Lys Lys Lys Val				
1052	1057	1062	1067	
ctt gaa att aag gat tta tgc tgt gga cac tgc ttc caa gaa ctt gaa				3445
Leu Glu Ile Lys Asp Leu Cys Cys Gly His Cys Phe Gln Glu Leu Glu				
1068	1073	1078	1083	
aag gca aag cag gaa tgt caa gat ctg aaa gga aaa ctg gag aaa tgc				3493
Lys Ala Lys Gln Glu Cys Gln Asp Leu Lys Gly Lys Leu Glu Lys Cys				
1084	1089	1094	1099	
tgt agg cat ctt cag cat tta gaa agg aag cac aaa gct gta gtg gaa				3541
Cys Arg His Leu Gln His Leu Glu Arg Lys His Lys Ala Val Val Glu				
1100	1105	1110	1115	
aaa att gga gaa gag aat aat aaa gtt gtt gaa gaa tta ata gaa gaa				3589
Lys Ile Gly Glu Glu Asn Asn Lys Val Val Glu Glu Leu Ile Glu Glu				
1116	1121	1126	1131	
aac aac gac atg aag aat aaa ttg gaa gaa ttg caa aca ctt tgt aaa				3637
Asn Asn Asp Met Lys Asn Lys Leu Glu Glu Leu Gln Thr Leu Cys Lys				
1132	1137	1142	1147	
aca cca cca agg tca ttg tca gca ggg gcc att gaa aat gct tgc ctg				3685
Thr Pro Pro Arg Ser Leu Ser Ala Gly Ala Ile Glu Asn Ala Cys Leu				
1148	1153	1158	1163	
cca tgc agt ggg gga gcc ttg gaa gaa ctt cgt ggg cag tac att aaa				3733
Pro Cys Ser Gly Gly Ala Leu Glu Glu Leu Arg Gly Gln Tyr Ile Lys				
1164	1169	1174	1179	
gct gta aaa aaa att aaa tgt gac atg ctt cgt tat att cag gag agt				3781
Ala Val Lys Lys Ile Lys Cys Asp Met Leu Arg Tyr Ile Gln Glu Ser				
1180	1185	1190	1195	
aag gaa cga gct gca gaa atg gta aaa gca gag gta ctg cga gaa cgt				3829
Lys Glu Arg Ala Ala Glu Met Val Lys Ala Glu Val Leu Arg Glu Arg				
1196	1201	1206	1211	
caa gaa acc gcc cga aag atg cgc aaa tat tat ttg att tgc ctc caa				3877
Gln Glu Thr Ala Arg Lys Met Arg Lys Tyr Tyr Leu Ile Cys Leu Gln				
1212	1217	1222	1227	
cag att ttg cag gat gat gga aaa gaa ggg gct gag aaa aag att atg				3925
Gln Ile Leu Gln Asp Asp Gly Lys Glu Gly Ala Glu Lys Lys Ile Met				
1228	1233	1238	1243	
aat gct gct agc aaa ctt gct aca atg gca aaa tta ctg gaa aca cct				3973
Asn Ala Ala Ser Lys Leu Ala Thr Met Ala Lys Leu Leu Glu Thr Pro				
1244	1249	1254	1259	

att tct agt aag tcc caa agc aaa act aca cag tca ggt atg tca aag 4021
 Ile Ser Ser Lys Ser Gln Ser Lys Thr Thr Gln Ser Gly Met Ser Lys
 1260 1265 1270 1275

tga gtcg ccaaattggtt tttctatctt ttcttcttta gctatttaat attttcagta 4078
 *
 1276

tgaagaaggc agggaaggta aggagtgaga gttaatttgt gaagttttgt atgttttact 4138

taaactagaa gtttacgcaa aaagagtaca cagtttccaa ttttaagtagg cagactgagc 4198

atgcccacatca gtttcctatt gctgcttcca tccctcgaaa tgatagaaaa gatttttaaac 4258

agccaaataa agaattgagaa aaagaagaaa ttataagtgg gtttttaaaaa gttgcagtgg 4318

gccaggcatc atggctcaca cctgtaatcc cagcactttg ggaggctgag gtgggaggat 4378

cccttgatcc caggaatttg aggttgcaat aagctatgat tgtgccactg tactccagcc 4438

tgggtgacag agtgaggccc tgtctcaaaa aaaaaa 4474

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gagaggagag cccagcccct ggtggaggcg gcttggcgga gattcggagc cgtcagcagc 180

tcagccagac gtccaggatc ccacccttg caaaagacca ggccgtggaa gcc atg 236
 Met
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ttc cca cca gcc agg ggg aag gag ctg ctc tcg ttt gag gat gtg gcg 284
 Phe Pro Pro Ala Arg Gly Lys Glu Leu Leu Ser Phe Glu Asp Val Ala
 2 7 12 17

atg tac ttc acc aga gag gag tgg ggc cac ctc aac tgg ggt cag aag 332
 Met Tyr Phe Thr Arg Glu Glu Trp Gly His Leu Asn Trp Gly Gln Lys
 18 23 28 33

gac ctc tac cga gat gtg atg ttg gag aac tac agg aac atg gtc ttg 380
 Asp Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Arg Asn Met Val Leu
 34 39 44 49

ctg gga ttt cag ttt ccc aaa cct gag atg atc tgt cag ctg gag aac 428
 Leu Gly Phe Gln Phe Pro Lys Pro Glu Met Ile Cys Gln Leu Glu Asn
 50 55 60 65

tgg gac gag cag tgg atc ctg gat cta ccg aga gct ggg aat agg aag 476
 Trp Asp Glu Gln Trp Ile Leu Asp Leu Pro Arg Ala Gly Asn Arg Lys
 66 71 76 81

gct tcc ggt agt gct tgc cca ggc gga ctc tcg ctc tgt cgc cag gct 524
 Ala Ser Gly Ser Ala Cys Pro Gly Gly Leu Ser Leu Cys Arg Gln Ala
 82 87 92 97

gtc tta gcc tcc tga gtggcttgga ctacaggcgc gcgccacccat gcccggtac 579
 Val Leu Ala Ser *
 98

tttctgtatt ttagtgagaga tgggggtttca ccatgttggc caggctgggc tggaactcct 639

gacctcgtga tccgcctgcc ccggcctccc aaagtgtcgg gattacaggc gtgagccgtg 699

cgcccagttg gaaaaagttt tgtttttttt ttaaaactaa gtgcttccat gtacatcaga 759

tgtaacgac tttgatccta acaaacaac aaaaaaaaaa aaa 802

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<211> 2152

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cacgcgtccg gcacaccctt tactggccgg ccccgcgctg ctctcctaag acccgcggg 180

ccagcgccgc gaccccttcc cagcgtcct cgcgctgtgt gggcgcgctc ctctcgccg 240

tgaccgggtg tgcgtggggt cgaggcgccg ggcggagtgg ctccgggccc aaacgcc 297

atg cgg agg ggc gag cgc agg gac gcc gga ggt ccg cgg ccc gag tcc 345

Met Arg Arg Gly Glu Arg Arg Asp Ala Gly Gly Pro Arg Pro Glu Ser
 1 5 10 15

ccg gtg ccc gcg ggc agg gcc tcg ctg gag gag ccg cct gac ggg ccg 393

Pro Val Pro Ala Gly Arg Ala Ser Leu Glu Glu Pro Pro Asp Gly Pro
 17 22 27 32

tct gcc ggc caa gcc acc ggg ccg ggc gag ggc cgc cgc agc acc gag 441

Ser Ala Gly Gln Ala Thr Gly Pro Gly Glu Gly Arg Arg Ser Thr Glu

33	38	43	48	
tcc gag gtc tac gac gac ggc acc aac acc ttc ttc tgg cga gcc cac				489
Ser Glu Val Tyr Asp Asp Gly Thr Asn Thr Phe Phe Trp Arg Ala His				
49	54	59	64	
acc tta acc gtg ctc ttc atc ctc acc tgt acg ctt ggc tat gtg acg				537
Thr Leu Thr Val Leu Phe Ile Leu Thr Cys Thr Leu Gly Tyr Val Thr				
65	70	75	80	
ctg ctg gag gaa aca cct cag gac acg gcc tac aac acc aag aga ggt				585
Leu Leu Glu Glu Thr Pro Gln Asp Thr Ala Tyr Asn Thr Lys Arg Gly				
81	86	91	96	
att gtg gcc agt att ttg gtt ttc tta tgt ttt gga gtc aca caa gct				633
Ile Val Ala Ser Ile Leu Val Phe Leu Cys Phe Gly Val Thr Gln Ala				
97	102	107	112	
aaa gac ggg cca ttt tcc aga cct cat cca gct tac tgg agg ttt tgg				681
Lys Asp Gly Pro Phe Ser Arg Pro His Pro Ala Tyr Trp Arg Phe Trp				
113	118	123	128	
ctc tgc gtg agt gtg gtc tac gag ctg ttt ctc atc ttt ata ctc ttc				729
Leu Cys Val Ser Val Val Tyr Glu Leu Phe Leu Ile Phe Ile Leu Phe				
129	134	139	144	
cag act gtc cag gac ggc cgg cag ttt cta aag tat gtt gac ccc aag				777
Gln Thr Val Gln Asp Gly Arg Gln Phe Leu Lys Tyr Val Asp Pro Lys				
145	150	155	160	
ctg gga gtc cca ctg cca gag aga gac tac ggg gga aac tgc ctc atc				825
Leu Gly Val Pro Leu Pro Glu Arg Asp Tyr Gly Gly Asn Cys Leu Ile				
161	166	171	176	
tac gac cca gac aat gag act gac ccc ttt cac aac atc tgg gac aag				873
Tyr Asp Pro Asp Asn Glu Thr Asp Pro Phe His Asn Ile Trp Asp Lys				
177	182	187	192	
ttg gat ggc ttt gtt ccc gcg cac ttt ctt ggc tgg tac ctg aag acc				921
Leu Asp Gly Phe Val Pro Ala His Phe Leu Gly Trp Tyr Leu Lys Thr				
193	198	203	208	
ctg atg atc cga gac tgg tgg atg tgc atg atc atc agc gtg atg ttc				969
Leu Met Ile Arg Asp Trp Trp Met Cys Met Ile Ile Ser Val Met Phe				
209	214	219	224	
gag ttc ctg gag tac agc ctg gag cac cag ctg ccc aac ttc agc gag				1017
Glu Phe Leu Glu Tyr Ser Leu Glu His Gln Leu Pro Asn Phe Ser Glu				
225	230	235	240	
tgc tgg tgg gat cac tgg atc atg gac gtg ctc gtc tgc aac ggg ctg				1065
Cys Trp Trp Asp His Trp Ile Met Asp Val Leu Val Cys Asn Gly Leu				
241	246	251	256	
ggc atc tac tgc ggc atg aag acc ctt gag tgg ctg tcc ctg aag acg				1113
Gly Ile Tyr Cys Gly Met Lys Thr Leu Glu Trp Leu Ser Leu Lys Thr				
257	262	267	272	

tac aag tgg cag ggc ctc tgg aac att ccg acc tac aag ggc aag atg	1161
Tyr Lys Trp Gln Gly Leu Trp Asn Ile Pro Thr Tyr Lys Gly Lys Met	
273 278 283 288	
aag agg atc gcc ttc cag ttc acg ccg tac agc tgg gtt cgc ttc gag	1209
Lys Arg Ile Ala Phe Gln Phe Thr Pro Tyr Ser Trp Val Arg Phe Glu	
289 294 299 304	
tgg aag ccg gcc tcc agc ctg cgt cgc tgg ctg gcc gtg tgc ggc atc	1257
Trp Lys Pro Ala Ser Ser Leu Arg Arg Trp Leu Ala Val Cys Gly Ile	
305 310 315 320	
atc ctg gtg ttc ctg ttg gca gaa ctg aac acg ttc tac ctg aag ttt	1305
Ile Leu Val Phe Leu Leu Ala Glu Leu Asn Thr Phe Tyr Leu Lys Phe	
321 326 331 336	
gtg ctg tgg atg ccc ccg gag cac tac ctg gtc ctc ctg cgg ctc gtc	1353
Val Leu Trp Met Pro Pro Glu His Tyr Leu Val Leu Leu Arg Leu Val	
337 342 347 352	
ttc ttc gtg aac gtg ggt ggc gtg gcc atg cgt gag atc tac gac ttc	1401
Phe Phe Val Asn Val Gly Gly Val Ala Met Arg Glu Ile Tyr Asp Phe	
353 358 363 368	
atg gat gac ccg aag ccc cac aag aag ctg ggc ccg cag gcc tgg ctg	1449
Met Asp Asp Pro Lys Pro His Lys Lys Leu Gly Pro Gln Ala Trp Leu	
369 374 379 384	
gtg gcg gcc atc acg gcc acg gag ctg ctc atc gtg gtg aag tac gac	1497
Val Ala Ala Ile Thr Ala Thr Glu Leu Leu Ile Val Val Lys Tyr Asp	
385 390 395 400	
ccc cac acg ctc acc ctg tcc ctg ccc ttc tac atc tcc cag tgc tgg	1545
Pro His Thr Leu Thr Leu Ser Leu Pro Phe Tyr Ile Ser Gln Cys Trp	
401 406 411 416	
acc ctc ggc tcc gtc ctg gcg ctc acc tgg acc gtc tgg cgc ttc ttc	1593
Thr Leu Gly Ser Val Leu Ala Leu Thr Trp Thr Val Trp Arg Phe Phe	
417 422 427 432	
ctg cgg gac atc aca ttg agg tac aag gag acc cgg tgg cag aag tgg	1641
Leu Arg Asp Ile Thr Leu Arg Tyr Lys Glu Thr Arg Trp Gln Lys Trp	
433 438 443 448	
cag aac aag gat gac cag ggc agc acc gtc ggc aac ggg gac cag cac	1689
Gln Asn Lys Asp Asp Gln Gly Ser Thr Val Gly Asn Gly Asp Gln His	
449 454 459 464	
cca ctg ggg ctg gac gaa gac ctg ctg ggg cct ggg gtg gcc gag ggc	1737
Pro Leu Gly Leu Asp Glu Asp Leu Leu Gly Pro Gly Val Ala Glu Gly	
465 470 475 480	
gag gga gca cca act cca aac tga cctggggccgt ggctgcctcg tgagcctccc	1791
Glu Gly Ala Pro Thr Pro Asn *	
481 486	

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agagcccagg cctccgtggc ctctctctgt gtgagtccca ccaggagcca cgtgcccgcc 1851
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tccaggcagc gatgctgagc cacctctctc gagccttctt ttcacacaga ccaccccgga 1971
ggacacgtgg atgatggggg cagagatcac tgagctgccc ctcaaggggg cctggaaccc 2031
gggtgctggg gtcattgctgc ctccgtggct ccaaggtgag ggtcatcttc acgagcaaag 2091
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a 2152

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<222> (51)..(2096)

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Arg Arg Ala Leu Arg Arg Leu Arg Gly Glu Gln Arg Gly Gln Glu Pro
  3              8              13              18

ctc ggg ccc ggc gcc ttg cat ttc gat ctc cgt gat gac gat gac gcg  152
Leu Gly Pro Gly Ala Leu His Phe Asp Leu Arg Asp Asp Asp Ala
  19              24              29              34

gaa gaa gaa ggg ccc aag cgg gag ctt ggt gtc cgg cgt ccc ggg ggc  200
Glu Glu Glu Gly Pro Lys Arg Glu Leu Gly Val Arg Arg Pro Gly Gly
  35              40              45              50

gca ggg aag gag ggc gtc cga gtc aac aac cgc ttc gag ctg ata aac  248
Ala Gly Lys Glu Gly Val Arg Val Asn Asn Arg Phe Glu Leu Ile Asn
  51              56              61              66

att gac gat ctt gag gat gac cct gtg gtg aac ggg gag agg tct ggc  296
Ile Asp Asp Leu Glu Asp Asp Pro Val Val Asn Gly Glu Arg Ser Gly
  67              72              77              82

tgt gcg ctc aca gac gct gtg gca cca ggg aac aaa gga agg ggt cag  344
Cys Ala Leu Thr Asp Ala Val Ala Pro Gly Asn Lys Gly Arg Gly Gln
  83              88              93              98

cgt gga aac aca gag agc aag acg gat gga gat gac acc gag aca gtg  392
Arg Gly Asn Thr Glu Ser Lys Thr Asp Gly Asp Asp Thr Glu Thr Val

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99	104	109	114	
ccc tca gag cag tct cat gca agt ggc aaa ctc cgg aag aag aaa aaa				440
Pro Ser Glu Gln Ser His Ala Ser Gly Lys		Leu Arg Lys Lys Lys Lys		
115	120	125	130	
aaa cag aaa aac aag aaa agc agc acg gga gaa gca tcg gaa aac gga				488
Lys Gln Lys Asn Lys Lys Ser Ser Thr Gly		Glu Ala Ser Glu Asn Gly		
131	136	141	146	
cta gaa gat atc gat cgc atc cta gag agg att gag gac agc act ggg				536
Leu Glu Asp Ile Asp Arg Ile Leu Glu Arg		Ile Glu Asp Ser Thr Gly		
147	152	157	162	
ttg aac cgt ccc ggc cca gct ccc ctg agc tcc agg aag cac gtt ctc				584
Leu Asn Arg Pro Gly Pro Ala Pro Leu Ser		Ser Arg Lys His Val Leu		
163	168	173	178	
tac gtg gag cac aga cac ttg aat cca gac aca gaa ctg aaa agg tat				632
Tyr Val Glu His Arg His Leu Asn Pro Asp Thr Glu Leu Lys Arg Tyr				
179	184	189	194	
ttt ggt gcc cgg gca atc ctg ggg gag caa agg cca cgg cag aga caa				680
Phe Gly Ala Arg Ala Ile Leu Gly Glu Gln Arg Pro Arg Gln Arg Gln				
195	200	205	210	
cgt gtg tac ccc aag tgc aca tgg ctg acc acc cct aaa agc acc tgg				728
Arg Val Tyr Pro Lys Cys Thr Trp Leu Thr Thr Pro Lys Ser Thr Trp				
211	216	221	226	
ccc cgc tac agc aaa cca ggt ctg tcc atg cgg ctg ctg gaa tca aaa				776
Pro Arg Tyr Ser Lys Pro Gly Leu Ser Met Arg Leu Leu Glu Ser Lys				
227	232	237	242	
aaa ggc ctc tcc ttc ttt gcg ttt gag cac agt gag gag tac cag cag				824
Lys Gly Leu Ser Phe Phe Ala Phe Glu His Ser Glu Glu Tyr Gln Gln				
243	248	253	258	
gct cag cac aag ttc ctg gtg gcc gtg gag tct atg gag ccg aac aac				872
Ala Gln His Lys Phe Leu Val Ala Val Glu Ser Met Glu Pro Asn Asn				
259	264	269	274	
atc gtg gtt ctg ctc cag acg agc cct tac cac gtt gac tca ctc ctg				920
Ile Val Val Leu Leu Gln Thr Ser Pro Tyr His Val Asp Ser Leu Leu				
275	280	285	290	
cag ctc agc gat gcc tgc cgc ttt caa gag gat cag gag atg gct cga				968
Gln Leu Ser Asp Ala Cys Arg Phe Gln Glu Asp Gln Glu Met Ala Arg				
291	296	301	306	
gac ctc gta gag aga gcg ctg tac agc atg gaa tgt gcg ttc cac ccc				1016
Asp Leu Val Glu Arg Ala Leu Tyr Ser Met Glu Cys Ala Phe His Pro				
307	312	317	322	
ctg ttc agt ctc acc agt ggg gcc tgc cgg ctg gat tac cgc aga ccc				1064
Leu Phe Ser Leu Thr Ser Gly Ala Cys Arg Leu Asp Tyr Arg Arg Pro				
323	328	333	338	

gag aac agg agc ttc tac ctg gcc ctc tac aag cag atg agc ttc ctg	1112
Glu Asn Arg Ser Phe Tyr Leu Ala Leu Tyr Lys Gln Met Ser Phe Leu	
339 344 349 354	
gag aag cga ggc tgc ccg cgc acg gcg ctg gag tac tgc aag ctc atc	1160
Glu Lys Arg Gly Cys Pro Arg Thr Ala Leu Glu Tyr Cys Lys Leu Ile	
355 360 365 370	
ctg agt ctc gag ccg gat gag gac ccc ctc tgc atg ctg ctg ctc atc	1208
Leu Ser Leu Glu Pro Asp Glu Asp Pro Leu Cys Met Leu Leu Leu Ile	
371 376 381 386	
gac cac ctg gcc ttg cgg gcc cgg aac tac gag tac ctg atc cgc ctc	1256
Asp His Leu Ala Leu Arg Ala Arg Asn Tyr Glu Tyr Leu Ile Arg Leu	
387 392 397 402	
ttc cag gag tgg gag gtg ggt gcg agc ctg gct cat cgg aac ctg tcc	1304
Phe Gln Glu Trp Glu Val Gly Ala Ser Leu Ala His Arg Asn Leu Ser	
403 408 413 418	
cag ctc cct aat ttt gcc ttc tct gtt cca ctg gcg tat ttc ctg ctg	1352
Gln Leu Pro Asn Phe Ala Phe Ser Val Pro Leu Ala Tyr Phe Leu Leu	
419 424 429 434	
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Ser Gln Gln Thr Asp Leu Pro Glu Cys Glu Gln Ser Ser Ala Arg Gln	
435 440 445 450	
aag gcc tct ctc ctg ata cag cag gcg ctc acc atg ttc cct gga gtc	1448
Lys Ala Ser Leu Leu Ile Gln Gln Ala Leu Thr Met Phe Pro Gly Val	
451 456 461 466	
ctc ctg ccc ctg ctc gag tct tgc agt gtg cgg ccc gac gcc agc gtt	1496
Leu Leu Pro Leu Leu Glu Ser Cys Ser Val Arg Pro Asp Ala Ser Val	
467 472 477 482	
tcc agt cac cgc ttc ttt gga ccc aat gct gaa ata agc cag ccc cct	1544
Ser Ser His Arg Phe Phe Gly Pro Asn Ala Glu Ile Ser Gln Pro Pro	
483 488 493 498	
gcc ctg agc cag ctg gtg aac ctg tac ctt ggg agg tca cac ttt ctc	1592
Ala Leu Ser Gln Leu Val Asn Leu Tyr Leu Gly Arg Ser His Phe Leu	
499 504 509 514	
tgg aaa gag ccc gcc acc atg agc tgg ctg gag gag aac gtc cac gag	1640
Trp Lys Glu Pro Ala Thr Met Ser Trp Leu Glu Glu Asn Val His Glu	
515 520 525 530	
gtt ctg caa gca gtg gac gcc ggg gac cca gcc gtg gaa gcc tgt gag	1688
Val Leu Gln Ala Val Asp Ala Gly Asp Pro Ala Val Glu Ala Cys Glu	
531 536 541 546	
aac cgg cgg aag gtg ctc tac cag cgt gca ccc agg aat atc cac cgc	1736
Asn Arg Arg Lys Val Leu Tyr Gln Arg Ala Pro Arg Asn Ile His Arg	
547 552 557 562	

cat gtg atc ctc tct gag atc aag gaa gcc gtc gct gcc ctg ccc ccg	1784
His Val Ile Leu Ser Glu Ile Lys Glu Ala Val Ala Ala Leu Pro Pro	
563 568 573 578	
gac gtg acc acg cag tct gtg atg ggg ttt gat cct ctg cct cct tcg	1832
Asp Val Thr Thr Gln Ser Val Met Gly Phe Asp Pro Leu Pro Pro Ser	
579 584 589 594	
gac aca atc tac tcc tac gtc agg cca gag agg cta agt cct atc agc	1880
Asp Thr Ile Tyr Ser Tyr Val Arg Pro Glu Arg Leu Ser Pro Ile Ser	
595 600 605 610	
cat gga aac acc att gct ctc ttc ttc cgg tca ctg ttg cca aac tat	1928
His Gly Asn Thr Ile Ala Leu Phe Phe Arg Ser Leu Leu Pro Asn Tyr	
611 616 621 626	
acc atg gag ggg gag agg ccc gag gaa gga gtg gct ggg ggt ctg aac	1976
Thr Met Glu Gly Glu Arg Pro Glu Glu Gly Val Ala Gly Gly Leu Asn	
627 632 637 642	
cgc aac cag ggc ctg aac agg ctg atg ctg gct gtg cgc gac atg atg	2024
Arg Asn Gln Gly Leu Asn Arg Leu Met Leu Ala Val Arg Asp Met Met	
643 648 653 658	
gcc aac ttc cac ctc aac gac ctg gag gcg ccg cac gag gac gac gct	2072
Ala Asn Phe His Leu Asn Asp Leu Glu Ala Pro His Glu Asp Asp Ala	
659 664 669 674	
gag ggg gag ggg gag tgg gac tga gcgtccgcag aggtgaccga aaagccgtat	2126
Glu Gly Glu Gly Glu Trp Asp *	
675 680	
gatgatgttc ccgatttctc tgttggtcgg agtcggccag ttgcctgaag tagggaagct	2186
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aaaa	2250

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Arg Arg Ala Leu Arg Arg Leu Arg Gly Glu Gln Arg Gly Gln Glu Pro	

3	8	13	18	
ctc ggg ccc ggc gcc ttg cat ttc gat ctc cgt gat gac gat gac gcg	152			
Leu Gly Pro Gly Ala Leu His Phe Asp Leu Arg Asp Asp Asp Ala				
19 24 29 34				
gaa gaa gaa ggg ccc aag cgg gag ctt ggt gtc cgg cgt ccc ggg ggc	200			
Glu Glu Glu Gly Pro Lys Arg Glu Leu Gly Val Arg Arg Pro Gly Gly				
35 40 45 50				
gca ggg aag gag ggc gtc cga gtc aac aac cgc ttc gag ctg ata aac	248			
Ala Gly Lys Glu Gly Val Arg Val Asn Asn Arg Phe Glu Leu Ile Asn				
51 56 61 66				
att gac gat ctt gag gat gac cct gtg gtg aac ggg gag agg tct ggc	296			
Ile Asp Asp Leu Glu Asp Asp Pro Val Val Asn Gly Glu Arg Ser Gly				
67 72 77 82				
tgt gcg ctc aca gac gct gtg gca cca ggg aac aaa gga agg ggt cag	344			
Cys Ala Leu Thr Asp Ala Val Ala Pro Gly Asn Lys Gly Arg Gly Gln				
83 88 93 98				
cgt gga aac aca gag agc aag acg gat gga gat gac acc gag aca gtg	392			
Arg Gly Asn Thr Glu Ser Lys Thr Asp Gly Asp Asp Thr Glu Thr Val				
99 104 109 114				
ccc tca gag cag tct cat gca agt ggc aaa ctc cgg aag aag aaa aaa	440			
Pro Ser Glu Gln Ser His Ala Ser Gly Lys Leu Arg Lys Lys Lys Lys				
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aaa cag aaa aac aag aaa agc agc acg gga gaa gca tcg gaa aac gga	488			
Lys Gln Lys Asn Lys Lys Ser Ser Thr Gly Glu Ala Ser Glu Asn Gly				
131 136 141 146				
cta gaa gat atc gat cgc atc cta gag agg att gag gac agc act ggg	536			
Leu Glu Asp Ile Asp Arg Ile Leu Glu Arg Ile Glu Asp Ser Thr Gly				
147 152 157 162				
ttg aac cgt ccc ggc cca gct ccc ctg agc tcc agg aag cac gtt ctc	584			
Leu Asn Arg Pro Gly Pro Ala Pro Leu Ser Ser Arg Lys His Val Leu				
163 168 173 178				
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Tyr Val Glu His Arg His Leu Asn Pro Asp Thr Glu Leu Lys Arg Tyr				
179 184 189 194				
ttt ggt gcc cgg gca atc ctg ggg gag caa agg cca cgg cag aga caa	680			
Phe Gly Ala Arg Ala Ile Leu Gly Glu Gln Arg Pro Arg Gln Arg Gln				
195 200 205 210				
cgt gtg tac ccc aag tgc aca tgg ctg acc acc cct aaa agc acc tgg	728			
Arg Val Tyr Pro Lys Cys Thr Trp Leu Thr Thr Pro Lys Ser Thr Trp				
211 216 221 226				
ccc cgc tac agc aaa cca ggt ctg tcc atg cgg ctg ctg gaa tca aaa	776			
Pro Arg Tyr Ser Lys Pro Gly Leu Ser Met Arg Leu Leu Glu Ser Lys				
227 232 237 242				

aaa ggc ctc tcc ttc ttt gcg ttt gag cac agt gag gag tac cag cag	824
Lys Gly Leu Ser Phe Phe Ala Phe Glu His Ser Glu Glu Tyr Gln Gln	
243 248 253 258	
gct cag cac aag ttc ctg gtg gcc gtg gag tct atg gag ccg aac aac	872
Ala Gln His Lys Phe Leu Val Ala Val Glu Ser Met Glu Pro Asn Asn	
259 264 269 274	
atc gtg ctc agc gat gcc tgc cgc ttt caa gag gat cag gag atg gct	920
Ile Val Leu Ser Asp Ala Cys Arg Phe Gln Glu Asp Gln Glu Met Ala	
275 280 285 290	
cga gac ctc gta gag aga gcg ctg tac agc atg gaa tgt gcg ttc cac	968
Arg Asp Leu Val Glu Arg Ala Leu Tyr Ser Met Glu Cys Ala Phe His	
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Gln Tyr Leu Val Glu Asp Ile Gln His Ile Leu Glu Arg Leu His Arg
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gtc cac atg cca cag aat ggg atc aac cac cct ggc atc act gcc ctg	1026
Val His Met Pro Gln Asn Gly Ile Asn His Pro Gly Ile Thr Ala Leu	
213 218 223 228	
gcc cag gct ttc gct gtc aac ccc ctg ctg cgg gtc atc aac ctg aat	1074
Ala Gln Ala Phe Ala Val Asn Pro Leu Leu Arg Val Ile Asn Leu Asn	
229 234 239 244	
gac aac acc ttc act gag aag ggc gcc gtg gcc atg gcc gag acc ttg	1122
Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met Ala Glu Thr Leu	
245 250 255 260	
aag acc ttg cgg cag gtg gag gtg att aat ttt ggg gac tgc ctg gtg	1170
Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly Asp Cys Leu Val	
261 266 271 276	

cgc tcc aag ggt gca gtt gcc att gca gat gcc atc cgc ggc ggc ctg	1218
Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile Arg Gly Gly Leu	
277 282 287 292	
ccc aag cta aag gag ctg aac ttg tca ttc tgt gaa atc aag agg gat	1266
Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu Ile Lys Arg Asp	
293 298 303 308	
gct gcc ctg gct gtt gct gag gcc atg gca gac aaa gct gag ctg gag	1314
Ala Ala Leu Ala Val Ala Glu Ala Met Ala Asp Lys Ala Glu Leu Glu	
309 314 319 324	
aag ctg gac ctg aat ggc aac acc ctg gga gaa gaa ggc tgt gaa cag	1362
Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu Gly Cys Glu Gln	
325 330 335 340	
ctt cag gag gtg ctg gag ggc ttc aac atg gcc aag gtg ctg gcg tcc	1410
Leu Gln Glu Val Leu Glu Gly Phe Asn Met Ala Lys Val Leu Ala Ser	
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ctc agt gat gac gag gac gag gag gag gag gag gaa gga gaa gag gaa	1458
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Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu Arg Leu Gly Pro Lys	
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Ser Ser Val Leu Ile Ala Gln Gln Thr Asp Thr Ser Asp Pro Glu Lys	
453 458 463 468	
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Val Val Ser Ala Phe Leu Lys Val Ser Ser Val Phe Lys Asp Glu Ala	
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Thr Val Arg Met Ala Val Gln Asp Ala Val Asp Ala Leu Met Gln Lys	
485 490 495 500	
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Ala Phe Asn Ser Ser Ser Phe Asn Ser Asn Thr Phe Leu Thr Arg Leu	
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ctc gtg cac atg ggt ctg ctc aag agt gaa gac aag gtc aag gcc att	1938
Leu Val His Met Gly Leu Leu Lys Ser Glu Asp Lys Val Lys Ala Ile	
517 522 527 532	
gcc aac ctg tac ggc ccc ctg atg gcg ctg aac cac atg gtg cag cag	1986
Ala Asn Leu Tyr Gly Pro Leu Met Ala Leu Asn His Met Val Gln Gln	
533 538 543 548	
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Asp Tyr Phe Pro Lys Ala Leu Ala Pro Leu Leu Leu Ala Phe Val Thr	
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Lys Pro Asn Ser Ala Leu Glu Ser Cys Ser Phe Ala Arg His Ser Leu	
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acatctggac cgctggatcc ggaggtggcg accccggcct gaccggacc ctaaattccgt	240
ccccgcccc gagggcggag gcgcgcgtc gattccccca acgcggcggc gccgcctgtt	300
tacgtctgca gatctccagg ggagcccacc agcctagtca ac atg gcc tcg gaa	354
Met Ala Ser Glu	
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gac att gcc aag ctg gca gag aca ctt gcc aag act cag gtg gcc ggg	402
Asp Ile Ala Lys Leu Ala Glu Thr Leu Ala Lys Thr Gln Val Ala Gly	
5 10 15 20	
gga cag ctg agt ttc aaa ggc aag agc ctc aaa ctc aac act gca gaa	450
Gly Gln Leu Ser Phe Lys Gly Lys Ser Leu Lys Leu Asn Thr Ala Glu	
21 26 31 36	
gat gct aaa gat gtg att aaa gag att gaa gac ttt gac agc ttg gag	498
Asp Ala Lys Asp Val Ile Lys Glu Ile Glu Asp Phe Asp Ser Leu Glu	
37 42 47 52	
gct ctg cgt ctg gaa ggc aac aca gtg ggc gtg gaa gca gcc agg gtc	546
Ala Leu Arg Leu Glu Gly Asn Thr Val Gly Val Glu Ala Ala Arg Val	
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atc gcc aag gcc tta gag aag aag tcg gag ttg aag cgc tgc cac tgg	594
Ile Ala Lys Ala Leu Glu Lys Lys Ser Glu Leu Lys Arg Cys His Trp	
69 74 79 84	
agt gac atg ttc acg gga agg ctg cgg acc gag atc cca cca gcc ctg	642
Ser Asp Met Phe Thr Gly Arg Leu Arg Thr Glu Ile Pro Pro Ala Leu	
85 90 95 100	
atc tca cta ggg gaa gga ctc atc aca gct ggg gct cag ctg gtg gag	690
Ile Ser Leu Gly Glu Gly Leu Ile Thr Ala Gly Ala Gln Leu Val Glu	
101 106 111 116	
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Leu Asp Leu Ser Asp Asn Ala Phe Gly Pro Asp Gly Val Gln Gly Phe	

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Glu Ala Leu Leu Lys Ser Ser Ala Cys Phe Thr Leu Gln Glu Leu Lys				
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Leu Asn Asn Cys Gly Met Gly Ile Gly Gly Gly Lys Ile Leu Ala Ala				
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gct ctg acc gaa tgt cac cgg aaa tcc agt gcc caa ggc aag cct ctg				882
Ala Leu Thr Glu Cys His Arg Lys Ser Ser Ala Gln Gly Lys Pro Leu				
165	170	175	180	
gcc ctg aag gtc ttt gtg gct ggc aga aac cgt ctg gag aat gat ggc				930
Ala Leu Lys Val Phe Val Ala Gly Arg Asn Arg Leu Glu Asn Asp Gly				
181	186	191	196	
gcc act gcc ttg gca gaa gct ttt agg gtc atc ggg acc ctg gag gag				978
Ala Thr Ala Leu Ala Glu Ala Phe Arg Val Ile Gly Thr Leu Glu Glu				
197	202	207	212	
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Val His Met Pro Gln Asn Gly Ile Asn His Pro Gly Ile Thr Ala Leu				
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229	234	239	244	
gac aac acc ttc act gag aag ggc gcc gtg gcc atg gcc gag acc ttg				1122
Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met Ala Glu Thr Leu				
245	250	255	260	
aag acc ttg cgg cag gtg gag gtg att aat ttt ggg gac tgc ctg gtg				1170
Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly Asp Cys Leu Val				
261	266	271	276	
cgc tcc aag ggt gca gtt gcc att gca gat gcc atc cgc ggc ggc ctg				1218
Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile Arg Gly Gly Leu				
277	282	287	292	
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Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu Ile Lys Arg Asp				
293	298	303	308	
gct gcc ctg gct gtt gct gag gcc atg gca gac aaa gct gag ctg gag				1314
Ala Ala Leu Ala Val Ala Glu Ala Met Ala Asp Lys Ala Glu Leu Glu				
309	314	319	324	
aag ctg gac ctg aat ggc aac acc ctg gga gaa gaa ggc tgt gaa cag				1362
Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu Gly Cys Glu Gln				
325	330	335	340	
ctt cag gag gtg ctg gag ggc ttc aac atg gcc aag gtg ctg gcg tcc				1410
Leu Gln Glu Val Leu Glu Gly Phe Asn Met Ala Lys Val Leu Ala Ser				
341	346	351	356	

ctc agt gat gac gag gac gag gag gag gag gag gaa gaa gag cct cag	1458
Leu Ser Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Pro Gln	
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Gln Arg Gly Gln Gly Glu Lys Ser Ala Thr Pro Ser Arg Lys Ile Leu	
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Asp Pro Asn Thr Gly Glu Pro Ala Pro Val Leu Ser Ser Pro Pro Pro	
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Ala Asp Val Ser Thr Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu	
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Arg Leu Gly Pro Lys Ser Ser Val Leu Ile Ala Gln Gln Thr Asp Thr	
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Ser Asp Pro Glu Lys Val Val Ser Ala Phe Leu Lys Val Ser Ser Val	
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Phe Lys Asp Glu Ala Thr Val Arg Met Ala Val Gln Asp Ala Val Asp	
453 458 463 468	
gcc ctg atg cag aag gct ttc aac tcc tcc tcc ttc aac tcc aac acc	1794
Ala Leu Met Gln Lys Ala Phe Asn Ser Ser Ser Phe Asn Ser Asn Thr	
469 474 479 484	
ttc ctc acc agg ctc ctc gtg cac atg ggt ctg ctc aag agt gaa gac	1842
Phe Leu Thr Arg Leu Leu Val His Met Gly Leu Leu Lys Ser Glu Asp	
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Lys Val Lys Ala Ile Ala Asn Leu Tyr Gly Pro Leu Met Ala Leu Asn	
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cac atg gtg cag cag gac tat ttc ccc aag gcc ctt gca ccc ctg ctg	1938
His Met Val Gln Gln Asp Tyr Phe Pro Lys Ala Leu Ala Pro Leu Leu	
517 522 527 532	
ctg gcg ttc gtg acc aag ccc aac agc gcc ctg gaa tcc tgc tcc ttc	1986
Leu Ala Phe Val Thr Lys Pro Asn Ser Ala Leu Glu Ser Cys Ser Phe	
533 538 543 548	
gcc cgc cac agt ctg ctg cag acg ctg tac aag gtc tag actcaaagcc	2035
Ala Arg His Ser Leu Leu Gln Thr Leu Tyr Lys Val *	
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gcctacgccca ttgccttggga caggactctg gccacaggca gggcgggtct gtgtcccatg	2155

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 gaggtgtcag taattaacac tgtggatacc toccatgagg ac atg att cac gac 234
 Met Ile His Asp
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 Ala Gln Met Asp Tyr Tyr Gly Thr Arg Leu Ala Thr Cys Ser Ser Asp
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Arg Ser Val Lys Ile Phe Asp Val Arg Asn Gly Gly Gln Ile Leu Ile	
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gcc gac ctc agg ggt cat gag ggt cct gtg tgg caa gtg gcc tgg gct	378
Ala Asp Leu Arg Gly His Glu Gly Pro Val Trp Gln Val Ala Trp Ala	
37 42 47 52	
cac ccc atg tac ggc aac atc ctg gca tgc tgc tcc tat gac cgg aaa	426
His Pro Met Tyr Gly Asn Ile Leu Ala Ser Cys Ser Tyr Asp Arg Lys	
53 58 63 68	
gtc att atc tgg aga gag gaa aac ggc acc tgg gag aag agc cac gag	474
Val Ile Ile Trp Arg Glu Glu Asn Gly Thr Trp Glu Lys Ser His Glu	
69 74 79 84	
cat gcg gga cac gac tcc tca gtg aac tgc gtg tgc tgg gcc ccc cat	522
His Ala Gly His Asp Ser Ser Val Asn Ser Val Cys Trp Ala Pro His	
85 90 95 100	
gac tac ggc ctg atc ctg gcc tgt ggg agc tgc gat ggg gcc atc tcc	570
Asp Tyr Gly Leu Ile Leu Ala Cys Gly Ser Ser Asp Gly Ala Ile Ser	
101 106 111 116	
ctg ctg act tac acc ggg gaa ggc caa tgg gaa gta aag aag atc aac	618
Leu Leu Thr Tyr Thr Gly Glu Gly Gln Trp Glu Val Lys Lys Ile Asn	
117 122 127 132	
aac gct cac acc att ggc tgc aat gcc gtc agc tgg gcc cct gct gtt	666
Asn Ala His Thr Ile Gly Cys Asn Ala Val Ser Trp Ala Pro Ala Val	
133 138 143 148	
gta cct gga agc ctc ata gac cac cca tgc ggg cag aaa ccc aat tac	714
Val Pro Gly Ser Leu Ile Asp His Pro Ser Gly Gln Lys Pro Asn Tyr	
149 154 159 164	
atc aag agg ttt gca tca ggt ggc tgt gac aac ctc atc aag ctg tgg	762
Ile Lys Arg Phe Ala Ser Gly Gly Cys Asp Asn Leu Ile Lys Leu Trp	
165 170 175 180	
aag gag gag gag gac ggc cag tgg aag gag gag cag aag cta gaa gcg	810
Lys Glu Glu Glu Asp Gly Gln Trp Lys Glu Glu Gln Lys Leu Glu Ala	
181 186 191 196	
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His Ser Asp Trp Val Arg Asp Val Ala Trp Ala Pro Ser Ile Gly Leu	
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Pro Thr Ser Thr Ile Ala Ser Cys Ser Gln Asp Gly Arg Val Phe Ile	
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Trp Thr Cys Asp Asp Ala Ser Ser Asn Thr Trp Ser Pro Lys Leu Leu	
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Asn Ile Leu Ala Val Ser Gly Gly Asp Asn Lys Val Thr Leu Trp Lys	
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Glu Ser Val Asp Gly Gln Trp Val Cys Ile Ser Asp Val Asn Lys Gly	
277 282 287 292	
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Gln Gly Ser Val Ser Ala Ser Val Thr Glu Gly Gln Gln Asn Glu Gln	
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Thr Ala Ser Arg Ser His Thr Thr Leu Gln Gly Gly Ser Cys Cys Pro	
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Val Leu Trp Thr Ala Lys Leu Arg Cys Arg Lys Leu Arg Phe Pro Leu	
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 Pro Pro Pro Pro Pro Ser Ser Ser Ala Trp Pro Trp Gln Gly Trp Gly
 45 50 55 60

atc aga ggt gaa cag gaa gca gaa gga ccc ctg ggg gag aca ggg cct 362
 Ile Arg Gly Glu Gln Glu Ala Glu Gly Pro Leu Gly Glu Thr Gly Pro
 61 66 71 76

cca gtg gga cca gag ctg agt ggc ctc agg cag tgg cgg aag ctg att 410
 Pro Val Gly Pro Glu Leu Ser Gly Leu Arg Gln Trp Arg Lys Leu Ile
 77 82 87 92

aaa gga agg tac ggg gag tgg agg gga agt gga caa aag aca gga cag 458
 Lys Gly Arg Tyr Gly Glu Trp Arg Gly Ser Gly Gln Lys Thr Gly Gln
 93 98 103 108

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 Pro Ser *
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 Met Met Gly His Arg Pro Val Leu Val Leu Ser
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 Gln Asn Thr Lys Arg Glu Ser Gly Arg Lys Val Gln Ser Gly Asn Ile
 12 17 22 27

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 Asn Ala Ala Lys Thr Ile Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro
 28 33 38 43

aag tcc atg atg aag atg ctt ttg gac cca atg gga ggc att gtg atg	375
Lys Ser Met Met Lys Met Leu Leu Asp Pro Met Gly Gly Ile Val Met	
44 49 54 59	
acc aat gat ggc aat gcc att ctt cga gag att caa gtc cag cat cca	423
Thr Asn Asp Gly Asn Ala Ile Leu Arg Glu Ile Gln Val Gln His Pro	
60 65 70 75	
gcg gcc aag tcc atg atc gaa att agc cgg acc cag gat gaa gag gtt	471
Ala Ala Lys Ser Met Ile Glu Ile Ser Arg Thr Gln Asp Glu Glu Val	
76 81 86 91	
gga gat ggg acc aca tca gta att att ctt gca ggg gaa atg ctg tct	519
Gly Asp Gly Thr Thr Ser Val Ile Ile Leu Ala Gly Glu Met Leu Ser	
92 97 102 107	
gta gct gag cac ttc ctg gag cag cag atg cac cca aca gtg gtg atc	567
Val Ala Glu His Phe Leu Glu Gln Gln Met His Pro Thr Val Val Ile	
108 113 118 123	
agt gct tac cgc aag gca ttg gat gat atg atc agc acc cta aag aaa	615
Ser Ala Tyr Arg Lys Ala Leu Asp Asp Met Ile Ser Thr Leu Lys Lys	
124 129 134 139	
ata agt atc cca gtc gac atc agt gac agt gat atg atg ctg aac atc	663
Ile Ser Ile Pro Val Asp Ile Ser Asp Ser Asp Met Met Leu Asn Ile	
140 145 150 155	
atc aac agc tct att act acc aaa gcc atc agt cgg tgg tca tct ttg	711
Ile Asn Ser Ser Ile Thr Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu	
156 161 166 171	
gct tgc aac att gcc ctg gat gct gtc aag atg gta cag ttt gag gag	759
Ala Cys Asn Ile Ala Leu Asp Ala Val Lys Met Val Gln Phe Glu Glu	
172 177 182 187	
aat ggt cgg aaa gag att gac ata aaa aaa tat gca aga gtg gaa aag	807
Asn Gly Arg Lys Glu Ile Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys	
188 193 198 203	
ata cct gga ggc atc att gaa gac tcc tgt gtc ttg cgt gga gtc atg	855
Ile Pro Gly Gly Ile Ile Glu Asp Ser Cys Val Leu Arg Gly Val Met	
204 209 214 219	
att aac aag gat gtg acc cat cca cgt atg cgg cgc tat atc aag aac	903
Ile Asn Lys Asp Val Thr His Pro Arg Met Arg Arg Tyr Ile Lys Asn	
220 225 230 235	
cct cgc att gtg ctg ctg gat tct tct ctg gaa tac aag aaa gga gaa	951
Pro Arg Ile Val Leu Leu Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu	
236 241 246 251	
agc cag act gac att gag att aca cga gag gag gac ttc acc cga att	999
Ser Gln Thr Asp Ile Glu Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile	
252 257 262 267	

ctc	cag	atg	gag	gaa	gag	tac	atc	cag	cag	ctc	tgt	gag	gac	att	atc	1047
Leu	Gln	Met	Glu	Glu	Glu	Tyr	Ile	Gln	Gln	Leu	Cys	Glu	Asp	Ile	Ile	
268					273					278					283	
caa	ctg	aag	ccc	gat	gtg	gtc	atc	act	gaa	aag	ggc	atc	tca	gat	tta	1095
Gln	Leu	Lys	Pro	Asp	Val	Val	Ile	Thr	Glu	Lys	Gly	Ile	Ser	Asp	Leu	
284					289					294					299	
gct	cag	cac	tac	ctt	atg	cgg	gcc	aat	atc	aca	gcc	atc	cgc	aga	gtc	1143
Ala	Gln	His	Tyr	Leu	Met	Arg	Ala	Asn	Ile	Thr	Ala	Ile	Arg	Arg	Val	
300					305					310					315	
cgg	aag	aca	gac	aat	aat	cgc	att	gct	aga	gcc	tgt	ggg	gcc	cgg	ata	1191
Arg	Lys	Thr	Asp	Asn	Asn	Arg	Ile	Ala	Arg	Ala	Cys	Gly	Ala	Arg	Ile	
316					321					326					331	
gtc	agc	cga	cca	gag	gaa	ctg	aga	gaa	gat	gat	gtt	gga	aca	gga	gca	1239
Val	Ser	Arg	Pro	Glu	Glu	Leu	Arg	Glu	Asp	Asp	Val	Gly	Thr	Gly	Ala	
332					337					342					347	
ggc	ctg	ttg	gaa	atc	aag	aaa	att	gga	gat	gaa	tac	ttt	act	ttc	atc	1287
Gly	Leu	Leu	Glu	Ile	Lys	Lys	Ile	Gly	Asp	Glu	Tyr	Phe	Thr	Phe	Ile	
348					353					358					363	
act	gac	tgc	aaa	gac	ccc	aag	gcc	tgc	acc	att	ctc	ctc	cgg	ggg	gct	1335
Thr	Asp	Cys	Lys	Asp	Pro	Lys	Ala	Cys	Thr	Ile	Leu	Leu	Arg	Gly	Ala	
364					369					374					379	
agc	aaa	gag	att	ctc	tcg	gaa	gta	gaa	cgc	aac	ctc	cag	gat	gcc	atg	1383
Ser	Lys	Glu	Ile	Leu	Ser	Glu	Val	Glu	Arg	Asn	Leu	Gln	Asp	Ala	Met	
380					385					390					395	
caa	gtg	tgt	cgc	aat	gtt	ctc	ctg	gac	cct	cag	ctg	gtg	cca	ggg	ggt	1431
Gln	Val	Cys	Arg	Asn	Val	Leu	Leu	Asp	Pro	Gln	Leu	Val	Pro	Gly	Gly	
396					401					406					411	
ggg	gcc	tcc	gag	atg	gct	gtg	gcc	cat	gcc	ttg	aca	gaa	aaa	tcc	aag	1479
Gly	Ala	Ser	Glu	Met	Ala	Val	Ala	His	Ala	Leu	Thr	Glu	Lys	Ser	Lys	
412					417					422					427	
gcc	atg	act	ggt	gtg	gaa	caa	tgg	cca	tac	agg	gct	gtt	gcc	cag	gcc	1527
Ala	Met	Thr	Gly	Val	Glu	Gln	Trp	Pro	Tyr	Arg	Ala	Val	Ala	Gln	Ala	
428					433					438					443	
cta	gag	gtc	att	cct	cgt	acc	ctg	atc	cag	aac	tgt	ggg	gcc	agc	acc	1575
Leu	Glu	Val	Ile	Pro	Arg	Thr	Leu	Ile	Gln	Asn	Cys	Gly	Ala	Ser	Thr	
444					449					454					459	
atc	cgt	cta	ctt	acc	tcc	ctt	cgg	gcc	aag	cac	acc	cag	gag	aac	tgt	1623
Ile	Arg	Leu	Leu	Thr	Ser	Leu	Arg	Ala	Lys	His	Thr	Gln	Glu	Asn	Cys	
460					465					470					475	
gag	acc	tgg	ggt	gta	aat	ggt	gag	acg	ggt	act	ttg	gtg	gac	atg	aag	1671
Glu	Thr	Trp	Gly	Val	Asn	Gly	Glu	Thr	Gly	Thr	Leu	Val	Asp	Met	Lys	
476					481					486					491	
gaa	ctg	ggc	ata	tgg	gag	cca	ttg	gct	gtg	aag	ctg	cag	act	tat	aag	1719

Glu Leu Gly Ile Trp	Glu Pro Leu Ala Val	Lys Leu Gln Thr Tyr Lys	
492	497	502	507
aca gca gtg gag acg	gca gtt ctg cta ctg	cga att gat gac atc gtt	1767
Thr Ala Val Glu Thr	Ala Val Leu Leu Leu	Arg Ile Asp Asp Ile Val	
508	513	518	523
tca ggc cac aaa aag	aaa ggc gat gac cag	agc cgg caa ggc ggg gct	1815
Ser Gly His Lys Lys	Lys Gly Asp Asp Gln	Ser Arg Gln Gly Gly Ala	
524	529	534	539
cct gat gct ggc cag	gag tga gt gctaggcaag	gctacttcaa tgcacagaac	1868
Pro Asp Ala Gly Gln	Glu *		
540	545		
cagcagagtc tccccttttc	ctgagccaga gtgccaggaa	cactgtggac gtctttgttc	1928
agaagggatc aggttggggg	gcagccccca gtccccttct	gtcccagctc agttttccaa	1988
aagacactga catgtaattc	ttctctattg taaggtttcc	atttagtttg cttccgatga	2048
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (188)..(1108)

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agccttctcg ggaccgggg	120
gacgcctaac cccgcgagaa	ccctgcaaatt tttcttctc
ataattggga gaagactcac	180
tggccga atg gca gca gta	gat gac ttg caa ttt gaa
gaa ttt ggc aat	229
Met Ala Ala Val Asp	Asp Leu Gln Phe Glu Glu
Phe Gly Asn	
1 5 10	
gca gcc act tct ctg	aca gca aac cca gat
gcc acc aca gta aac	att
Ala Ala Thr Ser Leu	Thr Ala Asn Pro Asp
Ala Thr Thr Val Asn	Ile
15 20 25 30	
gag gat cct ggt gaa	acc cca aaa cat cag
cca gga tcc cca aga	ggc
Glu Asp Pro Gly Glu	Thr Pro Lys His Gln
Pro Gly Ser Pro Arg	Gly
31 36 41 46	
tca gga aga gaa gaa	gat gat gag tta ctg
gga aat gat gac tct	gac
Ser Gly Arg Glu Glu	Asp Asp Glu Leu Leu
Gly Asn Asp Asp Ser	Asp
47 52 57 62	

aaa act gag tta ctt gct gga cag aag aaa agc tcc ccc ttc tgg aca	421
Lys Thr Glu Leu Leu Ala Gly Gln Lys Lys Ser Ser Pro Phe Trp Thr	
63 68 73 78	
ttt gaa tac tac caa aca ttc ttt gat gtg gac acc tac cag gtc ttt	469
Phe Glu Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe	
79 84 89 94	
gac aga att aaa gga tct ctt ttg cca ata ccc ggg aaa aac ttt gtg	517
Asp Arg Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val	
95 100 105 110	
agg tta tat atc cgc agc aat cca gat ctc tat ggc ccc ttt tgg ata	565
Arg Leu Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile	
111 116 121 126	
tgt gcc acg ttg gtc ttt gcc ata gca att agt ggg aat ctt tcc aac	613
Cys Ala Thr Leu Val Phe Ala Ile Ala Ile Ser Gly Asn Leu Ser Asn	
127 132 137 142	
ttc ttg atc cat ctg gga gag aag acg tac cat tat gtg ccc gaa ttc	661
Phe Leu Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe	
143 148 153 158	
cga aaa gtg tcc ata gca gct acc atc atc tat gcc tat gcc tgg ctg	709
Arg Lys Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu	
159 164 169 174	
gtt cct ctt gca ctc tgg ggt ttc ctc atg tgg aga aac agc aaa gtt	757
Val Pro Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val	
175 180 185 190	
atg aac atc gtc tcc tat tca ttt ctg gag att gtg tgt gtc tat gga	805
Met Asn Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly	
191 196 201 206	
tat tcc ctc ttc att tat atc ccc acc gca ata ctg tgg att atc ccc	853
Tyr Ser Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro	
207 212 217 222	
cag aaa gct gtt cgt tgg att cta gtc atg att gcc ctg ggc atc tca	901
Gln Lys Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser	
223 228 233 238	
gga tct ctc ttg gca atg aca ttt tgg cca gct gtt cgt gag gat aac	949
Gly Ser Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn	
239 244 249 254	
cga cgc gtt gca ttg gcc aca att gtg aca att gtg ttg ctc cat atg	997
Arg Arg Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met	
255 260 265 270	
ctg ctt tct gtg ggc tgc ttg gca tac ttt ttt gat gca cca gag atg	1045
Leu Leu Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met	
271 276 281 286	

gac cat ctc cca aca act aca gct act cca aac caa aca gtt gct gca 1093
 Asp His Leu Pro Thr Thr Thr Ala Thr Pro Asn Gln Thr Val Ala Ala
 287 292 297 302

gcc aag tcc agc taa tgaggaaaga ctcaacttgag ataccctctc cttgctgaag 1148
 Ala Lys Ser Ser *
 303

tttttcttga cttctccagt tctcttttgt tttttggagc atgggtcttt gggaagtggc 1208

atccactgca ggaaagcaga atgagcagag ccagcagaac tgatggagtg gcacaaattc 1268

ccagtgtctg gatggtgcca cactggcgcc taatcacccg ttttaacaagc agaaattaaa 1328

tggtgctcag cacatgtgtc tttcagctct tccttttcac ccatggatga tcattgagag 1388

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tgccaccaca gtcaaatgac atgcttcact gtggtacctt aatacctgaa atagaaccat 1508

ggaaaattct gatgtcctct ctctgaatta tgtacagact acctggggga tcctcttctc 1568

tcctaatgtt agccatcctg aagtagccga acagtagaaa ctttggtggg gattaaccgg 1628

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<220>
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<400> 263

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 Met Thr Ala His Ser Phe Ala Leu Pro
 1 5

gtc atc atc ttc acc acg ttc tgg ggc ctc gtc ggc atc gcc ggg ccc 160
 Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly Pro
 10 15 20 25

tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg ctg 208
 Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu
 26 31 36 41

gtc gcc acc gcc gtc tgc tgt tac ctc ttc tgg ctc atc gcc atc ctg 256
 Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu

42	47	52	57	
gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc atc				304
Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile				
58	63	68	73	
tggttacgtg cgc ttc ctg tgg gag tga cccgc ccccccgac ccaggtgccc				356
Trp Tyr Val Arg Phe Leu Trp Glu *				
74	79			
agctctcgga atgactgtgg ctccactgtc cctgacaacc ccttcgtccg gaccctcccc				416
cacacaacta tgtctggtca ccagctccct cctgctggca ccagagacc cggacccgca				476
gggcctgcct ggttcctgga agtcttccca gtcttccag ccagcccgga ccctggggag				536
ccctgggcac agcagcggcc gaggggatgt cctgctccaa taccgcact gctctggagt				596
ttgccctctt tcccaaggag atgctgctgg ggagctggta tgggtggggg ctttcccttt				656
acagacgggg cagatgccag gactcagccc atcctgagga ggacacgtgt cctcatggag				716
aggggtgctc ggcccaggcg ggggagtcgg tgcccagtca gcagctctgc caccatcctg				776
ctgggaactg ggggggcctc tattgggtta taggcaaggc cttttctctg gcatggaatt				836
gttaattttc tgacacgtct agatgtgaaa tttctgaaaa tgttgaagca gagaaacatt				896
cacacacaaa aagcaacata gtcattgtggg tccagatggc ctcagtccta gatgttgga				956
ccctttgctg tgtctcctca gagtatcctg ttccgctcc tgccacctgg acctccctca				1016
gtggatgtct tccctcccc gacccagcc tgctcagtc agcacagtgc aggtttggct				1076
ctgacttggg cctttggctg cagtgggggt ggatttcaga gcctctcatg gcagcatcta				1136
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ccagccctgc tcctgagcca gcccgcct ctgcccctg gccctgggct ctgtgctagg				1256
gatggtgaag aatgggggag tgccagcctg gcaggagtgg gaagcaacac gcaggggtcc				1316
cggacctctc cagccttgcc ctcacgctta cccagactcc cagtgtggtt agcacagagc				1376
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acgacagcct cacttctgta tggactgtg atgtggcctg ccattctgtt cagcgggcat				1496
tgtctttgga gcagcaggag aataggatgc ctctcactca catgccagtt cctggctggc				1556
cagctgctca gggctcaggc tggggcctcc cattgacatc cccccctac actccctctc				1616
tgagcctccg tcgcccctcc tgttgggtaa ggggtgtgag tgtgacttgt gctgaaaacc				1676
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<210> 264
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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 264

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caa acc caa aaa aag aga tct ctc gag gat ccg aat tgc cgg ccg cgt	95	
Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro Arg		
15 20 25 30		
cga ccg cgg tct atg gct gcg act tct cta atg tct gct ttg gct gcc	143	
Arg Pro Arg Ser Met Ala Ala Thr Ser Leu Met Ser Ala Leu Ala Ala		
31 36 41 46		
cgg ctg ctg cag ccc gcg cac agc tgc tcc ctt cgc ctt cgc cct ttc	191	
Arg Leu Leu Gln Pro Ala His Ser Cys Ser Leu Arg Leu Arg Pro Phe		
47 52 57 62		
cac ctc gcg gca gtt cga aat gaa gct gtt gtc att tct gga agg aaa	239	
His Leu Ala Ala Val Arg Asn Glu Ala Val Val Ile Ser Gly Arg Lys		
63 68 73 78		
ctg gcc cag cag atc aag cag gaa gtg cgg cag gag gta gaa gag tgg	287	
Leu Ala Gln Gln Ile Lys Gln Glu Val Arg Gln Glu Val Glu Glu Trp		
79 84 89 94		
gtg gcc tca ggc aac aaa cgg cca cac ctg agt gtg atc ctg gtt ggc	335	
Val Ala Ser Gly Asn Lys Arg Pro His Leu Ser Val Ile Leu Val Gly		
95 100 105 110		
gag aat cct gca agt cac tcc tat gtc ctc aac aaa acc agg gca gct	383	
Glu Asn Pro Ala Ser His Ser Tyr Val Leu Asn Lys Thr Arg Ala Ala		
111 116 121 126		
gca gtt gtg gga atc aac agt gag aca att atg aaa cca gct tca att	431	
Ala Val Val Gly Ile Asn Ser Glu Thr Ile Met Lys Pro Ala Ser Ile		
127 132 137 142		
tca gag gaa gaa ttg ttg aat tta atc aat aaa ctg aat aat gat gat	479	
Ser Glu Glu Glu Leu Leu Asn Leu Ile Asn Lys Leu Asn Asn Asp Asp		
143 148 153 158		
aat gta gat ggc ctc ctt gtt cag ttg cct ctt cca gag cat att gat	527	
Asn Val Asp Gly Leu Leu Val Gln Leu Pro Leu Pro Glu His Ile Asp		
159 164 169 174		
gag aga agg atc tgc aat gct gtt tct cca gac aag gat gtt gat ggc	575	

Glu	Arg	Arg	Ile	Cys	Asn	Ala	Val	Ser	Pro	Asp	Lys	Asp	Val	Asp	Gly	
175					180					185					190	
ttt	cat	gta	att	aat	gta	gga	cga	atg	tgt	ttg	gat	cag	tat	tcc	atg	623
Phe	His	Val	Ile	Asn	Val	Gly	Arg	Met	Cys	Leu	Asp	Gln	Tyr	Ser	Met	
191					196					201					206	
tta	ccg	gct	act	cca	tgg	ggt	gtg	tgg	gaa	ata	atc	aag	cga	act	ggc	671
Leu	Pro	Ala	Thr	Pro	Trp	Gly	Val	Trp	Glu	Ile	Ile	Lys	Arg	Thr	Gly	
207					212					217					222	
att	cca	acc	cta	ggg	aag	aat	gtg	gtt	gtg	gct	gga	agg	tca	aaa	aac	719
Ile	Pro	Thr	Leu	Gly	Lys	Asn	Val	Val	Val	Ala	Gly	Arg	Ser	Lys	Asn	
223					228					233					238	
gtt	gga	atg	ccc	att	gca	atg	tta	ctg	cac	aca	gat	ggg	gcg	cat	gaa	767
Val	Gly	Met	Pro	Ile	Ala	Met	Leu	Leu	His	Thr	Asp	Gly	Ala	His	Glu	
239					244					249					254	
cgt	ccc	gga	ggt	gat	gcc	act	gtt	aca	ata	tct	cat	cga	tat	act	ccc	815
Arg	Pro	Gly	Gly	Asp	Ala	Thr	Val	Thr	Ile	Ser	His	Arg	Tyr	Thr	Pro	
255					260					265					270	
aaa	gag	cag	ttg	aag	aaa	cat	aca	att	ctt	gca	gat	att	gta	ata	tct	863
Lys	Glu	Gln	Leu	Lys	Lys	His	Thr	Ile	Leu	Ala	Asp	Ile	Val	Ile	Ser	
271					276					281					286	
gct	gca	ggt	att	cca	aat	ctg	atc	aca	gca	gat	atg	atc	aag	gaa	gga	911
Ala	Ala	Gly	Ile	Pro	Asn	Leu	Ile	Thr	Ala	Asp	Met	Ile	Lys	Glu	Gly	
287					292					297					302	
gca	gca	gtc	att	gat	gtg	gga	ata	aat	aga	gtt	cac	gat	cct	gta	act	959
Ala	Ala	Val	Ile	Asp	Val	Gly	Ile	Asn	Arg	Val	His	Asp	Pro	Val	Thr	
303					308					313					318	
gcc	aaa	ccc	aag	ttg	gtt	gga	gat	gtg	gat	ttt	gaa	gga	gtc	aga	caa	1007
Ala	Lys	Pro	Lys	Leu	Val	Gly	Asp	Val	Asp	Phe	Glu	Gly	Val	Arg	Gln	
319					324					329					334	
aaa	gct	ggg	tat	atc	act	cca	gtt	cct	gga	ggt	gtt	ggc	ccc	atg	aca	1055
Lys	Ala	Gly	Tyr	Ile	Thr	Pro	Val	Pro	Gly	Gly	Val	Gly	Pro	Met	Thr	
335					340					345					350	
gtg	gca	atg	cta	atg	aag	aat	acc	att	att	gct	gca	aaa	aag	gtg	ctg	1103
Val	Ala	Met	Leu	Met	Lys	Asn	Thr	Ile	Ile	Ala	Ala	Lys	Lys	Val	Leu	
351					356					361					366	
agg	ctt	gaa	gag	cga	gaa	gtg	ctg	aag	tct	aaa	gag	ctt	ggg	gta	gcc	1151
Arg	Leu	Glu	Glu	Arg	Glu	Val	Leu	Lys	Ser	Lys	Glu	Leu	Gly	Val	Ala	
367					372					377					382	
act	aat	taa	ctactgt	gtcttctgtg	tcacaaacag	cactccaggc	cagctcaaga									1207
Thr	Asn	*														
383																
agcaaagcag	gccaatagaa	atgcaatatt	tttaatttat	tctactgaaa	tggtttaaaa											1267

tgatgccttg tatttattga aagcttaaata ggggtgggtgt ttctgcacat acctctgcag 1327
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 attaacctag tgattaatat gggagacatt accatatgga ggatggatgc ttcactttgt 1447
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 ttaaattttt gtattgtata gtttcttttg tgtatcttaa aacctatttt tgaaaaacaa 1987
 acttggttg ataatcattt gggcagcttg ggtaagtacg caacttactt ttccaccaa 2047
 gaactgtcag cagctgcctg cttttctgtg atgtatgtat cctgttgact tttccagaaa 2107
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 cggagaaacg tttctctttc ctctcagttt gcgcacacc atg gcg gcc cct gcc 114
 Met Ala Ala Pro Ala
 1
 cag cag act act cag cct ggc ggc ggg aag cgc aaa ggc aag gct cag 162
 Gln Gln Thr Thr Gln Pro Gly Gly Gly Lys Arg Lys Gly Lys Ala Gln
 6 11 16 21
 tat gtg ctg gcc aag cgc gct cgg cgc tgc gac gct ggc ggg ccc cgt 210
 Tyr Val Leu Ala Lys Arg Ala Arg Arg Cys Asp Ala Gly Gly Pro Arg

22	27	32	37	
cag cta gag ccc ggg cta cag ggc atc ctc atc acc tgc aat atg aac				258
Gln Leu Glu Pro Gly Leu Gln Gly Ile Leu Ile Thr Cys Asn Met Asn				
38	43	48	53	
gag cgc aag tgc gtg gag gag gcc tac agc ctc ctc aac gaa tac ggc				306
Glu Arg Lys Cys Val Glu Glu Ala Tyr Ser Leu Leu Asn Glu Tyr Gly				
54	59	64	69	
gac gac atg tat ggg cca gaa aag ttt aca gac aag gat cag cag ccc				354
Asp Asp Met Tyr Gly Pro Glu Lys Phe Thr Asp Lys Asp Gln Gln Pro				
70	75	80	85	
tct gga agt gag gga gag gat gat gat gcg gag gct gcc ttg aag aaa				402
Ser Gly Ser Glu Gly Glu Asp Asp Asp Ala Glu Ala Ala Leu Lys Lys				
86	91	96	101	
gaa gtt ggt gac att aag gca tct aca gag atg agg tta aga aga ttc				450
Glu Val Gly Asp Ile Lys Ala Ser Thr Glu Met Arg Leu Arg Arg Phe				
102	107	112	117	
cag tca gtg gaa agt gga gca aat aac gtt gtc ttc atc agg aca ctt				498
Gln Ser Val Glu Ser Gly Ala Asn Asn Val Val Phe Ile Arg Thr Leu				
118	123	128	133	
ggg ata gag cct gag aaa ttg gtg cat cat att ctc cag gat atg tac				546
Gly Ile Glu Pro Glu Lys Leu Val His His Ile Leu Gln Asp Met Tyr				
134	139	144	149	
aaa acc aag aaa aag aag act cga gtt att ttg cga atg tta ccc atc				594
Lys Thr Lys Lys Lys Lys Thr Arg Val Ile Leu Arg Met Leu Pro Ile				
150	155	160	165	
tca ggc aca tgc aag gct ttt tta gaa gat atg aaa aaa tat gca gaa				642
Ser Gly Thr Cys Lys Ala Phe Leu Glu Asp Met Lys Lys Tyr Ala Glu				
166	171	176	181	
aca ttt ttg gaa ccc tgg ttt aaa gct cca aac aaa ggg aca ttt cag				690
Thr Phe Leu Glu Pro Trp Phe Lys Ala Pro Asn Lys Gly Thr Phe Gln				
182	187	192	197	
att gtg tac aaa tct cga aat aac agt cat gtg aat aga gaa gaa gtt				738
Ile Val Tyr Lys Ser Arg Asn Asn Ser His Val Asn Arg Glu Glu Val				
198	203	208	213	
atc aga gaa ttg gca gga ata gtg tgc acc ctc aat tca gaa aat aaa				786
Ile Arg Glu Leu Ala Gly Ile Val Cys Thr Leu Asn Ser Glu Asn Lys				
214	219	224	229	
gtg gat ctc acc aat cca cag tac aca gtg gta gta gaa atc atc aaa				834
Val Asp Leu Thr Asn Pro Gln Tyr Thr Val Val Val Glu Ile Ile Lys				
230	235	240	245	
gct gtc tgt tgc ctg agt gtt gtg aaa gat tac atg ttg ttt aga aaa				882
Ala Val Cys Cys Leu Ser Val Val Lys Asp Tyr Met Leu Phe Arg Lys				
246	251	256	261	

tac aat ctc cag gag gtg gtg aag agc cct aag gat ccg tca cag ctt	930
Tyr Asn Leu Gln Glu Val Val Lys Ser Pro Lys Asp Pro Ser Gln Leu	
262 267 272 277	
aac tca aag cag gga aat ggg aaa gaa gct aaa ctg gaa tct gcg gac	978
Asn Ser Lys Gln Gly Asn Gly Lys Glu Ala Lys Leu Glu Ser Ala Asp	
278 283 288 293	
aaa tca gac caa aac aac aca gca gaa gga aaa aat aac cag cag gta	1026
Lys Ser Asp Gln Asn Asn Thr Ala Glu Gly Lys Asn Asn Gln Gln Val	
294 299 304 309	
cca gag aat act gag gag ctg ggg cag aca aaa cca acg tct aat cca	1074
Pro Glu Asn Thr Glu Glu Leu Gly Gln Thr Lys Pro Thr Ser Asn Pro	
310 315 320 325	
cag gtg gta aat gag gga gga gcc aaa cct gaa ctt gca agt caa gcc	1122
Gln Val Val Asn Glu Gly Gly Ala Lys Pro Glu Leu Ala Ser Gln Ala	
326 331 336 341	
aca gaa gga tcc aag tca aat gaa aat gac ttc tca tag gaagtcattt	1171
Thr Glu Gly Ser Lys Ser Asn Glu Asn Asp Phe Ser *	
342 347 352	
gggtgttgag ctgacagtcc agtgtcgcaa ttttgggaagg caagatgtga gagagacgag	1231
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Met	
1	
agg gca gac gag atc aaa gat gcc atc tac gtg acc atg gag atc ctg	166
Arg Ala Asp Glu Ile Lys Asp Ala Ile Tyr Val Thr Met Glu Ile Leu	
2 7 12 17	
tcc aac tgg ggc aac tcg tgg tgg gtg ggt ctc aca gaa gtc gag ttc	214
Ser Asn Trp Gly Asn Ser Trp Trp Val Gly Leu Thr Glu Val Glu Phe	
18 23 28 33	

ttt gac ttg aat gac aca aag ctt tat gtg tgc ccc cac gat gtg gat	262
Phe Asp Leu Asn Asp Thr Lys Leu Tyr Val Ser Pro His Asp Val Asp	
34 39 44 49	
atc cgg aac aca gcc acg cct ggg gag ctg ggc cgc ctc gtc aac agg	310
Ile Arg Asn Thr Ala Thr Pro Gly Glu Leu Gly Arg Leu Val Asn Arg	
50 55 60 65	
aac tta gct ggc aag aaa gac tcc tcc ccg tgg acc tgc ccc ttc cac	358
Asn Leu Ala Gly Lys Lys Asp Ser Ser Pro Trp Thr Cys Pro Phe His	
66 71 76 81	
cca cca ctc cag ctg ttt ttt gtt att cga aac aca aga cag ctg ggg	406
Pro Pro Leu Gln Leu Phe Phe Val Ile Arg Asn Thr Arg Gln Leu Gly	
82 87 92 97	
gac ttc cat ctg gcc aag atc aag gtt cgg aat tac tgg aca gct gat	454
Asp Phe His Leu Ala Lys Ile Lys Val Arg Asn Tyr Trp Thr Ala Asp	
98 103 108 113	
ggc gat ctt gac att ggt gcc aag aac gtg aag ctt tac gtc aac aga	502
Gly Asp Leu Asp Ile Gly Ala Lys Asn Val Lys Leu Tyr Val Asn Arg	
114 119 124 129	
aac ctc atc ttc aat ggc aag tta gac aaa gga gat agg gag gcc cca	550
Asn Leu Ile Phe Asn Gly Lys Leu Asp Lys Gly Asp Arg Glu Ala Pro	
130 135 140 145	
gct gac cac agc atc ctg gtt gac cag aag aac gag aag agc gag caa	598
Ala Asp His Ser Ile Leu Val Asp Gln Lys Asn Glu Lys Ser Glu Gln	
146 151 156 161	
cta gag gag gcc atg aac gct cac tgc gaa gaa agc aaa ggc acc cat	646
Leu Glu Glu Ala Met Asn Ala His Ser Glu Glu Ser Lys Gly Thr His	
162 167 172 177	
gag atg gct ggt gcc agc ggg gac aag gag ctt ggt ctc ggt tgc tca	694
Glu Met Ala Gly Ala Ser Gly Asp Lys Glu Leu Gly Leu Gly Cys Ser	
178 183 188 193	
ccg cca gct gaa aca tta gcg gat gca aag ctt tct tca caa gga aat	742
Pro Pro Ala Glu Thr Leu Ala Asp Ala Lys Leu Ser Ser Gln Gly Asn	
194 199 204 209	
gtg tct ggc aaa aga aag aat tct act aat tgc agg aaa gac agt ttg	790
Val Ser Gly Lys Arg Lys Asn Ser Thr Asn Cys Arg Lys Asp Ser Leu	
210 215 220 225	
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Ser Gln Leu Glu Glu Tyr Leu Arg Leu Ser Ala Val Pro Thr Ser Met	
226 231 236 241	
ggt gac atg ccc agt gct cct gcc act tcc cca cct gtg aag tgc cct	886
Gly Asp Met Pro Ser Ala Pro Ala Thr Ser Pro Pro Val Lys Cys Pro	
242 247 252 257	

cct gtc cat gag gag ccc tct ctc atc caa caa ctg gaa aac ctc atg	934
Pro Val His Glu Glu Pro Ser Leu Ile Gln Gln Leu Glu Asn Leu Met	
258 263 268 273	
ggc aga aaa atc tgt gag cca ccc ggg aaa acc cca tcc tgg tta caa	982
Gly Arg Lys Ile Cys Glu Pro Pro Gly Lys Thr Pro Ser Trp Leu Gln	
274 279 284 289	
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Pro Ser Pro Thr Gly Lys Asp Arg Lys Gln Gly Gly Arg Lys Pro Lys	
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ccc ctc tgg ctt agt ccc gag aag ccc ctg gcc tgg aag ggc agg ctc	1078
Pro Leu Trp Leu Ser Pro Glu Lys Pro Leu Ala Trp Lys Gly Arg Leu	
306 311 316 321	
cca tca gac gat gtc atc ggt gag ggt cct gga gag acc gag gcc agg	1126
Pro Ser Asp Asp Val Ile Gly Glu Gly Pro Gly Glu Thr Glu Ala Arg	
322 327 332 337	
gat aaa ggc cta cgg cat gag cca ggg tgg ggg acc agc cgg agt gtc	1174
Asp Lys Gly Leu Arg His Glu Pro Gly Trp Gly Thr Ser Arg Ser Val	
338 343 348 353	
aac acc aag gag aga ccc cag agg gca acc acc aaa gtc cac agt gat	1222
Asn Thr Lys Glu Arg Pro Gln Arg Ala Thr Thr Lys Val His Ser Asp	
354 359 364 369	
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Asp Ser Asp Ile Phe Asn Gln Pro Pro Asn Arg Glu Arg Pro Ala Ser	
370 375 380 385	
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Gly Arg Arg Gly Ser Arg Lys Asp Ala Gly Ser Ser Ser His Gly Asp	
386 391 396 401	
gac cag cca gcc agc aga gaa gac acc tgg tct tcc agg acg ccg tca	1366
Asp Gln Pro Ala Ser Arg Glu Asp Thr Trp Ser Ser Arg Thr Pro Ser	
402 407 412 417	
cgg tca agg tgg cgc agt gag cag gag cac aca ctt cac gag tca tgg	1414
Arg Ser Arg Trp Arg Ser Glu Gln Glu His Thr Leu His Glu Ser Trp	
418 423 428 433	
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Ser Ser Leu Ser Ala Phe Asp Arg Ser His Arg Gly Arg Ile Ser Asn	
434 439 444 449	
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Thr Glu Leu Pro Gly Asp Ile Leu Asp Glu Leu Leu Gln Gln Lys Ser	
450 455 460 465	
agc cgg cac agc gac ttg ccc ccc tcc aag aag ggg gag cag cca ggg	1558
Ser Arg His Ser Asp Leu Pro Pro Ser Lys Lys Gly Glu Gln Pro Gly	
466 471 476 481	
ctg tcg aga ggg cag gat ggc tac tct gga gag aca gac gct ggg ggt	1606

Leu Ser Arg Gly Gln Asp Gly Tyr Ser Gly Glu Thr Asp Ala Gly Gly	
482 487 492 497	
gac ttt aaa atc ccc gtc ttg cct tat gga cag cgc ttg gtc att gac	1654
Asp Phe Lys Ile Pro Val Leu Pro Tyr Gly Gln Arg Leu Val Ile Asp	
498 503 508 513	
atc aag tct acc tgg ggg gac aga cac tat gtc ggc ctc aac gga ata	1702
Ile Lys Ser Thr Trp Gly Asp Arg His Tyr Val Gly Leu Asn Gly Ile	
514 519 524 529	
gaa ata ttc agt tcc aag ggt gaa ccg gtg cag att tca aac ata aaa	1750
Glu Ile Phe Ser Ser Lys Gly Glu Pro Val Gln Ile Ser Asn Ile Lys	
530 535 540 545	
gca gac cct ccc gat atc aat att tta cca gcc tat ggg aaa gac ccc	1798
Ala Asp Pro Pro Asp Ile Asn Ile Leu Pro Ala Tyr Gly Lys Asp Pro	
546 551 556 561	
cgc gtg gtc acc aac ctc atc gac ggg gtg aac agg acc cag gat gac	1846
Arg Val Val Thr Asn Leu Ile Asp Gly Val Asn Arg Thr Gln Asp Asp	
562 567 572 577	
atg cat gtc tgg ctg gcc ccc ttc acg cgg ggc aga tcc cac tcc atc	1894
Met His Val Trp Leu Ala Pro Phe Thr Arg Gly Arg Ser His Ser Ile	
578 583 588 593	
acc att gac ttc acg cac cct tgc cac gtt gcc ctg atc aga att tgg	1942
Thr Ile Asp Phe Thr His Pro Cys His Val Ala Leu Ile Arg Ile Trp	
594 599 604 609	
aac tac aat aaa tct cgg ata cat tcc ttc cga ggc gtg aag gac atc	1990
Asn Tyr Asn Lys Ser Arg Ile His Ser Phe Arg Gly Val Lys Asp Ile	
610 615 620 625	
aca atg ctg tta gac acc cag tgc atc ttt gaa gga gaa atc gcc aag	2038
Thr Met Leu Leu Asp Thr Gln Cys Ile Phe Glu Gly Glu Ile Ala Lys	
626 631 636 641	
gcc tct gga acc ctg gcg gga gcc cca gag cac ttt gga gac acg atc	2086
Ala Ser Gly Thr Leu Ala Gly Ala Pro Glu His Phe Gly Asp Thr Ile	
642 647 652 657	
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Leu Phe Thr Thr Asp Asp Asp Ile Leu Glu Ala Ile Phe Tyr Ser Asp	
658 663 668 673	
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Glu Met Phe Asp Leu Asp Val Gly Ser Leu Asp Ser Leu Gln Asp Glu	
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Glu Ala Met Arg Arg Pro Ser Thr Ala Asp Gly Glu Gly Asp Glu Arg	
690 695 700 705	
ccc ttc acc cag gct ggc ttg ggg gct gat gaa cgg atc ccg gag cta	2278
Pro Phe Thr Gln Ala Gly Leu Gly Ala Asp Glu Arg Ile Pro Glu Leu	

706		711		716		721	
gag ctc cca tcc agt tcc cct gtc ccc caa gtc acc acg cca gag cca	2326						
Glu Leu Pro Ser Ser Ser Pro Val Pro Gln Val Thr Thr Pro Glu Pro							
722		727		732		737	
ggc atc tac cac gga atc tgc ctt cag ctg aat ttc act gcc tcc tgg	2374						
Gly Ile Tyr His Gly Ile Cys Leu Gln Leu Asn Phe Thr Ala Ser Trp							
738		743		748		753	
gga gac ttg cac tac ctg ggg ctc act ggc ctg gaa gtg gtg ggc aag	2422						
Gly Asp Leu His Tyr Leu Gly Leu Thr Gly Leu Glu Val Val Gly Lys							
754		759		764		769	
gag ggc cag gcg ctg ccc atc cac ctg cac cag atc tct gct tcc ccc	2470						
Glu Gly Gln Ala Leu Pro Ile His Leu His Gln Ile Ser Ala Ser Pro							
770		775		780		785	
aga gac tta aat gag ctc ccc gag tac tct gac gac tcc cgg acc ctg	2518						
Arg Asp Leu Asn Glu Leu Pro Glu Tyr Ser Asp Asp Ser Arg Thr Leu							
786		791		796		801	
gac aag tta att gat ggc acc aac atc acc atg gag gat gag cat atg	2566						
Asp Lys Leu Ile Asp Gly Thr Asn Ile Thr Met Glu Asp Glu His Met							
802		807		812		817	
tgg ctg atc ccc ttc tgc ccg ggg ctg gac cat gtg gtc acg atc cgc	2614						
Trp Leu Ile Pro Phe Ser Pro Gly Leu Asp His Val Val Thr Ile Arg							
818		823		828		833	
ctg gac agg gcc gaa agc atc gca ggc ctg cgc ttc tgg aac tac aat	2662						
Leu Asp Arg Ala Glu Ser Ile Ala Gly Leu Arg Phe Trp Asn Tyr Asn							
834		839		844		849	
aaa tct ccc gag gac acc tat cgc ggg gcc aag att gtc cac gtc tcc	2710						
Lys Ser Pro Glu Asp Thr Tyr Arg Gly Ala Lys Ile Val His Val Ser							
850		855		860		865	
ctg gat ggc ctg tgc gtc tcc ccg cca gag ggc ttt ctc atc cgg aag	2758						
Leu Asp Gly Leu Cys Val Ser Pro Pro Glu Gly Phe Leu Ile Arg Lys							
866		871		876		881	
ggg cca ggc aac tgc cac ttt gat ttt gct caa gaa atc ctc ttc gtg	2806						
Gly Pro Gly Asn Cys His Phe Asp Phe Ala Gln Glu Ile Leu Phe Val							
882		887		892		897	
gac tac cta cgg gct cag ctg ctg ccc cag ccg gcc agg agg ctg gac	2854						
Asp Tyr Leu Arg Ala Gln Leu Leu Pro Gln Pro Ala Arg Arg Leu Asp							
898		903		908		913	
atg aga agc ctg gag tgt gca agc atg gac tac gag gca ccg ctg atg	2902						
Met Arg Ser Leu Glu Cys Ala Ser Met Asp Tyr Glu Ala Pro Leu Met							
914		919		924		929	
ccc tgt ggc ttc att ttc cag ttt cag ctt ctc acc agc tgg ggc gac	2950						
Pro Cys Gly Phe Ile Phe Gln Phe Gln Leu Leu Thr Ser Trp Gly Asp							
930		935		940		945	

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Pro Tyr Tyr Ile Gly Leu Thr Gly Leu Glu Leu Tyr Asp Glu Arg Gly	
946 951 956 961	
gaa aaa atc ccc ttg tgc gaa aac aat att gcg gcc ttc ccc gac agc	3046
Glu Lys Ile Pro Leu Ser Glu Asn Asn Ile Ala Ala Phe Pro Asp Ser	
962 967 972 977	
gtg aac tcc ctg gag ggt gtg ggc ggg gac gtc cgc acc cca gac aag	3094
Val Asn Ser Leu Glu Gly Val Gly Gly Asp Val Arg Thr Pro Asp Lys	
978 983 988 993	
ctc atc gac caa gtg aac gac acc agt gat ggc cgg cac atg tgg ctg	3142
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Ala Pro Ile Leu Pro Gly Leu Val Asn Arg Val Tyr Val Ile Phe Asp	
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Leu Pro Thr Thr Val Ser Met Ile Lys Leu Trp Asn Tyr Ala Lys Thr	
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ccc cat cga ggg gtg aag gag ttt ggc ctc ctg gtg gac gac ctg ctt	3286
Pro His Arg Gly Val Lys Glu Phe Gly Leu Leu Val Asp Asp Leu Leu	
1042 1047 1052 1057	
gtg tac aat ggg atc ctg gcc atg gtg agc cac ctg gtg ggg ggc atc	3334
Val Tyr Asn Gly Ile Leu Ala Met Val Ser His Leu Val Gly Gly Ile	
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Leu Pro Thr Cys Glu Pro Thr Val Pro Tyr His Thr Ile Leu Phe Thr	
1074 1079 1084 1089	
gag gac agg gac atc cgc cac cag gag aaa cac acc acc atc agt aat	3430
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1090 1095 1100 1105	
cag gcc gag gat caa gat gtc cag atg atg aat gaa aac caa acc att	3478
Gln Ala Glu Asp Gln Asp Val Gln Met Met Asn Glu Asn Gln Thr Ile	
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acc aac gcg aaa cgg aag cag agc gtt gtt gac cca gcc tta cgt ccc	3526
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Lys Thr Cys Ile Ser Glu Lys Glu Thr Arg Arg Arg Arg Cys *	
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              Met Ala Ala Thr Leu Asp Leu Lys Ser Lys Glu Glu Lys
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gat gct gag ttg gac aag agg atc gag gct ctt cgg cgg aag aat gag      217
Asp Ala Glu Leu Asp Lys Arg Ile Glu Ala Leu Arg Arg Lys Asn Glu
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Ala Leu Ile Arg Arg Tyr Gln Glu Ile Glu Glu Asp Arg Lys Lys Ala
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Glu Leu Glu Gly Val Ala Val Thr Ala Pro Arg Lys Gly Arg Ser Val
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gag aag gag aac gtg gca gtg gag tcg gag aag aac ctg ggt cct tcc      361
Glu Lys Glu Asn Val Ala Val Glu Ser Glu Lys Asn Leu Gly Pro Ser
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cgg agg tct cct ggg acc cct cgg ccc cca ggg gcc agc aag ggg ggc      409
Arg Arg Ser Pro Gly Thr Pro Arg Pro Pro Gly Ala Ser Lys Gly Gly
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cgg act cct cca cag cag gga ggc cgg gcc ggc atg ggc cga gca tcg      457
Arg Thr Pro Pro Gln Gln Gly Gly Arg Ala Gly Met Gly Arg Ala Ser
  94              99              104             109

cgc agc tgg gag ggc agc ccc ggg gag cag cct cga gga gga gga gct      505
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Gly Ala Gly Asp Thr Ser Ile Ser Asp Arg Lys Ser Lys Glu Trp Glu
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gag cgg cgc agg cag aac att gag aag atg aat gag gag atg gag aag      649
Glu Arg Arg Arg Gln Asn Ile Glu Lys Met Asn Glu Glu Met Glu Lys
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Asn Trp Gly Gly Pro Asp Phe Glu Arg Val Arg Cys Gly Leu Glu His	
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Leu Ser Met Thr Gly Arg Glu Arg Ser Glu Tyr Leu Arg Trp Lys Gln	
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Pro Ala Gln Asp His Gln Ala Pro Glu Ala Ala Pro Thr Gly Ile Pro	
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Cys Ser Glu Gln Ala His Gly Val Pro Phe Ser Pro Glu Glu Pro Leu	
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Ser Gly His Gln Pro Val Ser Asp Trp Gly Glu Glu Val Glu Leu Asn	
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Ser Pro Arg Thr Thr His Leu Ala Gly Ala Leu Ser Pro Gly Glu Ala	
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Trp Pro Phe Glu Ser Val *	
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cta cct ttc aat acg gtt cag ggc gac ata gat gct atc ttt aag gat Leu Pro Phe Asn Thr Val Gln Gly Asp Ile Asp Ala Ile Phe Lys Asp 49 54 59 64	312
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aac tct gct atc ttc ggg ggt gcc agg cct aga gag gaa gtc gtt caa	792

Asn Ser Ala Ile Phe Gly Gly Ala Arg Pro Arg Glu Glu Val Val Gln
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 Lys Glu Gln Glu *
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 ggc ggc aga ggg tcc cgc ggc agt gct ggt ggc cat ggt tcc cgt agc 216
 Gly Gly Arg Gly Ser Arg Gly Ser Ala Gly Gly His Gly Ser Arg Ser
 17 22 27 32
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 Gln Lys Glu Leu Pro Thr Glu Pro Pro Tyr Thr Ala Tyr Val Gly Asn
 33 38 43 48
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 Leu Pro Phe Asn Thr Val Gln Gly Asp Ile Asp Ala Ile Phe Lys Asp
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 Leu Ser Ile Arg Ser Val Arg Leu Val Arg Asp Lys Asp Thr Asp Lys
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 Phe Lys Gly Phe Cys Tyr Val Glu Phe Asp Glu Val Asp Ser Leu Lys
 81 86 91 96
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 Glu Ala Leu Thr Tyr Asp Gly Ala Leu Leu Gly Asp Arg Ser Leu Arg
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Arg Lys Gly Gly Pro Asp Asp Arg Gly Met Gly Ser Ser Arg Glu Ser				
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Arg Gly Gly Trp Asp Ser Arg Asp Asp Phe Asn Ser Gly Phe Arg Asp				
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Asp Phe Leu Gly Gly Arg Gly Gly Ser Arg Pro Gly Asp Arg Arg Thr				
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Gly Pro Pro Met Gly Ser Arg Phe Arg Asp Gly Pro Pro Leu Arg Gly				
177	182	187	192	
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Ser Asn Met Asp Phe Arg Glu Pro Thr Glu Glu Glu Arg Ala Gln Arg				
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Pro Arg Leu Gln Leu Lys Pro Arg Thr Val Ala Thr Pro Leu Asn Gln				
209	214	219	224	
gta gcc aat ccc aac tct gct atc ttc ggg ggt gcc agg cct aga gag				840
Val Ala Asn Pro Asn Ser Ala Ile Phe Gly Gly Ala Arg Pro Arg Glu				
225	230	235	240	
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Glu Val Val Gln Lys Glu Gln Glu *				
241	246			
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Met Phe Leu Leu Leu
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Trp Pro Pro Arg Cys Asn Lys Leu Ala Val Tyr Leu Asp Leu Cys Leu
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Ile Phe Leu Leu Leu Arg Phe Ser Leu Arg Ile Arg Phe Phe Leu His
22 27 32 37

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Leu Ala Leu Met Ala Gln Arg Phe Pro Lys Lys Trp Arg Tyr Pro Arg
38 43 48 53

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Val Arg Pro Arg Val Arg Gly Arg Val Gly Phe Phe Gly Asn Leu Cys
54 59 64 69

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Ala Met Arg Ala Lys Trp Arg Lys Lys Arg Met Arg Arg Leu Lys Arg
70 75 80 85

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Lys Arg Arg Lys Met Arg Gln Arg Ser Lys *
86 91 96

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ctgccctgga cctgtgacat tctggactat ttctgtgttt atttgtggcc gagtgttaaca 944

accatataat aaatcacctc ttccgctggt ttagctgaag aattaaaaaa aaaaaaaa 1002

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cgagcgttgc cgggccaggg tcaagcggag ggctccgacg gcgcggacgg agcgaagcgc	180
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1 5 10	
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15 20 25 30	
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31 36 41 46	
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47 52 57 62	
gcc cag cag ccc tgc tac ctg ctc tac cgc ctc gac tca cag aat gct Ala Gln Gln Pro Cys Tyr Leu Leu Tyr Arg Leu Asp Ser Gln Asn Ala	420
63 68 73 78	
cag ggc ttc gaa tgg ctc ttc ctc gcc tgg tcg cct gat aac tcc ccc Gln Gly Phe Glu Trp Leu Phe Leu Ala Trp Ser Pro Asp Asn Ser Pro	468
79 84 89 94	
gtg cgg ctg aag atg ctg tac gcg gcc acg cgg gcc aca gtg aaa aag Val Arg Leu Lys Met Leu Tyr Ala Ala Thr Arg Ala Thr Val Lys Lys	516
95 100 105 110	
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111 116 121 126	
gat gac ctc tct ttt gct ggg tac cag aaa cac ctg tcg tcc tgt gcg Asp Asp Leu Ser Phe Ala Gly Tyr Gln Lys His Leu Ser Ser Cys Ala	612
127 132 137 142	
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175 180 185 190	
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191 196 201 206	

cta gag cgg gaa acc att gag ctg gtg cac aca gag ccc acg gat gtg	852
Leu Glu Arg Glu Thr Ile Glu Leu Val His Thr Glu Pro Thr Asp Val	
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Ala Gln Leu Pro Ser Arg Val Pro Arg Asp Ala Ala Arg Tyr His Phe	
223 228 233 238	
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Phe Leu Tyr Lys His Thr His Glu Gly Asp Pro Leu Glu Ser Val Val	
239 244 249 254	
ttc atc tac tcc atg ccg ggg tac aag tgc agc atc aag gag cga atg	996
Phe Ile Tyr Ser Met Pro Gly Tyr Lys Cys Ser Ile Lys Glu Arg Met	
255 260 265 270	
ctc tac tcc agc tgc aag agc cgc ctc ctc gac tcc gtg gag cag gac	1044
Leu Tyr Ser Ser Cys Lys Ser Arg Leu Leu Asp Ser Val Glu Gln Asp	
271 276 281 286	
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Phe His Leu Glu Ile Ala Lys Lys Ile Glu Ile Gly Asp Gly Ala Glu	
287 292 297 302	
ctg acg gca gag ttc ctc tac gac gag gtg cac ccc aag caa cac gcc	1140
Leu Thr Ala Glu Phe Leu Tyr Asp Glu Val His Pro Lys Gln His Ala	
303 308 313 318	
ttc aag cag gcc ttc gcc aag ccc aag ggc cca ggg ggc aag cgg ggc	1188
Phe Lys Gln Ala Phe Ala Lys Pro Lys Gly Pro Gly Gly Lys Arg Gly	
319 324 329 334	
cat aag cgc ctc atc cgc ggc ccg ggt gaa aat ggg gat gac agc tag	1236
His Lys Arg Leu Ile Arg Gly Pro Gly Glu Asn Gly Asp Asp Ser *	
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Met Val Leu Leu His Val Leu Phe Glu His
1 5

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Ala Val Gly Tyr Ala Leu Leu Ala Leu Lys Glu Val Glu Glu Ile Ser
11 16 21 26

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Leu Leu Gln Pro Gln Val Glu Glu Ser Val Leu Asn Leu Gly Lys Phe
27 32 37 42

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His Ser Ile Val Arg Leu Val Ala Phe Cys Pro Phe Ala Ser Ser Gln
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Val Ala Leu Glu Asn Ala Asn Ala Val Ser Glu Gly Val Val His Glu
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gac ctc cgc ctg ctc ttg gag acc cac ctg ccg tcc aaa aag aag aaa 351
Asp Leu Arg Leu Leu Leu Glu Thr His Leu Pro Ser Lys Lys Lys Lys
75 80 85 90

gta ctc ttg gga gtt ggg gat ccc aag att ggt gcc gca ata cag gag 399
Val Leu Leu Gly Val Gly Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu
91 96 101 106

gag tta ggg tac aac tgc cag act gga gga gtc ata gct gag atc ctg 447
Glu Leu Gly Tyr Asn Cys Gln Thr Gly Gly Val Ile Ala Glu Ile Leu
107 112 117 122

cga gga gtt cgt ctg cac ttc cac aat ctg gtg aag ggt ctg acc gat 495
Arg Gly Val Arg Leu His Phe His Asn Leu Val Lys Gly Leu Thr Asp
123 128 133 138

ctg tca gct tgt aaa gca cag ctg ggg ctg gga cac agc tat tcc cgt 543
Leu Ser Ala Cys Lys Ala Gln Leu Gly Leu Gly His Ser Tyr Ser Arg
139 144 149 154

gcc aaa gtt aag ttt aat gtg aac cgg gtg gac aat atg atc atc cag 591
Ala Lys Val Lys Phe Asn Val Asn Arg Val Asp Asn Met Ile Ile Gln

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tcc att agc ctc ctg gac cag ctg gat aag gac atc aat acc ttc tct				639
Ser Ile Ser Leu Leu Asp Gln Leu Asp Lys Asp Ile Asn Thr Phe Ser				
171	176	181	186	
atg cgt gtc agg gag tgg tac ggg tat cac ttt ccg gag ctg gtg aag				687
Met Arg Val Arg Glu Trp Tyr Gly Tyr His Phe Pro Glu Leu Val Lys				
187	192	197	202	
atc atc aac gac aat gcc aca tac tgc cgt ctt gcc cag ttt att gga				735
Ile Ile Asn Asp Asn Ala Thr Tyr Cys Arg Leu Ala Gln Phe Ile Gly				
203	208	213	218	
aac cga agg gaa ctg aat gag gac aag ctg gag aag ctg gag gag ctg				783
Asn Arg Arg Glu Leu Asn Glu Asp Lys Leu Glu Lys Leu Glu Glu Leu				
219	224	229	234	
aca atg gat ggg gcc aag gct aag gct att ctg gat gcc tca cgg tcc				831
Thr Met Asp Gly Ala Lys Ala Lys Ala Ile Leu Asp Ala Ser Arg Ser				
235	240	245	250	
tcc atg ggc atg gac ata tct gcc att gac ttg ata aac atc gag agc				879
Ser Met Gly Met Asp Ile Ser Ala Ile Asp Leu Ile Asn Ile Glu Ser				
251	256	261	266	
ttc tcc agt cgt gtg gtg tct tta tct gaa tac cgc cag agc cta cac				927
Phe Ser Ser Arg Val Val Ser Leu Ser Glu Tyr Arg Gln Ser Leu His				
267	272	277	282	
act tac ctg cgc tcc aag atg agc caa gta gcc ccc agc ctg tca gcc				975
Thr Tyr Leu Arg Ser Lys Met Ser Gln Val Ala Pro Ser Leu Ser Ala				
283	288	293	298	
cta att ggg gaa gcg gta ggt gca cgt ctc atc gca cat gct ggc agc				1023
Leu Ile Gly Glu Ala Val Gly Ala Arg Leu Ile Ala His Ala Gly Ser				
299	304	309	314	
ctc acc aac ctg gcc aag tat cca gca tcc aca gtg cag atc ctt ggg				1071
Leu Thr Asn Leu Ala Lys Tyr Pro Ala Ser Thr Val Gln Ile Leu Gly				
315	320	325	330	
gct gaa aag gcc ctg ttc aga gcc ctg aag aca agg ggt aac act cca				1119
Ala Glu Lys Ala Leu Phe Arg Ala Leu Lys Thr Arg Gly Asn Thr Pro				
331	336	341	346	
aaa tat gga ctc att ttc cac tcc acc ttc att ggc cga gca gct gcc				1167
Lys Tyr Gly Leu Ile Phe His Ser Thr Phe Ile Gly Arg Ala Ala Ala				
347	352	357	362	
aag aac aaa ggc cgc atc tcc cga tac ctg gca aac aaa tgc agt att				1215
Lys Asn Lys Gly Arg Ile Ser Arg Tyr Leu Ala Asn Lys Cys Ser Ile				
363	368	373	378	
gcc tca cga atc gat tgc ttc tct gag gtg ccc acg agt gta ttc ggg				1263
Ala Ser Arg Ile Asp Cys Phe Ser Glu Val Thr Ser Val Phe Gly				
379	384	389	394	

gag aag ctt cga gaa caa gtt gaa gag cga ctg tcc ttc tat gag act	1311
Glu Lys Leu Arg Glu Gln Val Glu Glu Arg Leu Ser Phe Tyr Glu Thr	
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Gly Glu Ile Pro Arg Lys Asn Leu Asp Val Met Lys Glu Ala Met Val	
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Gln Ala Glu Ala Glu Glu Ala Ala Ala Glu Ile Thr Arg Lys Leu Glu	
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Lys Gln Glu Lys Lys Arg Leu Lys Lys Glu Lys Lys Arg Leu Ala Ala	
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Leu Ala Leu Ala Ser Ser Glu Asn Ser Ser Ser Thr Pro Glu Glu Cys	
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Glu Glu Met Ser Glu Lys Pro Lys Lys Lys Lys Lys Gln Lys Pro Gln	
475 480 485 490	
gag gtt cct cag gag aat gga atg gaa gac cca tct atc tct ttc tcc	1599
Glu Val Pro Gln Glu Asn Gly Met Glu Asp Pro Ser Ile Ser Phe Ser	
491 496 501 506	
aaa ccc aag aaa aag aaa tct ttt tcc aag gag gag ttg atg agt agc	1647
Lys Pro Lys Lys Lys Lys Ser Phe Ser Lys Glu Glu Leu Met Ser Ser	
507 512 517 522	
gat ctt gaa gag acc gct ggc agc acc agt att ccc aag agg aag aag	1695
Asp Leu Glu Glu Thr Ala Gly Ser Thr Ser Ile Pro Lys Arg Lys Lys	
523 528 533 538	
tct aca ccc aag gag gaa aca gtt aat gac cct gag gag gca ggc cac	1743
Ser Thr Pro Lys Glu Glu Thr Val Asn Asp Pro Glu Glu Ala Gly His	
539 544 549 554	
aga agt ggc tcc aag aaa aag agg aaa ttc tcc aaa gag gag ccg gtc	1791
Arg Ser Gly Ser Lys Lys Lys Arg Lys Phe Ser Lys Glu Glu Pro Val	
555 560 565 570	
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Ser Ser Gly Pro Glu Glu Ala Ala Gly Lys Ser Ser Ser Lys Lys Lys	
571 576 581 586	
aaa aag ttc cat aaa gca tcc cag gaa gat tag aatgcaaa tggacattct	1890
Lys Lys Phe His Lys Ala Ser Gln Glu Asp *	
587 592 597	
ctgggaggtg gggcatacca tagcccaagg tgacatttcc caccctgtgc cgtgttcccc	1950
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ctgctcccca ctttcgttga tgtggtagtg gtgatgactg agccaaccac ctaatgtgga      180
aatgagagga cagcaagatt gtgggtatgg aatggggcaa agcaataagg gaaaattagt      240
gtggcagggt tcagtacagc agcctggggt cccatttccc cccatattca aatgctgaca      300
ctctcttctc ctcccaggtc cagcctgtgg tgtccaca      atg ccc cag gcc tct      353
                                   Met Pro Gln Ala Ser
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gag cac cgc ctg ggc cgt acc cga gag cca cct gtt aat atc cag ccc      401
Glu His Arg Leu Gly Arg Thr Arg Glu Pro Pro Val Asn Ile Gln Pro
   6                11                16                21

cga gtg gga tcc aag cta cca ttt gcc ccc agg gcc cgc agc aag gag      449
Arg Val Gly Ser Lys Leu Pro Phe Ala Pro Arg Ala Arg Ser Lys Glu
  22                27                32                37

cgc aga aac cca gcc tct ggg cca aac ccc atg tta cga cct ctg cct      497
Arg Arg Asn Pro Ala Ser Gly Pro Asn Pro Met Leu Arg Pro Leu Pro
  38                43                48                53

ccc cgg cca ggt ctg cct gat gaa cgg ctc aag aaa ctg gag ctg gga      545
Pro Arg Pro Gly Leu Pro Asp Glu Arg Leu Lys Lys Leu Glu Leu Gly
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cgg gga cgg acc tca ggc cct cgt ccc aga ggc ccc ctt cga gca gat      593
Arg Gly Arg Thr Ser Gly Pro Arg Pro Arg Gly Pro Leu Arg Ala Asp
  70                75                80                85

cat ggg gtt ccc ctg cct ggc tca cca ccc cca aca gtg gct ttg cct      641
His Gly Val Pro Leu Pro Gly Ser Pro Pro Pro Thr Val Ala Leu Pro
  86                91                96                101

ctc cca tct cgg acc aac tta gcc cgt tcc aag tct gtg agc agt ggg      689
Leu Pro Ser Arg Thr Asn Leu Ala Arg Ser Lys Ser Val Ser Ser Gly
  102                107                112                117

gac ttg cgt cca atg ggg att gcc ttg gga ggg cac cgt ggc acc gga      737
Asp Leu Arg Pro Met Gly Ile Ala Leu Gly Gly His Arg Gly Thr Gly

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134	139	144	149				
act ttg aga cgt agc	act tct ctc cgc cgc	cta ggg ggc ttt cct	gga	833			
Thr Leu Arg Arg Ser	Thr Ser Leu Arg Arg	Leu Gly Gly Phe Pro	Gly				
150	155	160	165				
ccc cct acc ctg ttc	agc ata cgg aca gag	ccc cct gct tcc cat	ggc	881			
Pro Pro Thr Leu Phe	Ser Ile Arg Thr Glu	Pro Pro Ala Ser His	Gly				
166	171	176	181				
tcc ttc cac atg ata	tcc gcc cgg tcc tct	gag cct ttc tac tct	gat	929			
Ser Phe His Met Ile	Ser Ala Arg Ser Ser	Glu Pro Phe Tyr Ser	Asp				
182	187	192	197				
gac aag atg gct cat	cac aca ctc ctt ctg	ggc tct ggt cat gtt	ggc	977			
Asp Lys Met Ala His	His Thr Leu Leu Leu	Gly Ser Gly His Val	Gly				
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ctt cga aac ctg gga	aac acg tgc ttc ctg	aat gct gtg ctg cag	tgt	1025			
Leu Arg Asn Leu Gly	Asn Thr Cys Phe Leu	Asn Ala Val Leu Gln	Cys				
214	219	224	229				
ctg agc agc act cga	cct ctt cgg gac ttc	tgt ctg aga agg gac	ttc	1073			
Leu Ser Ser Thr Arg	Pro Leu Arg Asp Phe	Cys Leu Arg Arg Asp	Phe				
230	235	240	245				
cgg caa gag gtg cct	gga gga ggc cga gcc	caa gag ctc act gaa	gcc	1121			
Arg Gln Glu Val Pro	Gly Gly Gly Arg Ala	Gln Glu Leu Thr Glu	Ala				
246	251	256	261				
ttt gca gat gtg att	ggt gcc ctc tgg cac	cct gac tcc tgc gaa	gct	1169			
Phe Ala Asp Val Ile	Gly Ala Leu Trp His	Pro Asp Ser Cys Glu	Ala				
262	267	272	277				
gtg aat cct act cga	ttc cga gct gtc ttc	cag aaa tat gtt ccc	ttc	1217			
Val Asn Pro Thr Arg	Phe Arg Ala Val Phe	Gln Lys Tyr Val Pro	Ser				
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Met Glu Arg Leu His	Leu Glu Ile Asn Arg	Arg Gly Arg Arg Ala	Pro				
310	315	320	325				
ccg ata ctt gcc aat	ggt cca gtt ccc tct	cca ccc cgc cga gga	ggg	1361			
Pro Ile Leu Ala Asn	Gly Pro Val Pro Ser	Pro Pro Arg Arg Gly	Gly				
326	331	336	341				
gct ctg cta gaa gaa	cct gag tta agt gat	gat gac cga gcc aac	cta	1409			
Ala Leu Leu Glu Glu	Pro Glu Leu Ser Asp	Asp Asp Arg Ala Asn	Leu				
342	347	352	357				

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Met Trp Lys Arg Tyr Leu Glu Arg Glu Asp Ser Lys Ile Val Asp Leu	
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374 379 384 389	
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Arg Ser Thr Thr Phe Glu Val Phe Cys Asp Leu Ser Leu Pro Ile Pro	
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Lys Lys Gly Phe Ala Gly Gly Lys Val Ser Leu Arg Asp Cys Phe Asn	
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Arg Phe Pro Arg Ile Leu Val Leu His Leu Asn Arg Phe Ser Ala Ser	
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486 491 496 501	
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Tyr Gln Leu Tyr Ala Leu Cys Asn His Ser Gly Ser Val His Tyr Gly	
502 507 512 517	
cac tac aca gcc ctg tgc cgg tgc cag act ggt tgg cat gtc tac aat	1937
His Tyr Thr Ala Leu Cys Arg Cys Gln Thr Gly Trp His Val Tyr Asn	
518 523 528 533	
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Asp Ser Arg Val Ser Pro Val Ser Glu Asn Gln Val Ala Ser Ser Glu	
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Gly Tyr Val Leu Phe Tyr Gln Leu Met Gln Glu Pro Pro Arg Cys Leu	
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caggtctcct	agatcagaaa atgaaaagcc gggTctcagc tccagatctg tatccatgat 180

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ttcgaagatg tagc atg cct tct gtc att tgt gaa cat acc aaa caa ttc	530
Met Pro Ser Val Ile Cys Glu His Thr Lys Gln Phe	
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caa aca ata tca gaa gag agc aat caa ggt agc tta tta act gtg cca	578
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Glu Arg Asp Leu Ser Asn Val Ser Asn Ile His Ser Ser Phe Ala Thr	
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Glu Met Pro Val Asp Arg Leu Glu Thr Leu Ser Thr Arg Asp Phe Ile	
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Cys Pro Asn Ser Asn Ile Pro Asp Gln Glu Ser Ser Leu Gln Ser Phe	
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Ser Phe Met Pro Pro Gln Gln Pro Cys Ser Phe Pro Ser Gln Ser Leu	
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Lys Glu Leu Phe Arg Gln Gln Glu Val Val Arg Met Lys Leu Arg Leu	
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Gln His Ser Ile Glu Arg Glu Lys Leu Ile Val Ser Asn Glu Gln Glu	
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Gln Glu Ile Thr Asp Asn Leu Thr Lys Lys Glu Ile Gln Ile Glu Lys	
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Ile His Leu Asp Thr Ser Ser Phe Val Glu Glu Leu Pro Gly Glu Lys	
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gac ctg atc gcc cat ctg gag caa gga aaa aaa cct ttg act atg aag      427
Asp Leu Ile Ala His Leu Glu Gln Gly Lys Lys Pro Leu Thr Met Lys
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aga cat gag atg gta gcc aac ccc tca ggg cca gtt ata tgt tct cat      475
Arg His Glu Met Val Ala Asn Pro Ser Gly Pro Val Ile Cys Ser His
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Phe Ala Gln Asp Leu Trp Pro Glu Gln Asn Ile Lys Asp Ser Phe Gln
   83              88              93              98

aaa gtg ata ctg aga aga tat gaa aaa cgt gga cat gga aat tta cag      571
Lys Val Ile Leu Arg Arg Tyr Glu Lys Arg Gly His Gly Asn Leu Gln
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tta ata aaa agg tgt gaa agt gta gat gag tgt aag gtg cac aca gga      619
Leu Ile Lys Arg Cys Glu Ser Val Asp Glu Cys Lys Val His Thr Gly
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Gly Tyr Asn Gly Leu Asn Gln Cys Ser Thr Thr Thr Gln Ser Lys Val
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Lys Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Glu Glu Cys Gly Lys	
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Ala	Phe	His	Leu	Ser	Thr	His	Leu	Thr	Thr	His	Lys	Ile	Leu	His	Thr	
547					552					557					562	
gga	gag	aaa	cct	tat	aga	tgt	aga	gaa	tgt	ggc	aaa	gct	ttt	aac	cat	1963
Gly	Glu	Lys	Pro	Tyr	Arg	Cys	Arg	Glu	Cys	Gly	Lys	Ala	Phe	Asn	His	
563					568					573					578	
tct	gca	acc	ctt	tct	tca	cat	aag	aaa	atc	cat	tct	gga	gag	aaa	cca	2011
Ser	Ala	Thr	Leu	Ser	Ser	His	Lys	Lys	Ile	His	Ser	Gly	Glu	Lys	Pro	
579					584					589					594	
tac	gag	tgt	gat	aaa	tgt	ggc	aaa	gcc	ttt	att	tca	ccc	tca	agc	ctt	2059
Tyr	Glu	Cys	Asp	Lys	Cys	Gly	Lys	Ala	Phe	Ile	Ser	Pro	Ser	Ser	Leu	

595	600	605	610	
agt aga cat gag ata att cat act ggg gag aaa ccc tag aagtgtgaag				2108
Ser Arg His Glu Ile Ile His Thr Gly Glu Lys Pro *				
611	616	621		
aatgtggcaa agctctcaag tggtcctcac accttactat acactgagag ttctgaactt				2168
actctgtaac catcccaaac tcctctcagg cacagtctgg cagaggtcct gccatttctg				2228
agacctggag gaagtggccc atttacagcc atgtaggcag gcctgcagac cttgggcttt				2288
actagggtag ctgaagtggg tcaatgactc agtttcaggt tactgagcca cagcttaagg				2348
tcagttctga ctatatagaa agcacacagt taacctgagg acatgctctc tgggtactcac				2408
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<220>
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ttagaggagt atagttacat aaaagaaggc aaaacgatgt ataaatgaaa gaaattgaga	180
tgggtgcacga tgcacagttg aagtgaactt gcgggggttt tcagtatcta cgattcatag	240
atctggaatt cgcggccgcg tcgacggcag cgggacgcac catttcagtt gtgttcttgg	300
ttcatttcgt gtctcggcg atg ttt cct aga gtc tcg acg ttc cta cct ctt	352
Met Phe Pro Arg Val Ser Thr Phe Leu Pro Leu	
1 5	
cgc ccc ctt tcc cgc cac cct ttg tcc tct gga agc ccg gag aca tca	400
Arg Pro Leu Ser Arg His Pro Leu Ser Ser Gly Ser Pro Glu Thr Ser	
12 17 22 27	
gcg gct gcg att atg cta ctc act gtt cgg cac gga aca gtc agg tac	448
Ala Ala Ala Ile Met Leu Leu Thr Val Arg His Gly Thr Val Arg Tyr	
28 33 38 43	
cgc agt tca gcg ctg ttg gcc cgg aca aaa aat aac atc caa aga tat	496
Arg Ser Ser Ala Leu Leu Ala Arg Thr Lys Asn Asn Ile Gln Arg Tyr	

44	49	54	59	
ttt ggc act aac agt gtg atc tgt agc aag aaa gat aag cag tct gtt				544
Phe Gly Thr Asn Ser Val Ile Cys Ser Lys Lys Asp Lys Gln Ser Val				
60	65	70	75	
cga act gag gag act tcc aag gag act tca gag agc caa gac agt gaa				592
Arg Thr Glu Glu Thr Ser Lys Glu Thr Ser Glu Ser Gln Asp Ser Glu				
76	81	86	91	
aag gaa aat acg aaa aaa gac ttg tta ggc att att aag ggc atg aaa				640
Lys Glu Asn Thr Lys Lys Asp Leu Leu Gly Ile Ile Lys Gly Met Lys				
92	97	102	107	
gtt gaa tta agc aca gta aat gta cga aca aca aag ccc ccc aaa aga				688
Val Glu Leu Ser Thr Val Asn Val Arg Thr Thr Lys Pro Pro Lys Arg				
108	113	118	123	
aga cca ctt aaa agt ttg gaa gct aca ctt ggc agg ctt cga aga gct				736
Arg Pro Leu Lys Ser Leu Glu Ala Thr Leu Gly Arg Leu Arg Arg Ala				
124	129	134	139	
aca gaa tat gct cca aag aag aga att gag ccc ctg agt cct gag ttg				784
Thr Glu Tyr Ala Pro Lys Lys Arg Ile Glu Pro Leu Ser Pro Glu Leu				
140	145	150	155	
gtg gca gct gca tct gct gtg gca gat tct ctc cct ttt gat aag caa				832
Val Ala Ala Ala Ser Ala Val Ala Asp Ser Leu Pro Phe Asp Lys Gln				
156	161	166	171	
aca acc aag tca gag ctg ctg agc cag ctc cag cag cat gag gaa gag				880
Thr Thr Lys Ser Glu Leu Leu Ser Gln Leu Gln Gln His Glu Glu Glu				
172	177	182	187	
tca agg gca cag aga gat gca aag cga cct aaa att agt ttc agt aac				928
Ser Arg Ala Gln Arg Asp Ala Lys Arg Pro Lys Ile Ser Phe Ser Asn				
188	193	198	203	
ata ata tca gat atg aaa gtt gcc aga tct gct aca gct aga gtt cgt				976
Ile Ile Ser Asp Met Lys Val Ala Arg Ser Ala Thr Ala Arg Val Arg				
204	209	214	219	
tca aga cca gag ctt cgg att cag ttt gat gaa ggc tat gac aat tat				1024
Ser Arg Pro Glu Leu Arg Ile Gln Phe Asp Glu Gly Tyr Asp Asn Tyr				
220	225	230	235	
cct ggc cag gag aag acg gat gat ctt aaa aaa agg aaa aat ata ttc				1072
Pro Gly Gln Glu Lys Thr Asp Asp Leu Lys Lys Arg Lys Asn Ile Phe				
236	241	246	251	
aca ggg aaa aga ctt aat att ttt gac atg atg gca gtt act aaa gaa				1120
Thr Gly Lys Arg Leu Asn Ile Phe Asp Met Met Ala Val Thr Lys Glu				
252	257	262	267	
gca cct gaa aca gac aca tca cct tca ctt tgg gat gtg gaa ttt gct				1168
Ala Pro Glu Thr Asp Thr Ser Pro Ser Leu Trp Asp Val Glu Phe Ala				
268	273	278	283	

aag cag tta gcc aca gta aat gaa caa ccc ctt cag aat gga ttt gaa	1216
Lys Gln Leu Ala Thr Val Asn Glu Gln Pro Leu Gln Asn Gly Phe Glu	
284 289 294 299	
gag ctg atc cag tgg aca aaa gag ggg aaa cta tgg gag ttc cca att	1264
Glu Leu Ile Gln Trp Thr Lys Glu Gly Lys Leu Trp Glu Phe Pro Ile	
300 305 310 315	
aac aat gaa gca ggt ttt gat gat gat ggt tca gaa ttt cat gaa cat	1312
Asn Asn Glu Ala Gly Phe Asp Asp Asp Gly Ser Glu Phe His Glu His	
316 321 326 331	
ata ttt ctg gag aaa cac ctg gag agc ttt cca aaa caa gga cca att	1360
Ile Phe Leu Glu Lys His Leu Glu Ser Phe Pro Lys Gln Gly Pro Ile	
332 337 342 347	
cgc cac ttc atg gag ctg gtg act tgt ggc ctt tcc aaa aac cca tat	1408
Arg His Phe Met Glu Leu Val Thr Cys Gly Leu Ser Lys Asn Pro Tyr	
348 353 358 363	
ctt agt gtt aaa cag aag gtt gaa cac ata gag tgg ttt aga aat tat	1456
Leu Ser Val Lys Gln Lys Val Glu His Ile Glu Trp Phe Arg Asn Tyr	
364 369 374 379	
ttt aat gaa aaa aag gat att cta aaa gaa agt aac ata cag ttc aat	1504
Phe Asn Glu Lys Lys Asp Ile Leu Lys Glu Ser Asn Ile Gln Phe Asn	
380 385 390 395	
taa gacc atggaaattt ttattttcaaa caattagaga tggatattac aactaaataa	1561
*	
396	
aataatttta ctagagtttg tatatgttat gttgattatt acatttgatt tggctggtat	1621
aaatgttaca ttgttttcaa aaatatgatg gtaactgaaa aatattcttg catggagaaa	1681
aatcatcagt attcataggt tcaaaagaat atctgggaat tagtaataca tttaagacaa	1741
caactcctaa ccttttttctt ttactctggt gaccatactt ctttgaaata caatacaatt	1801
actggatgat atcacagtac tatgttataa gagttgagat gatttataga cagatatata	1861
tgtacatacg tttatttggt tacattttata catatatattt aactaaatt aactaccctc	1921
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<210> 278
 <211> 1951
 <212> DNA
 <213> Homo sapiens

<220>
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<222> (320) .. (1480)

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tggtgcacga tgcacagttg aagtgaactt gcgggggtttt tcagtatcta cgattcatag	240
atctggaatt cgcgggccgcg tcgacggcag cgggacgcac catttcagtt gtgttcttgg	300
ttcatttcgt gtctcggcg atg ttt cct aga gtc tcg acg ttc cta cct ctt	352
Met Phe Pro Arg Val Ser Thr Phe Leu Pro Leu	
1 5	
cgc ccc ctt tcc cgc cac cct ttg tcc tct gga agc ccg gag aca tca	400
Arg Pro Leu Ser Arg His Pro Leu Ser Ser Gly Ser Pro Glu Thr Ser	
12 17 22 27	
gcg gct gcg att atg cta ctc act gtt cgg cac gga aca gtc cgg aca	448
Ala Ala Ala Ile Met Leu Leu Thr Val Arg His Gly Thr Val Arg Thr	
28 33 38 43	
aaa aat aac atc caa aga tat ttt ggc act aac agt gtg atc tgt agc	496
Lys Asn Asn Ile Gln Arg Tyr Phe Gly Thr Asn Ser Val Ile Cys Ser	
44 49 54 59	
aag aaa gat aag cag tct gtt cga act gag gag act tcc aag gag act	544
Lys Lys Asp Lys Gln Ser Val Arg Thr Glu Glu Thr Ser Lys Glu Thr	
60 65 70 75	
tca gag agc caa gac agt gaa aag gaa aat acg aaa aaa gac ttg tta	592
Ser Glu Ser Gln Asp Ser Glu Lys Glu Asn Thr Lys Lys Asp Leu Leu	
76 81 86 91	
ggc att att aag ggc atg aaa gtt gaa tta agc aca gta aat gta cga	640
Gly Ile Ile Lys Gly Met Lys Val Glu Leu Ser Thr Val Asn Val Arg	
92 97 102 107	
aca aca aag ccc ccc aaa aga aga cca ctt aaa agt ttg gaa gct aca	688
Thr Thr Lys Pro Pro Lys Arg Arg Pro Leu Lys Ser Leu Glu Ala Thr	
108 113 118 123	
ctt ggc agg ctt cga aga gct aca gaa tat gct cca aag aag aga att	736
Leu Gly Arg Leu Arg Arg Ala Thr Glu Tyr Ala Pro Lys Lys Arg Ile	
124 129 134 139	
gag ccc ctg agt cct gag ttg gtg gca gct gca tct gct gtg gca gat	784
Glu Pro Leu Ser Pro Glu Leu Val Ala Ala Ala Ser Ala Val Ala Asp	
140 145 150 155	
tct ctc cct ttt gat aag caa aca acc aag tca gag ctg ctg agc cag	832
Ser Leu Pro Phe Asp Lys Gln Thr Thr Lys Ser Glu Leu Leu Ser Gln	
156 161 166 171	

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Leu	Gln	Gln	His	Glu	Glu	Glu	Ser	Arg	Ala	Gln	Arg	Asp	Ala	Lys	Arg	
172					177					182					187	
cct	aaa	att	agt	ttc	agt	aac	ata	ata	tca	gat	atg	aaa	gtt	gcc	aga	928
Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met	Lys	Val	Ala	Arg	
188					193					198					203	
tct	gct	aca	gct	aga	gtt	cgt	tca	aga	cca	gag	ctt	cgg	att	cag	ttt	976
Ser	Ala	Thr	Ala	Arg	Val	Arg	Ser	Arg	Pro	Glu	Leu	Arg	Ile	Gln	Phe	
204					209					214					219	
gat	gaa	ggc	tat	gac	aat	tat	cct	ggc	cag	gag	aag	acg	gat	gat	ctt	1024
Asp	Glu	Gly	Tyr	Asp	Asn	Tyr	Pro	Gly	Gln	Glu	Lys	Thr	Asp	Asp	Leu	
220					225					230					235	
aaa	aaa	agg	aaa	aat	ata	ttc	aca	ggg	aaa	aga	ctt	aat	att	ttt	gac	1072
Lys	Lys	Arg	Lys	Asn	Ile	Phe	Thr	Gly	Lys	Arg	Leu	Asn	Ile	Phe	Asp	
236					241					246					251	
atg	atg	gca	gtt	act	aaa	gaa	gca	cct	gaa	aca	gac	aca	tca	cct	tca	1120
Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp	Thr	Ser	Pro	Ser	
252					257					262					267	
ctt	tgg	gat	gtg	gaa	ttt	gct	aag	cag	tta	gcc	aca	gta	aat	gaa	caa	1168
Leu	Trp	Asp	Val	Glu	Phe	Ala	Lys	Gln	Leu	Ala	Thr	Val	Asn	Glu	Gln	
268					273					278					283	
ccc	ctt	cag	aat	gga	ttt	gaa	gag	ctg	atc	cag	tgg	aca	aaa	gag	ggg	1216
Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp	Thr	Lys	Glu	Gly	
284					289					294					299	
aaa	cta	tgg	gag	ttc	cca	att	aac	aat	gaa	gca	ggt	ttt	gat	gat	gat	1264
Lys	Leu	Trp	Glu	Phe	Pro	Ile	Asn	Asn	Glu	Ala	Gly	Phe	Asp	Asp	Asp	
300					305					310					315	
ggt	tca	gaa	ttt	cat	gaa	cat	ata	ttt	ctg	gag	aaa	cac	ctg	gag	agc	1312
Gly	Ser	Glu	Phe	His	Glu	His	Ile	Phe	Leu	Glu	Lys	His	Leu	Glu	Ser	
316					321					326					331	
ttt	cca	aaa	caa	gga	cca	att	cgc	cac	ttc	atg	gag	ctg	gtg	act	tgt	1360
Phe	Pro	Lys	Gln	Gly	Pro	Ile	Arg	His	Phe	Met	Glu	Leu	Val	Thr	Cys	
332					337					342					347	
ggc	ctt	tcc	aaa	aac	cca	tat	ctt	agt	gtt	aaa	cag	aag	gtt	gaa	cac	1408
Gly	Leu	Ser	Lys	Asn	Pro	Tyr	Leu	Ser	Val	Lys	Gln	Lys	Val	Glu	His	
348					353					358					363	
ata	gag	tgg	ttt	aga	aat	tat	ttt	aat	gaa	aaa	aag	gat	att	cta	aaa	1456
Ile	Glu	Trp	Phe	Arg	Asn	Tyr	Phe	Asn	Glu	Lys	Lys	Asp	Ile	Leu	Lys	
364					369					374					379	
gaa	agt	aac	ata	cag	ttc	aat	taa	gaccatggaa	atgttttattt	caaacaatta						1510
Glu	Ser	Asn	Ile	Gln	Phe	Asn	*									
380					385											
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gaaaaatatt cttgcatgga gaaaaatcat cagtattcat aggttcaaaa gaatatctgg 1690
gaattagtaa tacatttaag acaacaactc ctaacctttt tcttttcact cggtgaccat 1750
acttctttga aatacaatac aattactgga tgatatcaca gtactatggtt ataagagttg 1810
agatgattta tagacagata tatatgtaca tacgtttatt tgtttacatt tatacatata 1870
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accacgtgcg gccggaaggg aagtaacgtc agcctgagaa ctgagtagct gtactgtgtg 180
gcgccttatt ctaggcactt gttgggcaga atg tca cac ctg ccg atg aaa 231
Met Ser His Leu Pro Met Lys
1 5
ctc ctg cgt aag aag atc gag aag cgg aac ctc aaa ttg cgg cag cgg 279
Leu Leu Arg Lys Lys Ile Glu Lys Arg Asn Leu Lys Leu Arg Gln Arg
8 13 18 23
aac cta aag ttt cag ggg gcc tca aat ctg acc cta tcg gaa act caa 327
Asn Leu Lys Phe Gln Gly Ala Ser Asn Leu Thr Leu Ser Glu Thr Gln
24 29 34 39
aat gga gat gta tct gaa gaa aca atg gga agt aga aag gtt aaa aaa 375
Asn Gly Asp Val Ser Glu Glu Thr Met Gly Ser Arg Lys Val Lys Lys
40 45 50 55
tca aaa caa aag ccc atg aat gtg ggc tta tca gaa act caa aat gga 423
Ser Lys Gln Lys Pro Met Asn Val Gly Leu Ser Glu Thr Gln Asn Gly
56 61 66 71
ggc atg tct caa gaa gca gtg gga aat ata aaa gtt aca aag tct ccc 471
Gly Met Ser Gln Glu Ala Val Gly Asn Ile Lys Val Thr Lys Ser Pro
72 77 82 87

cag aaa tcc act gta tta agc aat gga gaa gca gca atg cag tct tcc	519
Gln Lys Ser Thr Val Leu Ser Asn Gly Glu Ala Ala Met Gln Ser Ser	
88 93 98 103	
aat tca gaa tca aaa aag aaa aag aag aaa aag aga aaa atg gtg aat	567
Asn Ser Glu Ser Lys Lys Lys Lys Lys Lys Arg Lys Met Val Asn	
104 109 114 119	
gat gct gag cct gat acg aaa aaa gca aaa act gaa aac aaa ggg aaa	615
Asp Ala Glu Pro Asp Thr Lys Lys Ala Lys Thr Glu Asn Lys Gly Lys	
120 125 130 135	
tct gaa gaa gaa agt gcc gag act act aaa gaa aca gaa aat aat gtg	663
Ser Glu Glu Glu Ser Ala Glu Thr Thr Lys Glu Thr Glu Asn Asn Val	
136 141 146 151	
gag aag cca gat aat gat gaa gat gag agt gag gtg ccc agt ctg ccc	711
Glu Lys Pro Asp Asn Asp Glu Asp Glu Ser Glu Val Pro Ser Leu Pro	
152 157 162 167	
ctg gga ctg aca gga gct ttt gag gat act tcg ttt gct tct cta tgt	759
Leu Gly Leu Thr Gly Ala Phe Glu Asp Thr Ser Phe Ala Ser Leu Cys	
168 173 178 183	
aat ctt gtc aat gaa aac act ctg aag gca ata aaa gaa atg ggt ttt	807
Asn Leu Val Asn Glu Asn Thr Leu Lys Ala Ile Lys Glu Met Gly Phe	
184 189 194 199	
aca aac atg act gaa att cag cat aaa agt atc aga cca ctt ctg gaa	855
Thr Asn Met Thr Glu Ile Gln His Lys Ser Ile Arg Pro Leu Leu Glu	
200 205 210 215	
ggc agg gat ctt cta gca gct gca aaa aca ggc agt ggt aaa acc ctg	903
Gly Arg Asp Leu Leu Ala Ala Ala Lys Thr Gly Ser Gly Lys Thr Leu	
216 221 226 231	
gct ttt ctc atc cct gca gtt gaa ctc att gtt aag tta agg ttc atg	951
Ala Phe Leu Ile Pro Ala Val Glu Leu Ile Val Lys Leu Arg Phe Met	
232 237 242 247	
ccc agg aat gga aca gga gtc ctt att ctc tca cct act aga gaa cta	999
Pro Arg Asn Gly Thr Gly Val Leu Ile Leu Ser Pro Thr Arg Glu Leu	
248 253 258 263	
gcc atg caa acc ttt ggt gtt ctt aag gag ctg atg act cac cac gtg	1047
Ala Met Gln Thr Phe Gly Val Leu Lys Glu Leu Met Thr His His Val	
264 269 274 279	
cat acc tat ggc ttg ata atg ggt ggc agt aac aga tct gct gaa gca	1095
His Thr Tyr Gly Leu Ile Met Gly Gly Ser Asn Arg Ser Ala Glu Ala	
280 285 290 295	
cag aaa ctt ggt aat ggg atc aac atc att gtg gcc aca cca ggc cgt	1143
Gln Lys Leu Gly Asn Gly Ile Asn Ile Ile Val Ala Thr Pro Gly Arg	
296 301 306 311	

ctg ctg gac cat atg cag aat acc cca gga ttt atg tat aaa aac ctg	1191
Leu Leu Asp His Met Gln Asn Thr Pro Gly Phe Met Tyr Lys Asn Leu	
312 317 322 327	
cag tgt ctg gtt att gat gaa gct gat cgt atc ttg gat gtg ggg ttt	1239
Gln Cys Leu Val Ile Asp Glu Ala Asp Arg Ile Leu Asp Val Gly Phe	
328 333 338 343	
gaa gag gaa tta aag caa att att aaa ctt ttg cca aca cgt aga cag	1287
Glu Glu Glu Leu Lys Gln Ile Ile Lys Leu Leu Pro Thr Arg Arg Gln	
344 349 354 359	
act atg ctc ttt tct gcc acc caa act cga aaa gtt gaa gac ctg gca	1335
Thr Met Leu Phe Ser Ala Thr Gln Thr Arg Lys Val Glu Asp Leu Ala	
360 365 370 375	
agg att tct ctg aaa aag gag cca ttg tat gtt ggc gtt gat gat gat	1383
Arg Ile Ser Leu Lys Lys Glu Pro Leu Tyr Val Gly Val Asp Asp Asp	
376 381 386 391	
aaa gcg aat gca aca gtg gat ggt ctt gaa cag gga tat gtt gtt tgt	1431
Lys Ala Asn Ala Thr Val Asp Gly Leu Glu Gln Gly Tyr Val Val Cys	
392 397 402 407	
cct tct gaa aag aga ttc ctt ctg ctc ttt aca ttc ctt aag aag aac	1479
Pro Ser Glu Lys Arg Phe Leu Leu Leu Phe Thr Phe Leu Lys Lys Asn	
408 413 418 423	
cga aag aag aag ctt atg gtc ttc ttt tca tct tgt atg tct gtg aaa	1527
Arg Lys Lys Lys Leu Met Val Phe Phe Ser Ser Cys Met Ser Val Lys	
424 429 434 439	
tac cac tat gag ttg ctg aac tac att gat ttg ccc gtc ttg gcc att	1575
Tyr His Tyr Glu Leu Leu Asn Tyr Ile Asp Leu Pro Val Leu Ala Ile	
440 445 450 455	
cat gga aag caa aag caa aat aag cgt aca acc aca ttc ttc cag ttc	1623
His Gly Lys Gln Lys Gln Asn Lys Arg Thr Thr Thr Phe Phe Gln Phe	
456 461 466 471	
tgc aat gca gat tgc gga aca cta ttg tgt acg gat gtg gca gcg aga	1671
Cys Asn Ala Asp Ser Gly Thr Leu Leu Cys Thr Asp Val Ala Ala Arg	
472 477 482 487	
gga cta gac att cct gaa gtc gac tgg att gtt cag tat gac cct ccg	1719
Gly Leu Asp Ile Pro Glu Val Asp Trp Ile Val Gln Tyr Asp Pro Pro	
488 493 498 503	
gat gac cct aag gaa tat att cat cgt gtg ggt aga aca gcc aga ggc	1767
Asp Asp Pro Lys Glu Tyr Ile His Arg Val Gly Arg Thr Ala Arg Gly	
504 509 514 519	
cta aat ggg aga ggg cat gcc ttg ctc att ttg cgc cca gaa gaa ttg	1815
Leu Asn Gly Arg Gly His Ala Leu Leu Ile Leu Arg Pro Glu Glu Leu	
520 525 530 535	
ggg ttt ctt cgt tac ttg aaa caa tcc aag gtt cca tta agt gaa ttt	1863

Gly Phe Leu Arg Tyr Leu Lys Gln Ser Lys Val Pro Leu Ser Glu Phe	
536 541 546 551	
gac ttt tcc tgg tct aaa att tct gac att cag tct cag ctt gag aaa	1911
Asp Phe Ser Trp Ser Lys Ile Ser Asp Ile Gln Ser Gln Leu Glu Lys	
552 557 562 567	
ttg att gaa aag aat tac ttt ctt cat aag tca gcc cag gaa gca tat	1959
Leu Ile Glu Lys Asn Tyr Phe Leu His Lys Ser Ala Gln Glu Ala Tyr	
568 573 578 583	
aag tca tac ata cga gcc tat gat tcc cat tct ctg aaa cag atc ttt	2007
Lys Ser Tyr Ile Arg Ala Tyr Asp Ser His Ser Leu Lys Gln Ile Phe	
584 589 594 599	
aat gtt aat aac cta aat ttg cct cag gtt gct ctg tca ttt ggt ttc	2055
Asn Val Asn Asn Leu Asn Leu Pro Gln Val Ala Leu Ser Phe Gly Phe	
600 605 610 615	
aag gtg cct ccc ttc gtt gat ctg aac gtc aac agt aat gaa ggc aag	2103
Lys Val Pro Pro Phe Val Asp Leu Asn Val Asn Ser Asn Glu Gly Lys	
616 621 626 631	
cag aaa aag cga gga ggt ggt ggt gga ttt ggc tac cag aaa acc aag	2151
Gln Lys Lys Arg Gly Gly Gly Gly Phe Gly Tyr Gln Lys Thr Lys	
632 637 642 647	
aaa gtt gag aaa tcc aaa atc ttt aaa cac att agc aag aaa tca tct	2199
Lys Val Glu Lys Ser Lys Ile Phe Lys His Ile Ser Lys Lys Ser Ser	
648 653 658 663	
gac agc agg cag ttc tct cac tga acacatgcct tcctttcatc ttgaataact	2253
Asp Ser Arg Gln Phe Ser His *	
664 669	
ttgtcctaaa atgaattttt tttccccttg atttaacagg atttttgtag actttagaat	2313
ttggacttac ctaacaagag tataaattga cttgggttgc aagcactgag cactgttact	2373
tctatcacgt ctctctttta tttctgggat ataaaacagg ctttaagttt cttgggttgc	2433
caagggcaga gcaaggaata tctggtgttt cttgtgatga taatatttta attttaata	2493
tccctccctc atacaagtgt atgttaccat tttaatatataa ttctttttgt atctttcctt	2553
cttggtttgt gaagattttt gtggcatgga ttgctgtgct cactgctgta aaaggtgacc	2613
tagtgactg ggcagctggt ggtggtgcag aaaagagtct caggttattt tagatttgtt	2673
taattcaagg tggtttggat ttggttaagcc tttgcactct gtagagtact tagaagacaa	2733
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agcttctttc tgagaaaaaa atacctcttc caggccctga aacaaaaaat acatttgctg	2853
tgaagattga aaatgaacaa agttagaaaa aaaaacagca aaatcagtga tttagtcaat	2913

gagtttttcg ttgtaggagc acttgatttc tagtgtgttt tgtacagtat ataactacaa 2973
 gatagtacat tttgtagcag ttcaaagcca aagttgctag catcattttg ctgttgtgcc 3033
 agttaatcat aggatcccat taaataagtg tgctaacatc gaatatagag aaaactggta 3093
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 ttgggttcct aattcctggt gtttaataat tctctccacg atcatgtttt tctgattttt 3273
 tttttcagaa ataatgtttt ttaaaagaca aaaacaaagg gaagaatatt taattactga 3333
 gcagaagtaa atactgttgg tattttgtac ataatctaata ttttatatgc atgttcatgc 3393
 tttttaattt ttttatcaaa aattaagtca tctacctact acttgtaacc agcttgtttc 3453
 ataacatggt attttcctgt gtcattaaat aattacttca aaaaaaaaaa a 3504

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 cagtttacat atattcttga taacctctcc aacttt atg tct cac cac ccc cac 174
 Met Ser His His Pro His
 1
 tca ctt cgt aat tcg tgc ctt atc aga atg gac ctg tta tac tgg cag 222
 Ser Leu Arg Asn Ser Cys Leu Ile Arg Met Asp Leu Leu Tyr Trp Gln
 7 12 17 22
 ttc acc ata tat acc att aca ttt tgt ttc tcc cat ctc tca ggt aga 270
 Phe Thr Ile Tyr Thr Ile Thr Phe Cys Phe Ser His Leu Ser Gly Arg
 23 28 33 38
 ctt aca ctt tcg gcc cag cac atc agt cat cgc cct tgc ttg ctt tcc 318
 Leu Thr Leu Ser Ala Gln His Ile Ser His Arg Pro Cys Leu Leu Ser
 39 44 49 54
 tat tca ctc ctg ttc tgg aag gtg cac cac ctt ttc ttg gaa ggc ttc 366
 Tyr Ser Leu Leu Phe Trp Lys Val His His Leu Phe Leu Glu Gly Phe
 55 60 65 70

cct tgc tct ccc agg cta gat gag atg tcc ttc cat cag ttc cca cag	414
Pro Cys Ser Pro Arg Leu Asp Glu Met Ser Phe His Gln Phe Pro Gln	
71 76 81 86	
cac cct gtg cat gta tct gtt gtg cac tta cca ata gta tac aag gga	462
His Pro Val His Val Ser Val Val His Leu Pro Ile Val Tyr Lys Gly	
87 92 97 102	
tct atg acc caa gtc tct ccc cac tag cttgt aagctcctca cagacaggaa	514
Ser Met Thr Gln Val Ser Pro His *	
103 108	
ccatgttttg tctttgtact ccagtgccta gtatataaga gatactcaat aaataaatat	574
ttgtcaaadc aactaattga ttccttgtga cctaattcta gagaatggga agaaggcctg	634
ttattttgtt gtcctttatg gttcttttagg aaagctctcc aagcttggca tttgtcaggg	694
tgggaggaaa actggtgaag tattaagact ggacacatgg ctgctaattc atcagcttat	754
cattgaaaaa gtccatagcc aaaacctgac tgtgcactta ctataggacc ctgacctgcc	814
tgggtctccc tgtctctcca gccagtatat ttaaaggtaa tgagataatg atgagtgttt	874
tgaaaaatgt ttagtggtca aatagaaacc attcgtgtcc cttcactctc tgaacatagt	934
ctgcaaatct ctccctctct ggtatgtttc tgttttgtgg attagactgc taaataagcg	994
aagagttaat tttgaagttc aggtcaacaa attcctgttt ggagacgggc tgttcctgaa	1054
taccaggttg ttatctgtct attacagccc cttcacttct gggctcctgg ccctttgcga	1114
agtacttcag aaagcctaga gagaagagag ggccctcaaa tcccattcca gccctaaat	1174
gaaagtggca tcacaaggag aaaagtggag gtagaaatgt accatggggg acgttgcccc	1234
attgcctttc tccccctgac tactgggctt cctctatcag ctttaacgct ggaagtagct	1294
gagtctccag tcaactgggtg ccttcccca gtgagctcag cagcatgtgc taataggtgc	1354
caatactgtg ctggtccag tgggattcct ctctgcaaag ctgctggctt agcttgactg	1414
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attatgtcat atgggctgac tgggttaggt ttggtaggcc tcaactgctct ccagaggcta	1594
gtgttcctat cccaggatgg ctgttgggat taggagtgga atgaggaata gtttaggacc	1654
acaagagatt tggcctcctt ggaacatgta ggaaggcctc aaggatgtaa ttctagccca	1714
gggaagaaaa tccttttcag cagacgcttc ccttcccttc ccctagggaa tgtgtcccta	1774
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cttaatgttg ttcctatgg	1853

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (37)..(963)

<400> 281

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Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser		
7 12 17 22		
gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa		150
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys		
23 28 33 38		
ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta		198
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu		
39 44 49 54		
ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga		246
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg		
55 60 65 70		
cag tcg gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac		294
Gln Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp		
71 76 81 86		
cca aag gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg		342
Pro Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val		
87 92 97 102		
gcc tcc ttt tct gaa aga gtt cgg aac atg tcg cct gat gaa atc aag		390
Ala Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys		
103 108 113 118		
atc ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag		438
Ile Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys		
119 124 129 134		
atc cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac		486
Ile Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn		
135 140 145 150		
tac att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag		534
Tyr Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu		
151 156 161 166		

aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca	582
Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro	
167 172 177 182	
aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag	630
Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu	
183 188 193 198	
gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc	678
Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala	
199 204 209 214	
aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc aaa aaa ggc	726
Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly	
215 220 225 230	
acc acg acc aac gcc acg tcc acc acc act acc act gcc agc aca gct	774
Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala	
231 236 241 246	
gtt gca gat gct cag aag aga aag agc aag tgg gat tcg gct atc cca	822
Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro	
247 252 257 262	
gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca gcc acc ctg	870
Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu	
263 268 273 278	
cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc aag acc acc	918
Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr	
279 284 289 294	
gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag cag tga cct	966
Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys Gln *	
295 300 305	
gagggggccac cctaggactt gaaaggaccg tgcagcccag tgaccactgc ccagtgggag	1026
gcgccacttt gtatatttca ggactgggac ctactcccca gatgccacct gagaggagct	1086
tctgttttggc attccagatg gaaggacagg cagcacggga gccaggcgct gtggacaggg	1146
tctgtccacg caccacctgg ggtctgccgc ctattaaaag tgccgtattc ttacctcttg	1206
gcattctcaga tgcaactggc tctcctgcat tctgtttgca ggcaaatgct tcagctcaca	1266
tgtcccccaa gactcaatag tcttggttgg gactattgcc tcagggttga caacaggggtg	1326
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at	1388

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 <212> DNA
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<220>
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 <222> (37)..(1137)

<400> 282

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 Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser
 7 12 17 22

gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa 150
 Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys
 23 28 33 38

ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta 198
 Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu
 39 44 49 54

ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga 246
 Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg
 55 60 65 70

cag tcg aga cgg tgt ttc act atg ttt ccc agt ctg gtt tca aac ttc 294
 Gln Ser Arg Arg Cys Phe Thr Met Phe Pro Ser Leu Val Ser Asn Phe
 71 76 81 86

tgg cct caa gca att ccc ctg cct cac cct ccc aaa gtg ctg gga tta 342
 Trp Pro Gln Ala Ile Pro Leu Pro His Pro Pro Lys Val Leu Gly Leu
 87 92 97 102

cag gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac cca 390
 Gln Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp Pro
 103 108 113 118

aag gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg gcc 438
 Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val Ala
 119 124 129 134

tcc ttt tct gaa aga gtt cgg aac atg tcg cct gat gaa atc aag atc 486
 Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys Ile
 135 140 145 150

ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag atc 534
 Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys Ile
 151 156 161 166

cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac tac 582
 Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn Tyr
 167 172 177 182

att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag aag	630
Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu Lys	
183 188 193 198	
ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca aag	678
Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro Lys	
199 204 209 214	
gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag gca	726
Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu Ala	
215 220 225 230	
tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc aaa	774
Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala Lys	
231 236 241 246	
aag gag cga aca aaa gct tgt tgc agg gac gtg tct gca gcg cct ggg	822
Lys Glu Arg Thr Lys Ala Cys Cys Arg Asp Val Ser Ala Ala Pro Gly	
247 252 257 262	
gaa ccg agc tgt cct tcc cct gtg cgg gcg ggc acc gcc tcc tcc tgg	870
Glu Pro Ser Cys Pro Ser Pro Val Arg Ala Gly Thr Ala Ser Ser Trp	
263 268 273 278	
att gag ttt gtg acg ggc acc aaa aaa ggc acc acg acc aac gcc acg	918
Ile Glu Phe Val Thr Gly Thr Lys Lys Gly Thr Thr Thr Asn Ala Thr	
279 284 289 294	
tcc acc acc act acc act gcc agc aca gct gtt gca gat gct cag aag	966
Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala Val Ala Asp Ala Gln Lys	
295 300 305 310	
aga aag agc aag tgg gat tcg gct atc cca gtg aca acg ata gcc cag	1014
Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro Val Thr Thr Ile Ala Gln	
311 316 321 326	
ccc acc atc ctc acc acc aca gcc acc ctg cca gct gtt gtc acg gtc	1062
Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu Pro Ala Val Val Thr Val	
327 332 337 342	
acc acc agc gcc agc ggc tcc aag acc acc gtc atc tct gct gtg ggc	1110
Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr Val Ile Ser Ala Val Gly	
343 348 353 358	
acc att gtg aag aag gcc aag cag tga cctga ggggccaccc taggacttga	1162
Thr Ile Val Lys Lys Ala Lys Gln *	
359 364	
aaggaccgtg cagcccagtg accactgccc agtgggaggc gccactttgt atatttcagg	1222
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aggacaggca gcacgggagc caggcgctgt ggacagggtc tgtccacgca ccacctgggg	1342
tctgccgctt attaaaagtg ccgtattctt acctcttggc atctcagatg cactggcctc	1402
tcctgcattc tgtttgcagg caaatgcttc agctcacatg tcccccaaga ctcaatagtc	1462

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(1152)

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Met Ala Glu Arg Gln Glu Glu Gln Arg Gly Ser Pro
1 5 10
ccc ttg agg gcg gaa ggc aag gcc gac gcg gag gtt aag ctc att ctg 159
Pro Leu Arg Ala Glu Gly Lys Ala Asp Ala Glu Val Lys Leu Ile Leu
13 18 23 28
tac cat tgg acg cat tcc ttc agc tct caa aag gtg cgc ttg gta att 207
Tyr His Trp Thr His Ser Phe Ser Ser Gln Lys Val Arg Leu Val Ile
29 34 39 44
gct gaa aag gca ttg aag tgc gag gaa cat gat gta agt ctg ccc ttg 255
Ala Glu Lys Ala Leu Lys Cys Glu Glu His Asp Val Ser Leu Pro Leu
45 50 55 60
agt gag cac aat gag cct tgg ttt atg cgt ttg aac tca act gga gaa 303
Ser Glu His Asn Glu Pro Trp Phe Met Arg Leu Asn Ser Thr Gly Glu
61 66 71 76
gtg cct gtc ctt atc cac ggg gaa aac ata att tgt gag gcc act cag 351
Val Pro Val Leu Ile His Gly Glu Asn Ile Ile Cys Glu Ala Thr Gln
77 82 87 92
atc att gat tat ctt gaa cag act ttc ctg gat gaa aga aca ccc agg 399
Ile Ile Asp Tyr Leu Glu Gln Thr Phe Leu Asp Glu Arg Thr Pro Arg
93 98 103 108
tta atg cct gat aaa gaa agc atg tat tac cca cgg gta caa cat tac 447
Leu Met Pro Asp Lys Glu Ser Met Tyr Tyr Pro Arg Val Gln His Tyr
109 114 119 124
cga gag ctg ctt gac tcc ttg cca atg gat gcc tat aca cat ggc tgc 495
Arg Glu Leu Leu Asp Ser Leu Pro Met Asp Ala Tyr Thr His Gly Cys
125 130 135 140
att tta cat cct gag tta act gtg gac tcc atg atc ccg gct tat gca 543

Ile	Leu	His	Pro	Glu	Leu	Thr	Val	Asp	Ser	Met	Ile	Pro	Ala	Tyr	Ala	
141					146					151					156	
act	aca	agg	att	cgt	agc	caa	att	gga	aac	aca	gag	tct	gag	ctg	aag	591
Thr	Thr	Arg	Ile	Arg	Ser	Gln	Ile	Gly	Asn	Thr	Glu	Ser	Glu	Leu	Lys	
157					162					167					172	
aaa	ctt	gct	gaa	gaa	aac	cca	gat	tta	caa	gaa	gca	tac	att	gca	aaa	639
Lys	Leu	Ala	Glu	Glu	Asn	Pro	Asp	Leu	Gln	Glu	Ala	Tyr	Ile	Ala	Lys	
173					178					183					188	
cag	aaa	cga	ctt	aaa	tca	aag	ctg	ctt	gat	cat	gac	aat	gtc	aag	tat	687
Gln	Lys	Arg	Leu	Lys	Ser	Lys	Leu	Leu	Asp	His	Asp	Asn	Val	Lys	Tyr	
189					194					199					204	
ttg	aag	aaa	att	ctt	gat	gag	ttg	gag	aaa	gtc	ttg	gat	cag	gtt	gaa	735
Leu	Lys	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Lys	Val	Leu	Asp	Gln	Val	Glu	
205					210					215					220	
act	gaa	ttg	caa	aga	aga	aat	gaa	gaa	acc	cca	gaa	gag	ggc	cag	caa	783
Thr	Glu	Leu	Gln	Arg	Arg	Asn	Glu	Glu	Thr	Pro	Glu	Glu	Gly	Gln	Gln	
221					226					231					236	
cct	tgg	ctc	tgc	ggc	gaa	tcc	ttc	acc	ctg	gca	gac	gtc	tca	ctc	gct	831
Pro	Trp	Leu	Cys	Gly	Glu	Ser	Phe	Thr	Leu	Ala	Asp	Val	Ser	Leu	Ala	
237					242					247					252	
gtc	aca	ttg	cat	cga	ctg	aag	ttc	ctg	ggg	ttt	gca	agg	aga	aac	tgg	879
Val	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Phe	Ala	Arg	Arg	Asn	Trp	
253					258					263					268	
gga	aac	gga	aag	cga	cca	aac	ttg	gaa	acc	tat	tac	gag	cgt	gtc	ttg	927
Gly	Asn	Gly	Lys	Arg	Pro	Asn	Leu	Glu	Thr	Tyr	Tyr	Glu	Arg	Val	Leu	
269					274					279					284	
aag	aga	aaa	aca	ttt	aac	aag	gtt	tta	gga	cat	gtc	aac	aat	ata	tta	975
Lys	Arg	Lys	Thr	Phe	Asn	Lys	Val	Leu	Gly	His	Val	Asn	Asn	Ile	Leu	
285					290					295					300	
atc	tct	gca	gtg	ctg	cca	aca	gca	ttc	cgg	gtg	gcc	aag	aaa	agg	gcc	1023
Ile	Ser	Ala	Val	Leu	Pro	Thr	Ala	Phe	Arg	Val	Ala	Lys	Lys	Arg	Ala	
301					306					311					316	
cca	aaa	gtt	ctt	ggc	acg	acc	ctt	gtg	gtt	ggc	ttg	ctt	gca	gga	gtg	1071
Pro	Lys	Val	Leu	Gly	Thr	Thr	Leu	Val	Val	Gly	Leu	Leu	Ala	Gly	Val	
317					322					327					332	
gga	tat	ttt	gct	ttt	atg	ctt	ttc	aga	aag	aga	ctt	ggc	agc	atg	ata	1119
Gly	Tyr	Phe	Ala	Phe	Met	Leu	Phe	Arg	Lys	Arg	Leu	Gly	Ser	Met	Ile	
333					338					343					348	
tta	gca	ctt	aga	ccc	aga	cca	aat	tat	ttc	tag						1152
Leu	Ala	Leu	Arg	Pro	Arg	Pro	Asn	Tyr	Phe	*						
349					354					359						

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (50)..(1774)

<400> 284
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 Pro Arg Ala Ala Arg Ala Pro Ala Thr Leu Leu Leu Ala Leu Gly Ala
 3 8 13 18

gtg ctg tgg cct gcg gct ggc gcc tgg gag ctt acg att ttg cac acc 151
 Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu His Thr
 19 24 29 34

aac gac gtg cac agc cgg ctg gag cag acc agc gag gac tcc agc aag 199
 Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser Ser Lys
 35 40 45 50

tgc gtc aac gcc agc cgc tgc atg ggt ggc gtg gct cgg ctc ttc acc 247
 Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu Phe Thr
 51 56 61 66

aag gtt cag cag atc cgc cgc gcc gaa ccc aac gtg ctg ctg ctg gac 295
 Lys Val Gln Gln Ile Arg Arg Ala Glu Pro Asn Val Leu Leu Leu Asp
 67 72 77 82

gcc ggc gac cag tac cag ggc act atc tgg ttc acc gtg tac aag ggc 343
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Leu	Leu	His	Thr	Ser	Arg	Ser	Phe	Ser	Cys	Leu	Asn	Arg	Ser	Leu	Ser	
815					820					825					830	
tcg	ggg	gag	agc	ctc	cca	ggg	tcc	ccc	act	cat	agc	ttg	tct	ccc	cgg	2724
Ser	Gly	Glu	Ser	Leu	Pro	Gly	Ser	Pro	Thr	His	Ser	Leu	Ser	Pro	Arg	
831					836					841					846	
tct	cca	aca	cca	agc	tac	cgc	tcc	acc	cct	gac	ttc	cca	tct	ggg	act	2772
Ser	Pro	Thr	Pro	Ser	Tyr	Arg	Ser	Thr	Pro	Asp	Phe	Pro	Ser	Gly	Thr	
847					852					857					862	
aat	tcc	tcc	cag	agc	agc	tcc	cct	agt	tct	agt	gcc	ccc	aat	tcc	cca	2820
Asn	Ser	Ser	Gln	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Ala	Pro	Asn	Ser	Pro	
863					868					873					878	
gca	ggg	tcc	ggg	cac	atc	cgg	ccc	agc	act	ctc	cac	ggg	ctt	gca	ccc	2868
Ala	Gly	Ser	Gly	His	Ile	Arg	Pro	Ser	Thr	Leu	His	Gly	Leu	Ala	Pro	
879					884					889					894	
aaa	ctc	ggc	ggg	cag	cgg	tac	cgg	tcc	gga	agg	cga	aag	tcc	gcc	ggc	2916
Lys	Leu	Gly	Gly	Gln	Arg	Tyr	Arg	Ser	Gly	Arg	Arg	Lys	Ser	Ala	Gly	
895					900					905					910	
aac	atc	cca	ctg	tcc	ccg	ctg	gcc	cgg	acg	ccc	tct	cca	acc	ccg	caa	2964
Asn	Ile	Pro	Leu	Ser	Pro	Leu	Ala	Arg	Thr	Pro	Ser	Pro	Thr	Pro	Gln	

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ccc acc tcc ccg cag cgg tca cca tcc cct ctt ctg gga cac tca ctg				3012
Pro Thr Ser Pro Gln Arg Ser Pro Ser Pro Leu Leu Gly His Ser Leu				
927	932	937	942	
ggc aat tcc aag atc gcg caa gcc ttt ccc agc aag atg cac tcc ccg				3060
Gly Asn Ser Lys Ile Ala Gln Ala Phe Pro Ser Lys Met His Ser Pro				
943	948	953	958	
ccc acc atc gtc aga cac atc gtg agg ccc aag agt gcg gag ccc ccc				3108
Pro Thr Ile Val Arg His Ile Val Arg Pro Lys Ser Ala Glu Pro Pro				
959	964	969	974	
agg tcc ccg ctg ctc aag cgc gtg cag tcc gag gag aag ctg tcg ccc				3156
Arg Ser Pro Leu Leu Lys Arg Val Gln Ser Glu Glu Lys Leu Ser Pro				
975	980	985	990	
tct tac ggc agt gac aag aag cac ctg tgc tcc cgc aag cac agc ctg				3204
Ser Tyr Gly Ser Asp Lys Lys His Leu Cys Ser Arg Lys His Ser Leu				
991	996	1001	1006	
gag gtg acc caa gag gag gtg cag cgg gag cag tcc cag cgg gag gcg				3252
Glu Val Thr Gln Glu Glu Val Gln Arg Glu Gln Ser Gln Arg Glu Ala				
1007	1012	1017	1022	
ccg ctg cag agc ctg gat gag aac gtg tgc gac gtg ccg ccg ctc agc				3300
Pro Leu Gln Ser Leu Asp Glu Asn Val Cys Asp Val Pro Pro Leu Ser				
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cgc gcc cgg cca gtg gag caa ggc tgc ctg aaa cgc cca gtc tcc ccg				3348
Arg Ala Arg Pro Val Glu Gln Gly Cys Leu Lys Arg Pro Val Ser Arg				
1039	1044	1049	1054	
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Lys Val Gly Arg Gln Glu Ser Val Asp Asp Leu Asp Arg Asp Lys Leu				
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Lys Ala Lys Val Val Lys Lys Ala Asp Gly Phe Pro Glu Lys Gln				
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gaa tcc cac cag aaa tcc cat gga ccc ggg agt gat ttg gaa aac ttt				3492
Glu Ser His Gln Lys Ser His Gly Pro Gly Ser Asp Leu Glu Asn Phe				
1087	1092	1097	1102	
gct ctg ttt aag ctg gaa gag aga gag aag aaa gtc tat ccg aag gct				3540
Ala Leu Phe Lys Leu Glu Glu Arg Glu Lys Lys Val Tyr Pro Lys Ala				
1103	1108	1113	1118	
gtg gaa agg tca agt act ttt gaa aac aaa gcg tct atg cag gag gcg				3588
Val Glu Arg Ser Ser Thr Phe Glu Asn Lys Ala Ser Met Gln Glu Ala				
1119	1124	1129	1134	
cca ccg ctg ggc agc ctg ctg aag gat gct ctt cac aag cag gcc agc				3636
Pro Pro Leu Gly Ser Leu Leu Lys Asp Ala Leu His Lys Gln Ala Ser				
1135	1140	1145	1150	

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Val Arg Ala Ser Glu Gly Ala Met Ser Asp Gly Pro Val Pro Ala Glu	
1151 1156 1161 1166	
cac cgc cag ggt ggc ggg gac ttc aga cgg gcc ccc gct cct ggc acc	3732
His Arg Gln Gly Gly Gly Asp Phe Arg Arg Ala Pro Ala Pro Gly Thr	
1167 1172 1177 1182	
ctc cag gat ggt ctc tgc cac tcc ctc gac agg ggc atc tct ggg aag	3780
Leu Gln Asp Gly Leu Cys His Ser Leu Asp Arg Gly Ile Ser Gly Lys	
1183 1188 1193 1198	
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Gly Glu Gly Thr Glu Lys Ser Ser Gln Ala Lys Glu Leu Leu Arg Cys	
1199 1204 1209 1214	
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Glu Lys Leu Asp Ser Lys Leu Ala Asn Ile Asp Tyr Leu Arg Lys Lys	
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Met Ser Leu Glu Asp Lys Glu Asp Asn Leu Cys Pro Val Leu Lys Pro	
1231 1236 1241 1246	
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Lys Met Thr Ala Gly Ser His Glu Cys Leu Pro Gly Asn Pro Val Arg	
1247 1252 1257 1262	
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Pro Thr Gly Gly Gln Gln Glu Pro Pro Pro Ala Ser Glu Ser Arg Ala	
1263 1268 1273 1278	
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Phe Val Ser Ser Thr His Ala Ala Gln Met Ser Ala Val Ser Phe Val	
1279 1284 1289 1294	
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Pro Leu Lys Ala Leu Thr Gly Arg Val Asp Ser Gly Thr Glu Lys Pro	
1295 1300 1305 1310	
ggc ttg gtt gct cct gag tcc cct gtt agg aag agc ccc tcc gag tat	4164
Gly Leu Val Ala Pro Glu Ser Pro Val Arg Lys Ser Pro Ser Glu Tyr	
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Lys Leu Glu Gly Arg Ser Val Ser Cys Leu Glu Pro Ile Glu Gly Thr	
1327 1332 1337 1342	
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Leu Asp Ile Ala Leu Leu Ser Gly Pro Gln Ala Ser Lys Thr Glu Leu	
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Pro Ser Pro Glu Ser Ala Gln Ser Pro Ser Pro Ser Gly Asp Val Arg	
1359 1364 1369 1374	

gcc tct gtg cca cca gtt ctc ccc agc agc agt ggg aaa aag aac gat	4356
Ala Ser Val Pro Pro Val Leu Pro Ser Ser Ser Gly Lys Lys Asn Asp	
1375 1380 1385 1390	
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Thr Thr Ser Ala Arg Glu Leu Ser Pro Ser Ser Leu Lys Met Asn Lys	
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Ser Tyr Leu Leu Glu Pro Trp Phe Leu Pro Pro Ser Arg Gly Leu Gln	
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Asn Ser Pro Ala Val Ser Leu Pro Asp Pro Glu Phe Lys Arg Asp Arg	
1423 1428 1433 1438	
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Lys Gly Pro His Pro Thr Ala Arg Ser Pro Gly Thr Val Met Glu Ser	
1439 1444 1449 1454	
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Asn Pro Gln Gln Arg Glu Gly Ser Ser Pro Lys His Gln Asp His Thr	
1455 1460 1465 1470	
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Thr Asp Pro Lys Leu Leu Thr Cys Leu Gly Gln Asn Leu His Ser Pro	
1471 1476 1481 1486	
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Asp Leu Ala Arg Pro Arg Cys Pro Leu Pro Pro Glu Ala Ser Pro Ser	
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Arg Glu Lys Pro Gly Leu Arg Glu Ser Ser Glu Arg Gly Pro Pro Thr	
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Ala Arg Ser Glu Arg Ser Ala Ala Arg Ala Asp Thr Cys Arg Glu Pro	
1519 1524 1529 1534	
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Ser Met Glu Leu Cys Phe Pro Glu Thr Ala Lys Thr Ser Asp Asn Ser	
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Thr Gln Ala Met Glu Lys Ala Trp Ala Pro Gly Gly Lys Thr Asn His	
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Lys Asp Gly Pro Gly Glu Ala Arg Pro Pro Pro Arg Asp Asn Ser Ser	
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Gln	Pro	Pro	Gly	Ile	Glu	Ser	Glu	Lys	Ser	Glu	Lys	Leu	Ser	Ser	Phe		
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Pro	Leu	Gln	Arg	His	Pro	Ser	Ser	Ile	Pro	Pro	Pro	Pro	Leu	Thr	Ala		
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Lys	Asp	Leu	Ser	Ser	Pro	Ala	Ala	Arg	Gln	His	Cys	Ser	Ser	Pro	Ser		
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Gly	Gly	Pro	Ser	Val	Pro	Leu	His	Thr	Asp	Arg	Ala	Pro	Leu	Asp	Ala		
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Pro Val His Leu Pro Arg Pro Gly His Pro Gly Pro Ser Glu Pro Ala				
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Asp Gln Lys Leu Ser Ala Val Gly Glu Lys Gln Thr Leu Ser Pro Lys				
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His Pro Lys Pro Ser Thr Val Lys Asp Cys Pro Thr Leu Cys Lys Gln				
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Thr Asp Asn Arg Gln Thr Asp Lys Ser Pro Ser Gln Pro Ala Ala Asn				
1887	1892	1897	1902	
acc gac aga agg gcg gaa ggg aag aaa tgc act gaa gca ctt tat gct				5940
Thr Asp Arg Arg Ala Glu Gly Lys Lys Cys Thr Glu Ala Leu Tyr Ala				
1903	1908	1913	1918	
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Pro Ala Glu Gly Asp Lys Leu Glu Ala Gly Leu Ser Phe Val His Ser				
1919	1924	1929	1934	
gag aac cgg ttg aaa ggc gcg gag cgg cca gcc gcg ggg gtg ggg aag				6036
Glu Asn Arg Leu Lys Gly Ala Glu Arg Pro Ala Ala Gly Val Gly Lys				
1935	1940	1945	1950	
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Gly Phe Pro Glu Ala Arg Gly Lys Gly Pro Gly Pro Gln Lys Pro Pro				
1951	1956	1961	1966	
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Thr Glu Ala Asp Lys Pro Asn Gly Met Lys Arg Ser Pro Ser Ala Thr				
1967	1972	1977	1982	
ggg cag agt tct ttc cga tcc acg gcc ctc ccg gaa aag tct ctg agc				6180
Gly Gln Ser Ser Phe Arg Ser Thr Ala Leu Pro Glu Lys Ser Leu Ser				
1983	1988	1993	1998	
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Cys Ser Ser Ser Phe Pro Glu Thr Arg Ala Gly Val Arg Glu Ala Ser				
1999	2004	2009	2014	
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Ala Ala Ser Ser Asp Thr Ser Ser Ala Lys Ala Ala Gly Gly Met Leu				
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Glu Leu Pro Ala Pro Ser Asn Arg Asp His Arg Lys Ala Gln Pro Ala				
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Gly Glu Gly Arg Thr His Met Thr Lys Ser Asp Ser Leu Pro Ser Phe				
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Met	Gly	Gly	Ala	Ser	His	Arg	Asp	Arg	Ala	Leu	Ser	Val	Thr	Ala	Thr															
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Val	Gly	Glu	Thr	Lys	Gly	Lys	Asp	Pro	Ala	Pro	Ala	Gln	Pro	Pro	Pro															
2095					2100				2105					2110																
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Ala	Arg	Lys	Gln	Asn	Val	Gly	Arg	Asp	Val	Thr	Lys	Pro	Ser	Pro	Ala															
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c	a	a	a	c	t	g	a	c	c	a	t	c	t	c	t	a	a	g	a	g	a	c	t	t	c	a	a		6612	
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Val	Arg	Gln	Arg	Arg	Gly	Lys	Glu	Ser	Leu	Arg	Ser	Ser	Pro	His	Lys															
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Lys	Ala	Leu	*																											
2159																														
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Met	Pro	Ala	Ser	Phe	Pro	Leu	Ser	Arg	Asn	Ala	Gly	Thr	Arg	Gly	Gly																		
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Asn	Pro	Ala	Pro	Ser	Pro	Pro	Leu	Arg	Ser	Pro	Gly	Lys	Gly	Arg	Leu																		
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Ala Ser Pro Ile Leu Pro Gln Arg Ser Gly Asn Ile Pro Glu Ala Pro	
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Arg Arg Tyr Asp Pro Gly Val Arg Ile Gly Leu Gly Gly Ala Ala Ala	
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Ser Leu Ser Thr Ser Gly Arg Asp Cys Arg Val Met Arg Tyr Ser Val	
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Asp Lys Tyr Asp Ala Arg Asp Val Glu Arg Leu Gln Gln Asp Asp Asn	
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Asn Val Trp Ile Arg Val Lys Tyr His Val Lys Asp Gln Lys Thr Ile	
225 230 235 240	
ttg gac aaa aag aag ctc ata gca ttc tgg ttg gaa cgt tat gct aag	768
Leu Asp Lys Lys Lys Leu Ile Ala Phe Trp Leu Glu Arg Tyr Ala Lys	
241 246 251 256	

agg gaa aat ggg aaa cct gta aca gtg atg ttt gac ctg tca gaa act	816
Arg Glu Asn Gly Lys Pro Val Thr Val Met Phe Asp Leu Ser Glu Thr	
257 262 267 272	
gga ata aat agc att gac atg gac ttt gta cgc ttt atc atc aac tgc	864
Gly Ile Asn Ser Ile Asp Met Asp Phe Val Arg Phe Ile Ile Asn Cys	
273 278 283 288	
ttt aag gtt tat tac cct aaa tac ctc tct gct ttc aaa att gtg aaa	912
Phe Lys Val Tyr Tyr Pro Lys Tyr Leu Ser Ala Phe Lys Ile Val Lys	
289 294 299 304	
acc tgg ctt ggt cca gaa gca gtg agc ttg ttg aag ttt aca agc aaa	960
Thr Trp Leu Gly Pro Glu Ala Val Ser Leu Leu Lys Phe Thr Ser Lys	
305 310 315 320	
aat gaa gtc cag gac tat gtc agt gta gaa tac ctg cct ccc cac atg	1008
Asn Glu Val Gln Asp Tyr Val Ser Val Glu Tyr Leu Pro Pro His Met	
321 326 331 336	
ggg gga act gat cct ttc aag tat agc tat cca cca cta gta gat gat	1056
Gly Gly Thr Asp Pro Phe Lys Tyr Ser Tyr Pro Pro Leu Val Asp Asp	
337 342 347 352	
gac ttc cag acc cca ctg tgt gag aat ggg cct att acc agt gag gat	1104
Asp Phe Gln Thr Pro Leu Cys Glu Asn Gly Pro Ile Thr Ser Glu Asp	
353 358 363 368	
gaa act tca agt aaa gaa gac ata gaa agt gat ggc aaa gaa aca ttg	1152
Glu Thr Ser Ser Lys Glu Asp Ile Glu Ser Asp Gly Lys Glu Thr Leu	
369 374 379 384	
gaa aca att tct aat gaa gaa caa aca cct ctt ctt aaa aag att aac	1200
Glu Thr Ile Ser Asn Glu Glu Gln Thr Pro Leu Leu Lys Lys Ile Asn	
385 390 395 400	
cca acc gaa tct act tcc aaa gca gaa gaa aat gaa aaa gtt gat tca	1248
Pro Thr Glu Ser Thr Ser Lys Ala Glu Glu Asn Glu Lys Val Asp Ser	
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Lys Val Lys Ala Phe Lys Lys Pro Leu Ser Val Phe Lys Gly Pro Leu	
417 422 427 432	
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Leu His Ile Ser Pro Ala Glu Glu Leu Tyr Phe Gly Ser Thr Glu Ser	
433 438 443 448	
gga gag aag aaa acc tta ata gtg ttg aca aat gta act aaa aat ata	1392
Gly Glu Lys Lys Thr Leu Ile Val Leu Thr Asn Val Thr Lys Asn Ile	
449 454 459 464	
gtg gca ttt aag gtg aga aca aca gct cca gaa aaa tac aga gtc aag	1440
Val Ala Phe Lys Val Arg Thr Thr Ala Pro Glu Lys Tyr Arg Val Lys	
465 470 475 480	
cca agc aat agc agc tgt gac ccg ggt gca tca gtg gat ata gtt gtg	1488

Pro	Ser	Asn	Ser	Ser	Cys	Asp	Pro	Gly	Ala	Ser	Val	Asp	Ile	Val	Val	
481					486					491					496	
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Ser	Pro	His	Gly	Gly	Leu	Thr	Val	Ser	Ala	Gln	Asp	Arg	Phe	Leu	Ile	
497					502					507					512	
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Met	Ala	Ala	Glu	Met	Glu	Gln	Ser	Ser	Gly	Thr	Gly	Pro	Ala	Glu	Leu	
513					518					523					528	
act	cag	ttt	tgg	aaa	gaa	gtt	ccc	aga	aac	aaa	gtg	atg	gaa	cat	agg	1632
Thr	Gln	Phe	Trp	Lys	Glu	Val	Pro	Arg	Asn	Lys	Val	Met	Glu	His	Arg	
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tta	aga	tgc	cat	act	gtt	gaa	agc	agt	aaa	cca	aac	act	ctt	acg	tta	1680
Leu	Arg	Cys	His	Thr	Val	Glu	Ser	Ser	Lys	Pro	Asn	Thr	Leu	Thr	Leu	
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aaa	gac	aat	gct	ttc	aat	atg	tca	gat	aaa	acc	agt	gaa	gat	ata	tgt	1728
Lys	Asp	Asn	Ala	Phe	Asn	Met	Ser	Asp	Lys	Thr	Ser	Glu	Asp	Ile	Cys	
561					566					571					576	
cta	caa	ctc	agt	cgt	tta	cta	gaa	agc	aat	agg	aag	ctt	gaa	gac	caa	1776
Leu	Gln	Leu	Ser	Arg	Leu	Leu	Glu	Ser	Asn	Arg	Lys	Leu	Glu	Asp	Gln	
577					582					587					592	
gtt	cag	cgt	tgt	atc	tgg	ttc	cag	cag	ctg	ctg	ctt	tcc	tta	aca	atg	1824
Val	Gln	Arg	Cys	Ile	Trp	Phe	Gln	Gln	Leu	Leu	Leu	Ser	Leu	Thr	Met	
593					598					603					608	
ctc	ttg	ctt	gct	ttt	gtc	acc	tct	ttc	ttc	tat	tta	ttg	tac	agt	taa	1872
Leu	Leu	Leu	Ala	Phe	Val	Thr	Ser	Phe	Phe	Tyr	Leu	Leu	Tyr	Ser	*	
609					614					619					624	
agaagtgggtg	ccgggtagga	accacggttc	cttcgtccat	tagttggaaa	aagtaacaga											1932
cctaaaactc	taccaagcta	ctaaaaacat	tgacacatctg	tgcttcctaa	aaggaaatat											1992
gcagcacgtg	gaggggaaca	catacatgtc	ttgaaaataa	actgctagaa	taaagaaatg											2052
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	Met Gln Lys Leu Gln Thr Arg Ser	
	1 5	
cct gcc atg tcc ctg tct gac cca ggc ctg ggg tac cac ccc acg tgc	160	
Pro Ala Met Ser Leu Ser Asp Pro Gly Leu Gly Tyr His Pro Thr Cys		
9 14 19 24		
tgg acc cta cgc tgg cca ccc ctg tgc tcc ctc cac gcc ctc cac gtg	208	
Trp Thr Leu Arg Trp Pro Pro Leu Cys Ser Leu His Ala Leu His Val		
25 30 35 40		
ttc cac tgc ctc ttc tct tct cgc ttg gga act cca gtc tca cct cgg	256	
Phe His Cys Leu Phe Ser Ser Arg Leu Gly Thr Pro Val Ser Pro Arg		
41 46 51 56		
ctt gca atg gac ccc aac tgc tcc tgc gag gct ggt ggc tcc tgc gcc	304	
Leu Ala Met Asp Pro Asn Cys Ser Cys Glu Ala Gly Gly Ser Cys Ala		
57 62 67 72		
tgc gcc ggc tcc tgc aag tgc aaa aag tgc aaa tgc acc tcc tgc aag	352	
Cys Ala Gly Ser Cys Lys Cys Lys Lys Cys Lys Cys Thr Ser Cys Lys		
73 78 83 88		
aag agc tgc tgc tcc tgt tgc ccc ctg ggc tgt gcc aag tgt gcc cag	400	
Lys Ser Cys Cys Ser Cys Cys Pro Leu Gly Cys Ala Lys Cys Ala Gln		
89 94 99 104		
ggc tgc atc tgc aaa ggg gcg tca gag aag tgc agc tgc tgt gcc tga	448	
Gly Cys Ile Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Ala *		
105 110 115 120		
tgtcggggaca gccctgctgt cagatgaaaa cagaatgaca cgtaaaatcc aggatttttt	508	
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Leu Gln Gln Gly Lys Gly Asn Val Asp Gly Val Ala Ala Thr Pro Thr	
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gct gcc tcg gcc tcc tgc cag tac agg tgc atc gaa tgc aac cag gag	149
Ala Ala Ser Ala Ser Cys Gln Tyr Arg Cys Ile Glu Cys Asn Gln Glu	
25 30 35 40	
gcc aaa gag ttg tac cga gac tat aac cac ggt gtg ctg aag ata acc	197
Ala Lys Glu Leu Tyr Arg Asp Tyr Asn His Gly Val Leu Lys Ile Thr	
41 46 51 56	
atc tgt aaa tcc tgc cag aaa cct gta gac aaa tat atc gag tat gat	245
Ile Cys Lys Ser Cys Gln Lys Pro Val Asp Lys Tyr Ile Glu Tyr Asp	
57 62 67 72	
cct gtt atc atc ttg att aat gct ata ttg tgc aaa gct cag gcc tac	293
Pro Val Ile Ile Leu Ile Asn Ala Ile Leu Cys Lys Ala Gln Ala Tyr	
73 78 83 88	
aga cat att ctt ttc aat act caa ata aat atc cat gga aaa ctc tgc	341
Arg His Ile Leu Phe Asn Thr Gln Ile Asn Ile His Gly Lys Leu Cys	
89 94 99 104	
ata ttt tgt ttg ctt tgt gaa gca tac ctg agg tgg tgg cag ctt caa	389
Ile Phe Cys Leu Leu Cys Glu Ala Tyr Leu Arg Trp Trp Gln Leu Gln	
105 110 115 120	
gat tcc aac cag aat act gcc cct gat gac ttg atc aga tat gct aag	437
Asp Ser Asn Gln Asn Thr Ala Pro Asp Asp Leu Ile Arg Tyr Ala Lys	
121 126 131 136	
gaa tgg gat ttc tat aga atg ttt gcg att gct gct tta gaa caa act	485
Glu Trp Asp Phe Tyr Arg Met Phe Ala Ile Ala Ala Leu Glu Gln Thr	
137 142 147 152	
gcc tat ttt att ggc att ttt acc ttc ctg tgg gta gaa cgg ccc atg	533
Ala Tyr Phe Ile Gly Ile Phe Thr Phe Leu Trp Val Glu Arg Pro Met	
153 158 163 168	
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Thr Ala Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu Lys Ala Leu Leu	
169 174 179 184	
tta tct agc tac gga aaa ctc ttg ctg att cca gct gtc att tgg gaa	629
Leu Ser Ser Tyr Gly Lys Leu Leu Leu Ile Pro Ala Val Ile Trp Glu	
185 190 195 200	
cat gac tac aca tct gtg tgc ctc aaa ctc att aaa gta ttt gtt ctt	677
His Asp Tyr Thr Ser Val Cys Leu Lys Leu Ile Lys Val Phe Val Leu	
201 206 211 216	
aca tca aat ttt cag gca att aga gtg acc cta aac atc aac cgt aag	725
Thr Ser Asn Phe Gln Ala Ile Arg Val Thr Leu Asn Ile Asn Arg Lys	

217	222	227	232	
ctc tcc ttc ttg gcc gtg ttg agt ggc tta ctg ctg gaa agc atc atg				773
Leu Ser Phe Leu Ala Val Leu Ser Gly Leu Leu Leu Glu Ser Ile Met				
233	238	243	248	
gtc tac ttc ttc cag agt atg gaa tgg gat gtt gga agt gat tat gcc				821
Val Tyr Phe Phe Gln Ser Met Glu Trp Asp Val Gly Ser Asp Tyr Ala				
249	254	259	264	
atc ttt aaa tct cag gac ttc tga agagttttat tcttcttcac tatctgtggc				875
Ile Phe Lys Ser Gln Asp Phe *				
265	270			
atgaccagct gtatctgaaa gagaaaagac atgaaatata aaccaacctc ctcatttctg				935
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ggtggatacc cccccccaca aatgcaccca agagacaagc catttacata cagatattca				1055
cagtcacaca tagaaacacc cacatggaca caaggaatgt tgctgcagag actgaatgac				1115
atgcaacagg tgaaggttta tacgtttatac acaaggccag gtaagcgctc ataattcaca				1175
cataataaaa catctagggtt tcattccttt gacatgttta tatcttttta atttaaattgt				1235
tgttactggc ttaaaatatt ttgtgttctt acaatagaaa cgcttttaaat aaagtctttc				1295
agaataaacc aagtttttgt aaattttcaa ttcaataatt aaggtaattct ttaaaattgg				1355
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gaacctattg tttcagaagt cggtgacctt tgaggacgtg gctgtgtact tcaccaggc	180
ggaatgggat ggctgtccc ctgcacagag gacctgtac agggatgtg	235
	atg ctg
	Met Leu

gag aat tat ggg aat gtg gca tcc ctg gga ttt cca ctt ctc aaa cct	283
Glu Asn Tyr Gly Asn Val Ala Ser Leu Gly Phe Pro Leu Leu Lys Pro	
3 8 13 18	
gct gtg atc tca caa ctg gag gga gga agt gag ctg ggg ggc tca tct	331
Ala Val Ile Ser Gln Leu Glu Gly Gly Ser Glu Leu Gly Gly Ser Ser	
19 24 29 34	
cca ctg gct gca gga aca ggc ctc cag ggc ctc cag act gta gat att	379
Pro Leu Ala Ala Gly Thr Gly Leu Gln Gly Leu Gln Thr Val Asp Ile	
35 40 45 50	
cag act gac aat gat ttg aca aag gaa atg tat gaa gga aaa gag aat	427
Gln Thr Asp Asn Asp Leu Thr Lys Glu Met Tyr Glu Gly Lys Glu Asn	
51 56 61 66	
gta tca ttt gaa ctt caa aga gac ttt tcc cag gaa aca gac ttt tca	475
Val Ser Phe Glu Leu Gln Arg Asp Phe Ser Gln Glu Thr Asp Phe Ser	
67 72 77 82	
gaa gcc tct ctt cta gag aaa caa cag gaa gtc cac tca gca gga aat	523
Glu Ala Ser Leu Leu Glu Lys Gln Gln Glu Val His Ser Ala Gly Asn	
83 88 93 98	
ata aag aag gag aag agc aac acc att gat gga aca gtg aaa gat gag	571
Ile Lys Lys Glu Lys Ser Asn Thr Ile Asp Gly Thr Val Lys Asp Glu	
99 104 109 114	
aca agc ccc gtg gag gag tgt ttt ttt agt caa agt tca aac tca tat	619
Thr Ser Pro Val Glu Glu Cys Phe Phe Ser Gln Ser Ser Asn Ser Tyr	
115 120 125 130	
cag tgt cat acc atc act gga gag cag ccc tct ggg tgt aca gga ttg	667
Gln Cys His Thr Ile Thr Gly Glu Gln Pro Ser Gly Cys Thr Gly Leu	
131 136 141 146	
ggg aaa tcc atc agc ttt gat aca aaa ctc gtg aag cat gaa ata att	715
Gly Lys Ser Ile Ser Phe Asp Thr Lys Leu Val Lys His Glu Ile Ile	
147 152 157 162	
aat tct gag gaa aga cct ttc aaa tgt gaa gaa tta gta gag ccc ttt	763
Asn Ser Glu Glu Arg Pro Phe Lys Cys Glu Glu Leu Val Glu Pro Phe	
163 168 173 178	
agg tgt gac tct caa ctt att caa cat caa gag aac aac act gag gaa	811
Arg Cys Asp Ser Gln Leu Ile Gln His Gln Glu Asn Asn Thr Glu Glu	
179 184 189 194	
aag cct tat cag tgt tcg gag tgt ggc aaa gct ttc agc att aat gag	859
Lys Pro Tyr Gln Cys Ser Glu Cys Gly Lys Ala Phe Ser Ile Asn Glu	
195 200 205 210	
aaa tta att tgg cat cag aga ctt cac agt ggg gag aaa ccc ttc aaa	907
Lys Leu Ile Trp His Gln Arg Leu His Ser Gly Glu Lys Pro Phe Lys	
211 216 221 226	
tgt gtg gag tgt ggg aaa agc ttc agc tac agt tcc cat tat atc aca	955

Cys Val Glu Cys Gly Lys Ser Phe Ser Tyr Ser Ser His Tyr Ile Thr	
227 232 237 242	
cat cag aca atc cac agt ggg gag aag ccc tat cag tgt aag atg tgt	1003
His Gln Thr Ile His Ser Gly Glu Lys Pro Tyr Gln Cys Lys Met Cys	
243 248 253 258	
ggg aag gcc ttc agt gtt aat gga agc cta agt agg cat cag aga atc	1051
Gly Lys Ala Phe Ser Val Asn Gly Ser Leu Ser Arg His Gln Arg Ile	
259 264 269 274	
cat acg gga gag aag ccc tat cag tgc aag gaa tgt gga aat ggc ttc	1099
His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys Gly Asn Gly Phe	
275 280 285 290	
agc tgt agt tct gca tat att aca cat cag aga gtc cac act gga gag	1147
Ser Cys Ser Ser Ala Tyr Ile Thr His Gln Arg Val His Thr Gly Glu	
291 296 301 306	
aaa cct tac gag tgt aat gac tgt ggg aaa gcg ttc aat gtt aat gca	1195
Lys Pro Tyr Glu Cys Asn Asp Cys Gly Lys Ala Phe Asn Val Asn Ala	
307 312 317 322	
aaa tta att caa cat cag aga atc cat act gga gag aaa cct tat gaa	1243
Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu	
323 328 333 338	
tgt aat gaa tgt gga aaa ggc ttc agg tgc agc tcc cag ctt agg cag	1291
Cys Asn Glu Cys Gly Lys Gly Phe Arg Cys Ser Ser Gln Leu Arg Gln	
339 344 349 354	
cat cag agc atc cac aca gga gaa aag ccc tat cag tgt aaa gag tgt	1339
His Gln Ser Ile His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys	
355 360 365 370	
gga aaa ggc ttc aat aat aat aca aaa ctc att cag cat cag aga atc	1387
Gly Lys Gly Phe Asn Asn Asn Thr Lys Leu Ile Gln His Gln Arg Ile	
371 376 381 386	
cac aca ggt gag aaa ccc tat gaa tgc act gaa tgt gga aaa gcc ttc	1435
His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Ala Phe	
387 392 397 402	
agt gtc aaa ggg aag tta atc caa cac cag aga att cac aca ggc gag	1483
Ser Val Lys Gly Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu	
403 408 413 418	
aaa ccc tat gag tgt aat gaa tgc ggg aaa gcc ttc aga tgt aac tcc	1531
Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg Cys Asn Ser	
419 424 429 434	
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Gln Phe Arg Gln His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu	
435 440 445 450	
tgt aat gag tgt gga aag gcc ttc agc gtt aat ggg aaa cta atg cgg	1627
Cys Asn Glu Cys Gly Lys Ala Phe Ser Val Asn Gly Lys Leu Met Arg	

451	456	461	466	
cat cag aga att cac	act ggg gag aaa cct	ttt gaa tgt aat gag	tgt	1675
His Gln Arg Ile His	Thr Gly Glu Lys Pro	Phe Glu Cys Asn Glu	Cys	
467	472	477	482	
ggg aga tgc ttt act	tct aaa aga aac cta	ctt gat cat cac cga	atc	1723
Gly Arg Cys Phe Thr	Ser Lys Arg Asn Leu	Leu Asp His His Arg	Ile	
483	488	493	498	
cat act gga gaa aag	ccc tat caa tgt aag	gaa tgt ggg aaa gcc	ttc	1771
His Thr Gly Glu Lys	Pro Tyr Gln Cys Lys	Glu Cys Gly Lys Ala	Phe	
499	504	509	514	
agt atc aat gcc aaa	cta act agg cat cag	agg ata cat act ggg	gag	1819
Ser Ile Asn Ala Lys	Leu Thr Arg His Gln	Arg Ile His Thr Gly	Glu	
515	520	525	530	
aaa cct ttc aaa tgt	atg gaa tgt gag aaa	gca ttc agc tgt agt	tct	1867
Lys Pro Phe Lys Cys	Met Glu Cys Glu Lys	Ala Phe Ser Cys Ser	Ser	
531	536	541	546	
aac tat att gtg cac	cag aga atc cat aca	gga gag aaa ccc ttt	cag	1915
Asn Tyr Ile Val His	Gln Arg Ile His Thr	Gly Glu Lys Pro Phe	Gln	
547	552	557	562	
tgt aag gag tgt gga	aaa gcc ttc cat gtt	aat gcc cat tta att	cgg	1963
Cys Lys Glu Cys Gly	Lys Ala Phe His Val	Asn Ala His Leu Ile	Arg	
563	568	573	578	
cat cag aga agc cac	act ggg gag aaa ccc	ttc aga tgt gtg gaa	tgt	2011
His Gln Arg Ser His	Thr Gly Glu Lys Pro	Phe Arg Cys Val Glu	Cys	
579	584	589	594	
ggc aaa ggc ttc agc	ttt agt tct gac tac	att ata cat cag aca	gtc	2059
Gly Lys Gly Phe Ser	Phe Ser Ser Asp Tyr	Ile Ile His Gln Thr	Val	
595	600	605	610	
cac act tgg aag aaa	ccc tat atg tgt agt	gtg tgt ggg aaa gca	ttc	2107
His Thr Trp Lys Lys	Pro Tyr Met Cys Ser	Val Cys Gly Lys Ala	Phe	
611	616	621	626	
agg ttt agc ttc cag	ctc agt cag cat cag	agt gtc cat agt gaa	gga	2155
Arg Phe Ser Phe Gln	Leu Ser Gln His Gln	Ser Val His Ser Glu	Gly	
627	632	637	642	
aaa tcc taa taatgag	aaagatatag aaaactctta	aggttaatgc caaaatggat		2211
Lys Ser *				
643				
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gagaaacatc caaaaatagc	tttgttttgt accaacagga	attagaaaat ataataaaaa		2391
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His Ala Tyr Val Ser Leu Asp Pro Leu Glu Arg Pro Pro Thr Thr Thr
2 7 12 17

aaa ttc gcg gcc gcg tcc gac cgc cgc cgc gcc gcc atc atg gac acc 151
Lys Phe Ala Ala Ala Ser Asp Arg Arg Arg Ala Ala Ile Met Asp Thr
18 23 28 33

agc cgt gtg cag cct atc aag ctg gcc agg gtc acc aag gtc ctg ggc 199
Ser Arg Val Gln Pro Ile Lys Leu Ala Arg Val Thr Lys Val Leu Gly
34 39 44 49

agg acc ggt tct cag gga cag tgc acg cag gtg cgc gtg gaa ttc atg 247
Arg Thr Gly Ser Gln Gly Gln Cys Thr Gln Val Arg Val Glu Phe Met
50 55 60 65

gac gac acg agc cga tcc atc atc cgc aat gta aaa ggc ccc gtg cgc 295
Asp Asp Thr Ser Arg Ser Ile Ile Arg Asn Val Lys Gly Pro Val Arg
66 71 76 81

gag ggc gac gtg ctc acc ctt ttg gag tca gag cga gaa gcc cgg agg 343
Glu Gly Asp Val Leu Thr Leu Leu Glu Ser Glu Arg Glu Ala Arg Arg
82 87 92 97

ttg cgc tga gcttggc tgctcgtgg gtcttggatg tcgggttcga ccacttggcc 399
Leu Arg *
98

gatgggaatg gtctgtcaca atctgtcct tttttttgtc cgccacacgt aactgagatg 459
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        Met Ala Asp Asp Ala Gly Ala Ala Gly Gly Pro Gly Gly Pro
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ggg ggc cct ggg atg ggg aac cgc ggt ggc ttc cgc gga ggt ttc ggc 156
Gly Gly Pro Gly Met Gly Asn Arg Gly Gly Phe Arg Gly Gly Phe Gly
 15              20              25              30

agt ggc atc cgg ggc cgg ggt cgc ggc cgt gga cgg ggc cgg ggc cga 204
Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 31              36              41              46

ggc cgc gga gct cgc gga ggc aag gcc gag gat aag gag tgg atg ccc 252
Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu Asp Lys Glu Trp Met Pro
 47              52              57              62

gtc acc aag ttg ggc cgc ttg gtc aag gac atg aag atc aag tcc ctg 300
Val Thr Lys Leu Gly Arg Leu Val Lys Asp Met Lys Ile Lys Ser Leu
 63              68              73              78

gag gag atc tat ctc ttc tcc ctg ccc att aag gaa tca gag atc att 348
Glu Glu Ile Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile
 79              84              89              94

gat ttc ttc ctg ggg gcc tct ctc aag gat gag gtt ttg aag att atg 396
Asp Phe Phe Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met
 95              100             105             110

cca gtg cag aag cag acc cgt gcc ggc cag cgc acc agg ttc aag gca 444
Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala
111              116             121             126

ttt gtt gct atc ggg gac tac aat ggc cac gtc ggt ctg ggt gtt aag 492
Phe Val Ala Ile Gly Asp Tyr Asn Gly His Val Gly Leu Gly Val Lys
127              132             137             142

tgc tcc aag gag gtg gcc acc gcc atc cgt ggg gcc atc atc ctg gcc 540
Cys Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala
143              148             153             158

aag ctc tcc atc gtc ccc gtg cgc aga ggc tac tgg ggg aac aag atc 588

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Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val	Thr	Gly	Arg	Cys	Gly	Ser	
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gtg	ctg	gta	cgc	ctc	atc	cct	gca	ccc	agg	ggc	act	ggc	atc	gtc	tcc	684
Val	Leu	Val	Arg	Leu	Ile	Pro	Ala	Pro	Arg	Gly	Thr	Gly	Ile	Val	Ser	
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Tyr	Thr	Ser	Ala	Arg	Gly	Cys	Thr	Ala	Thr	Leu	Gly	Asn	Phe	Ala	Lys	
223					228					233					238	
gcc	acc	ttt	gat	gcc	att	tct	aag	acc	tac	agc	tac	ctg	acc	ccc	gac	828
Ala	Thr	Phe	Asp	Ala	Ile	Ser	Lys	Thr	Tyr	Ser	Tyr	Leu	Thr	Pro	Asp	
239					244					249					254	
ctc	tgg	aag	gag	act	gta	ttc	acc	aag	tct	ccc	tat	cag	gag	ttc	act	876
Leu	Trp	Lys	Glu	Thr	Val	Phe	Thr	Lys	Ser	Pro	Tyr	Gln	Glu	Phe	Thr	
255					260					265					270	
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Asp	His	Leu	Val	Lys	Thr	His	Thr	Arg	Val	Ser	Val	Gln	Arg	Thr	Gln	
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gcatgagacc	gtgagacgag	agacgggtcg	gggccgccga	c	atg ttt ggc cgc	173
					Met Phe Gly Arg	

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Ser Arg Ser Trp Val Gly Gly Gly His Gly Lys Thr Ser Arg Asn Ile	
5 10 15 20	
cac tcc ttg gac cac ctc aag tat ctg tac cac gtt ttg acc aaa aac	269
His Ser Leu Asp His Leu Lys Tyr Leu Tyr His Val Leu Thr Lys Asn	
21 26 31 36	
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Thr Thr Val Thr Glu Gln Asn Arg Asn Leu Leu Val Glu Thr Ile Arg	
37 42 47 52	
tcc atc act gag atc ctg atc tgg gga gat caa aat gac agc tct gta	365
Ser Ile Thr Glu Ile Leu Ile Trp Gly Asp Gln Asn Asp Ser Ser Val	
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Phe Asp Phe Phe Leu Glu Lys Asn Met Phe Val Phe Phe Leu Asn Ile	
69 74 79 84	
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Leu Arg Gln Lys Ser Gly Arg Tyr Val Cys Val Gln Leu Leu Gln Thr	
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Leu Asn Ile Leu Phe Glu Asn Ile Ser His Glu Thr Ser Leu Tyr Tyr	
101 106 111 116	
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Phe Ser Asp Glu Glu Ile Met Ala Tyr Tyr Ile Ser Phe Leu Lys Thr	
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Leu Ser Leu Lys Leu Asn Asn His Thr Val His Phe Phe Tyr Asn Glu	
149 154 159 164	
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His Thr Asn Asp Phe Ala Leu Tyr Thr Glu Ala Ile Lys Phe Phe Asn	
165 170 175 180	
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His Pro Glu Ser Met Val Arg Ile Ala Val Arg Thr Ile Thr Leu Asn	
181 186 191 196	
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Val Tyr Lys Val Ser Leu Asp Asn Gln Ala Met Leu His Tyr Ile Arg	
197 202 207 212	
gat aaa act gct gtt cct tac ttc tcc aat ttg gtc tgg ttc att ggg	845
Asp Lys Thr Ala Val Pro Tyr Phe Ser Asn Leu Val Trp Phe Ile Gly	
213 218 223 228	

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Ser His Val Ile Glu Leu Asp Asp Cys Val Gln Thr Asp Glu Glu His	
229 234 239 244	
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Arg Asn Arg Gly Lys Leu Ser Asp Leu Val Ala Glu His Leu Asp His	
245 250 255 260	
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Leu His Tyr Leu Asn Asp Ile Leu Ile Ile Asn Cys Glu Phe Leu Asn	
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Asp Val Leu Thr Asp His Leu Leu Asn Arg Leu Phe Leu Pro Leu Tyr	
277 282 287 292	
gtg tac tca ctg gag aac cag gac aag gga gga gaa cgg ccg aaa att	1085
Val Tyr Ser Leu Glu Asn Gln Asp Lys Gly Gly Glu Arg Pro Lys Ile	
293 298 303 308	
agc ctg ccg gtg tct ctt tat ctt ctg tca cag gtc ttc tta att ata	1133
Ser Leu Pro Val Ser Leu Tyr Leu Leu Ser Gln Val Phe Leu Ile Ile	
309 314 319 324	
cat cat gca ccg ctg gtg aac tcg tta gct gaa gtc att ctg aat ggt	1181
His His Ala Pro Leu Val Asn Ser Leu Ala Glu Val Ile Leu Asn Gly	
325 330 335 340	
gat ctg tct gag atg tac gct aag act gaa cag gat att cag aga agt	1229
Asp Leu Ser Glu Met Tyr Ala Lys Thr Glu Gln Asp Ile Gln Arg Ser	
341 346 351 356	
tct gcc aag ccc agc att cgg tgc ttc att aaa ccc acc gag aca ctc	1277
Ser Ala Lys Pro Ser Ile Arg Cys Phe Ile Lys Pro Thr Glu Thr Leu	
357 362 367 372	
gag cgg tcc ctt gag atg aac aag cac aag ggc aag agg cgg gtg caa	1325
Glu Arg Ser Leu Glu Met Asn Lys His Lys Gly Lys Arg Arg Val Gln	
373 378 383 388	
aag aga ccc aac tac aaa aac gtt ggg gaa gaa gaa gat gag gag aaa	1373
Lys Arg Pro Asn Tyr Lys Asn Val Gly Glu Glu Glu Asp Glu Glu Lys	
389 394 399 404	
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Gly Pro Thr Glu Asp Ala Gln Glu Asp Ala Glu Lys Ala Lys Gly Thr	
405 410 415 420	
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Glu Gly Gly Ser Lys Gly Ile Lys Thr Ser Gly Glu Ser Glu Glu Ile	
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Glu Met Val Ile Met Glu Arg Ser Lys Leu Ser Glu Leu Ala Ala Ser	
437 442 447 452	
acc tcc gtg cag gag cag aac acc acg gac gag gag aaa agc gcc gcc	1565

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Ala	Thr	Cys	Ser	Glu	Ser	Thr	Gln	Trp	Ser	Arg	Pro	Phe	Leu	Asp	Met	
469					474					479					484	
gtg	tac	cac	gcg	ctg	gac	agc	ccg	gat	gat	gat	tac	cat	gcc	ctg	ttc	1661
Val	Tyr	His	Ala	Leu	Asp	Ser	Pro	Asp	Asp	Asp	Tyr	His	Ala	Leu	Phe	
485					490					495					500	
gtg	ctc	tgc	ctc	ctc	tat	gcc	atg	tct	cat	aat	aaa	ggc	atg	gat	cct	1709
Val	Leu	Cys	Leu	Leu	Tyr	Ala	Met	Ser	His	Asn	Lys	Gly	Met	Asp	Pro	
501					506					511					516	
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Glu	Lys	Leu	Glu	Arg	Ile	Gln	Leu	Pro	Val	Pro	Asn	Ala	Ala	Glu	Lys	
517					522					527					532	
acc	acc	tac	aac	cac	ccg	cta	gct	gaa	aga	ctc	atc	agg	atc	atg	aac	1805
Thr	Thr	Tyr	Asn	His	Pro	Leu	Ala	Glu	Arg	Leu	Ile	Arg	Ile	Met	Asn	
533					538					543					548	
aac	gct	gcc	cag	cca	gat	ggg	aag	atc	cgg	ctg	gcg	acg	ctg	gag	ctg	1853
Asn	Ala	Ala	Gln	Pro	Asp	Gly	Lys	Ile	Arg	Leu	Ala	Thr	Leu	Glu	Leu	
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agc	tgc	ctg	ctt	ctg	aag	cag	caa	gtc	ctg	atg	agt	gct	ggc	tgc	atc	1901
Ser	Cys	Leu	Leu	Leu	Lys	Gln	Gln	Val	Leu	Met	Ser	Ala	Gly	Cys	Ile	
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Met	Lys	Asp	Val	His	Leu	Ala	Cys	Leu	Glu	Gly	Ala	Arg	Glu	Glu	Ser	
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gtt	cac	ctt	gta	cga	cat	ttt	tat	aag	gga	gaa	gac	att	ttt	ttg	gac	1997
Val	His	Leu	Val	Arg	His	Phe	Tyr	Lys	Gly	Glu	Asp	Ile	Phe	Leu	Asp	
597					602					607					612	
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Met	Phe	Glu	Asp	Glu	Tyr	Arg	Ser	Met	Thr	Met	Lys	Pro	Met	Asn	Val	
613					618					623					628	
gaa	tat	ctc	atg	atg	gac	gcc	tcc	atc	ctg	ctg	ccc	cca	aca	ggc	acg	2093
Glu	Tyr	Leu	Met	Met	Asp	Ala	Ser	Ile	Leu	Leu	Pro	Pro	Thr	Gly	Thr	
629					634					639					644	
cca	ctg	acg	ggc	att	gac	ttc	gtg	aag	cgg	ctg	ccg	tgt	ggc	gat	gtg	2141
Pro	Leu	Thr	Gly	Ile	Asp	Phe	Val	Lys	Arg	Leu	Pro	Cys	Gly	Asp	Val	
645					650					655					660	
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Glu	Lys	Thr	Arg	Arg	Ala	Ile	Arg	Val	Phe	Phe	Met	Leu	Arg	Ser	Leu	
661					666					671					676	
tca	ctg	caa	ttg	cga	ggg	gag	cct	gag	aca	cag	ttg	ccg	ctg	act	cgg	2237
Ser	Leu	Gln	Leu	Arg	Gly	Glu	Pro	Glu	Thr	Gln	Leu	Pro	Leu	Thr	Arg	

677	682	687	692	
gag gag gac ctg atc	aag act gat gat gtc	ctg gat ctg aat aac agc		2285
Glu Glu Asp Leu Ile	Lys Thr Asp Asp Val	Leu Asp Leu Asn Asn Ser		
693	698	703	708	
gac ttg att gca tgt	aca gtg atc acc aag	gat ggc ggc atg gtc cag		2333
Asp Leu Ile Ala Cys	Thr Val Ile Thr Lys	Asp Gly Gly Met Val Gln		
709	714	719	724	
cga ttc ctg gct gtg	gat att tac cag atg	agt ttg gtg gag cct gat		2381
Arg Phe Leu Ala Val	Asp Ile Tyr Gln Met	Ser Leu Val Glu Pro Asp		
725	730	735	740	
gtg tcc agg ctt ggc	tgg gga gtg gtc aag	ttt gca ggc cta ttg cag		2429
Val Ser Arg Leu Gly	Trp Gly Val Val Lys	Phe Ala Gly Leu Leu Gln		
741	746	751	756	
gac atg cag gtg act	ggc gtg gag gac gac	agc cgt gcc ctg aac atc		2477
Asp Met Gln Val Thr	Gly Val Glu Asp Asp	Ser Arg Ala Leu Asn Ile		
757	762	767	772	
acc atc cac aag cct	gcg tcc agc ccc cat	tcc aag ccc ttc ccc atc		2525
Thr Ile His Lys Pro	Ala Ser Ser Pro His	Ser Lys Pro Phe Pro Ile		
773	778	783	788	
ctc cag gcc acc ttc	atc ttc tca gac cac	atc cgc tgc atc atc gcc		2573
Leu Gln Ala Thr Phe	Ile Phe Ser Asp His	Ile Arg Cys Ile Ile Ala		
789	794	799	804	
aag cag cgc ctg gcc	aaa ggc cgc atc cag	gca agg cgc atg aag atg		2621
Lys Gln Arg Leu Ala	Lys Gly Arg Ile Gln	Ala Arg Arg Met Lys Met		
805	810	815	820	
cag aga ata gct gcc	ctc ctg gac ctc cca	atc cag ccc acc act gaa		2669
Gln Arg Ile Ala Ala	Leu Leu Asp Leu Pro	Ile Gln Pro Thr Thr Glu		
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Val Leu Gly Phe Gly	Leu Gly Ser Ser Thr	Ser Thr Gln His Leu Pro		
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Phe Arg Phe Tyr Asp	Gln Gly Arg Arg Gly	Ser Ser Asp Pro Thr Val		
853	858	863	868	
cag cgc tcc gtg ttt	gca tcg gtg gac aag	gtg cca ggc ttc gcc gtg		2813
Gln Arg Ser Val Phe	Ala Ser Val Asp Lys	Val Pro Gly Phe Ala Val		
869	874	879	884	
gcc cag tgc ata aac	cag cac agc tcc ccg	tcc ctg tcc tca cag tcg		2861
Ala Gln Cys Ile Asn	Gln His Ser Ser Pro	Ser Leu Ser Ser Gln Ser		
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cca ccc tcc gcc agc	ggg agc ccc agc ggc	agc ggg agc acc agc cac		2909
Pro Pro Ser Ala Ser	Gly Ser Pro Ser Gly	Ser Gly Ser Thr Ser His		
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Cys Asp Ser Gly Gly Thr Ser Ser Ser Ser Thr Pro Ser Thr Ala Gln	
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Ser Pro Ala Asp Ala Pro Met Ser Pro Glu Leu Pro Lys Pro His Leu	
933 938 943 948	
cct gac cag ttg gta atc gtc aac gaa acg gaa gca gac tct aag ccc	3053
Pro Asp Gln Leu Val Ile Val Asn Glu Thr Glu Ala Asp Ser Lys Pro	
949 954 959 964	
agc aag aac gtg gcc agg agc gca gcc gtg gag aca gcc agc ctg tcc	3101
Ser Lys Asn Val Ala Arg Ser Ala Ala Val Glu Thr Ala Ser Leu Ser	
965 970 975 980	
ccc agc ctc gtc cct gcc cgg cag ccc acc att tcc ctg ctc tgc gag	3149
Pro Ser Leu Val Pro Ala Arg Gln Pro Thr Ile Ser Leu Leu Cys Glu	
981 986 991 996	
gac acg gct gac acg ctg agc gtc gaa tcg ctg acc ctt gtc ccc cca	3197
Asp Thr Ala Asp Thr Leu Ser Val Glu Ser Leu Thr Leu Val Pro Pro	
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Val Asp Pro His Ser Leu Arg Ser Leu Thr Gly Met Pro Pro Leu Ser	
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Thr Pro Ala Ala Ala Cys Thr Glu Pro Val Gly Glu Glu Ala Ala Cys	
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gccaaaaata ctgagtaact tcacattcag agggactgtt ttttctctct atatatagca	180

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Glu Leu Asp Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu				
30	35	40	45	
gct gca gag tac atc tcc acg gtg aag acg ctg tct cca gac cag cgc				433
Ala Ala Glu Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg				
46	51	56	61	
gtg gag cgc ctg cag aag atc cag aac gcc tac agc aag tgc aag gaa				481
Val Glu Arg Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu				
62	67	72	77	
tac agt gac gac aaa gtg cag ctg gcc atg cag acc tac gag atg gtg				529
Tyr Ser Asp Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val				
78	83	88	93	
gat aaa cac att cga agg ctt gat gca gac ctg gcg cgc ttt gaa gca				577
Asp Lys His Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala				
94	99	104	109	
gat ctg aag gac aag atg gag ggc agt gat ttt gaa agc tcc gga ggg				625
Asp Leu Lys Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly				
110	115	120	125	
cga ggg tta aaa aaa ggc ctg cgt cag aaa gaa aaa aga ggg tcc cgg				673
Arg Gly Leu Lys Lys Gly Leu Arg Gln Lys Glu Lys Arg Gly Ser Arg				
126	131	136	141	
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Gly Arg Gly Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys				
142	147	152	157	
cac aaa gga ggg tct gag ttc act gac acc atc ctg tcc gtg cac ccc				769
His Lys Gly Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro				
158	163	168	173	
tct gat gtg ctg gac atg ccc gtg gac cca aac gaa ccc acg tac tgc				817
Ser Asp Val Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys				
174	179	184	189	
ctg tgc cac cag gtc tcc tat ggg gag atg att ggc tgt gac aat cca				865
Leu Cys His Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro				
190	195	200	205	
gac tgt cca att gag tgg ttt cac ttt gcc tgc gtg gac ctt acc acg				913
Asp Cys Pro Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr				
206	211	216	221	
aaa ccc aaa gga aaa tga tttcat ttaaataaaa acctgtagtc tgggcaacat				967
Lys Pro Lys Gly Lys *				
222	227			
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Met Pro Ala Val Arg Val Trp Asp
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Val Ala Glu His Ser Gln Val Ala Glu Leu Gln Glu His Lys Tyr Gly
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Val Ala Cys Val Ala Phe Ser Pro Ser Ala Lys Tyr Ile Val Ser Val
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Gly Tyr Gln His Asp Met Ile Val Asn Val Trp Ala Trp Lys Lys Asn
41 46 51 56
att gtg gtg gcc tcc aac aag gtg tcc agt cgg gtg aca gca gtg tcc 303
Ile Val Val Ala Ser Asn Lys Val Ser Ser Arg Val Thr Ala Val Ser
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Phe Ser Glu Asp Cys Ser Tyr Phe Val Thr Ala Gly Asn Arg His Ile
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Lys Phe Trp Tyr Leu Asp Asp Ser Lys Thr Ser Lys Val Asn Ala Thr
89 94 99 104

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Val Pro Leu Leu Gly Arg Ser Gly Leu Leu Gly Glu Leu Arg Asn Asn	
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Leu Phe Thr Asp Val Ala Cys Gly Arg Gly Lys Lys Ala Asp Ser Thr	
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Phe Cys Ile Thr Ser Ser Gly Leu Leu Cys Glu Phe Ser Asp Arg Arg	
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Ser Thr Leu His Arg Asn Ile Leu Ser Ser Asp Leu Ile Lys Ile Ile	
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Tyr Val Asp Gly Asn Thr Gln Ala Leu Leu Asp Thr Glu Leu Pro Gly	
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Ser Val Cys Val Ser Pro Asn Gly Gln His Leu Ala Ser Gly Asp Arg	
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Met Gly Thr Leu Arg Val His Glu Leu Gln Ser Leu Ser Glu Met Leu	
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Lys Val Glu Ala His Asp Ser Glu Ile Leu Cys Leu Glu Tyr Ser Lys	
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Pro Asp Thr Gly Leu Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu	
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Ile His Val Leu Asp Ala Gly Arg Glu Tyr Ser Leu Gln Gln Thr Leu	
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Trp Lys Tyr Thr Ala Ile Gly Cys Gln Asp Arg Asn Ile Arg Ile Phe	
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Glu Asp Gly Thr Leu Ile Lys Val Gln Thr Asp Pro Ser Gly Ile Tyr	
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Ile Ala Thr Ser Cys Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser	
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Ser Gly Glu Cys Val Ala Thr Met Phe Gly His Ser Glu Ile Val Thr	
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Gly Met Lys Phe Ser Asn Asp Cys Lys His Leu Ile Ser Val Ser Gly	
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Asp Ser Cys Ile Phe Val Trp Arg Leu Ser Ser Glu Met Thr Ile Ser	
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Pro Val Leu Ala Lys	Ser Thr Lys Lys Ala	Leu Ala Ser Val Pro Ser	
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Pro Ala Leu Pro Arg	Ser Leu Ser His Trp	Glu Met Ser Arg Ala Gln	
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Asp Pro Ser Gln Asp	Ser Leu Ala Ile Ile	Pro Ser Gly Pro Arg Lys	
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His Gly Gln Glu Ala	Leu Glu Thr Ser Leu	Thr Ser Gln Asn Glu Lys	
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ccc cct cgg cct cag	gct tcc caa cct tgt	tcc tat ccc cat att atc	2175
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Pro Gln Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr				
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356 361 366 371	
gac aag cca gaa ata ggg cct caa gtg gtt ggg aat ttg ttt ctc gaa	1326
Asp Lys Pro Glu Ile Gly Pro Gln Val Val Gly Asn Leu Phe Leu Glu	
372 377 382 387	
gtc atc agg gcc ttt tat tct tac tgc aga gat gcc ctt ggc tct gat	1374
Val Ile Arg Ala Phe Tyr Ser Tyr Cys Arg Asp Ala Leu Gly Ser Asp	
388 393 398 403	
ctt aaa ctt agc tac acc cag agt gga aat tcg ctg ata agt gca atc	1422
Leu Lys Leu Ser Tyr Thr Gln Ser Gly Asn Ser Leu Ile Ser Ala Ile	
404 409 414 419	
aag gaa aac aga aat gcc tct gag att gtc aaa acg gta aat ttg ctg	1470
Lys Glu Asn Arg Asn Ala Ser Glu Ile Val Lys Thr Val Asn Leu Leu	
420 425 430 435	
ata act tct cta agc aca gac ttt ctc tgg gat tat atg aca agg tgt	1518
Ile Thr Ser Leu Ser Thr Asp Phe Leu Trp Asp Tyr Met Thr Arg Cys	
436 441 446 451	
ttt gag gaa tgc ttt aga cca gtg aag cag cgt tac agc gtg agg aac	1566
Phe Glu Glu Cys Phe Arg Pro Val Lys Gln Arg Tyr Ser Val Arg Asn	
452 457 462 467	
agc gtc agc cct ccc ccc acg gtc tcg gag ctc tgc gcc ctc ctg gtc	1614
Ser Val Ser Pro Pro Thr Val Ser Glu Leu Cys Ala Leu Leu Val	
468 473 478 483	
ttc ctg ctg gat gtc att cct ttg gaa ctt tac tct gag gtg cat acc	1662
Phe Leu Leu Asp Val Ile Pro Leu Glu Leu Tyr Ser Glu Val His Thr	
484 489 494 499	
cag tat ctc cct cag gtg ctc ggc tgc ctg gtg cag cct ctt gct gag	1710
Gln Tyr Leu Pro Gln Val Leu Gly Cys Leu Val Gln Pro Leu Ala Glu	
500 505 510 515	
gac atg gag gcc tta agt tta cct gaa ctc acg cat gcc ttg aag acg	1758
Asp Met Glu Ala Leu Ser Leu Pro Glu Leu Thr His Ala Leu Lys Thr	
516 521 526 531	
tgt ttc aag gtg ctc agc aaa gtc cag atg cct cct tcc tac ctc gac	1806

Cys	Phe	Lys	Val	Leu	Ser	Lys	Val	Gln	Met	Pro	Pro	Ser	Tyr	Leu	Asp	
532					537					542					547	
acg	gag	tcc	acc	agc	gga	acc	tcg	agt	cca	gta	aaa	ggg	gaa	aac	ggc	1854
Thr	Glu	Ser	Thr	Ser	Gly	Thr	Ser	Ser	Pro	Val	Lys	Gly	Glu	Asn	Gly	
548					553					558					563	
aaa	ata	att	ttg	gaa	aca	aag	gca	gtg	att	ccc	ggg	gac	gaa	gat	gct	1902
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ala	Val	Ile	Pro	Gly	Asp	Glu	Asp	Ala	
564					569					574					579	
tcg	ttt	ccc	cct	ctg	aag	tct	gag	gac	agt	ggg	atc	ggg	ctc	agt	gcc	1950
Ser	Phe	Pro	Pro	Leu	Lys	Ser	Glu	Asp	Ser	Gly	Ile	Gly	Leu	Ser	Ala	
580					585					590					595	
tcg	tca	ccg	gag	ctc	tct	gag	cac	ttg	agg	ggt	cct	cga	ggt	tct	ctg	1998
Ser	Ser	Pro	Glu	Leu	Ser	Glu	His	Leu	Arg	Val	Pro	Arg	Val	Ser	Leu	
596					601					606					611	
gaa	agg	gac	gac	gtt	tgg	aag	aag	ggc	ggg	agc	atg	cag	agg	acg	ttt	2046
Glu	Arg	Asp	Asp	Val	Trp	Lys	Lys	Gly	Gly	Ser	Met	Gln	Arg	Thr	Phe	
612					617					622					627	
ctt	tgc	atc	caa	gag	cta	atc	gcc	aac	ttt	gcc	agc	aag	aac	att	ttt	2094
Leu	Cys	Ile	Gln	Glu	Leu	Ile	Ala	Asn	Phe	Ala	Ser	Lys	Asn	Ile	Phe	
628					633					638					643	
gga	gta	cag	ctg	aca	gcg	tca	gga	gaa	gaa	agc	aag	tcc	gag	gag	cct	2142
Gly	Val	Gln	Leu	Thr	Ala	Ser	Gly	Glu	Glu	Ser	Lys	Ser	Glu	Glu	Pro	
644					649					654					659	
gca	ggg	aag	agg	gac	agg	gat	ggg	acg	cag	agc	ctg	gca	gcc	aat	gat	2190
Ala	Gly	Lys	Arg	Asp	Arg	Asp	Gly	Thr	Gln	Ser	Leu	Ala	Ala	Asn	Asp	
660					665					670					675	
tcc	agc	agg	aag	aac	tct	tgg	gag	ccc	aag	ccc	atc	act	gtg	cct	cag	2238
Ser	Ser	Arg	Lys	Asn	Ser	Trp	Glu	Pro	Lys	Pro	Ile	Thr	Val	Pro	Gln	
676					681					686					691	
ttc	aag	cag	atg	ctg	tca	gac	ttg	ttc	aca	gca	cga	ggg	tct	cca	ttc	2286
Phe	Lys	Gln	Met	Leu	Ser	Asp	Leu	Phe	Thr	Ala	Arg	Gly	Ser	Pro	Phe	
692					697					702					707	
aag	aca	aaa	agt	tca	gag	tca	cca	tcg	tct	tcg	ccc	agc	agc	cct	gcc	2334
Lys	Thr	Lys	Ser	Ser	Glu	Ser	Pro	Ser	Ser	Ser	Pro	Ser	Ser	Pro	Ala	
708					713					718					723	
agg	aaa	aac	ggg	gga	gaa	tgg	gat	gtt	gag	aag	gtg	gtc	att	gac	ctg	2382
Arg	Lys	Asn	Gly	Gly	Glu	Trp	Asp	Val	Glu	Lys	Val	Val	Ile	Asp	Leu	
724					729					734					739	
ggg	ggg	tcc	agg	gag	gaa	cgc	agg	gag	gcc	ttt	gcc	gcc	gcc	tgc	cac	2430
Gly	Gly	Ser	Arg	Glu	Glu	Arg	Arg	Glu	Ala	Phe	Ala	Ala	Ala	Cys	His	
740					745					750					755	
ctg	ctg	ctg	gat	tgt	gcc	act	ttc	cct	gtc	tac	ctg	tcc	gag	gaa	gag	2478
Leu	Leu	Leu	Asp	Cys	Ala	Thr	Phe	Pro	Val	Tyr	Leu	Ser	Glu	Glu	Glu	

756	761	766	771	
acc gag cag ctc tgt gca acg ctc ttc cag ctg cca gga gcc ggt gat				2526
Thr Glu Gln Leu Cys Ala Thr Leu Phe Gln Leu Pro Gly Ala Gly Asp				
772	777	782	787	
tcc agt ttt cca tct tgg ctg aag tcc ctc atg act att tgc tgc tgt				2574
Ser Ser Phe Pro Ser Trp Leu Lys Ser Leu Met Thr Ile Cys Cys Cys				
788	793	798	803	
gtg act gac tgc tac ctc cag aac gtg gcc att tcc act ctg ctg gaa				2622
Val Thr Asp Cys Tyr Leu Gln Asn Val Ala Ile Ser Thr Leu Leu Glu				
804	809	814	819	
gtg ata aac cat tcc cag tcc ctg gcg ctt gtc att gaa gac aag atg				2670
Val Ile Asn His Ser Gln Ser Leu Ala Leu Val Ile Glu Asp Lys Met				
820	825	830	835	
aaa cgc tat aag agc tct gga cac aac cct ttt ttt ggc aag ctg cag				2718
Lys Arg Tyr Lys Ser Ser Gly His Asn Pro Phe Phe Gly Lys Leu Gln				
836	841	846	851	
atg gtg acg gtt cct ccc att gct cca ggg ata ttg aaa gtc att gca				2766
Met Val Thr Val Pro Pro Ile Ala Pro Gly Ile Leu Lys Val Ile Ala				
852	857	862	867	
gag aaa aca gat ttc tat cag agg gtg gct cgc gtg ctt tgg aat cag				2814
Glu Lys Thr Asp Phe Tyr Gln Arg Val Ala Arg Val Leu Trp Asn Gln				
868	873	878	883	
ctg aac aaa gag acc cgg gag cat cac gtc acc tgc gta gaa ttg ttc				2862
Leu Asn Lys Glu Thr Arg Glu His His Val Thr Cys Val Glu Leu Phe				
884	889	894	899	
tac cgg ctg cac tgc ctg gcc cct acg gcc aac atc tgc gag gac atc				2910
Tyr Arg Leu His Cys Leu Ala Pro Thr Ala Asn Ile Cys Glu Asp Ile				
900	905	910	915	
atc tgc cat gcc ctc ctg gac cct gac aag gga aca agg ctg gaa gct				2958
Ile Cys His Ala Leu Leu Asp Pro Asp Lys Gly Thr Arg Leu Glu Ala				
916	921	926	931	
ctg ttt aga ttt tcc gtg atc tgg cat ctg aca aga gag atc caa ggc				3006
Leu Phe Arg Phe Ser Val Ile Trp His Leu Thr Arg Glu Ile Gln Gly				
932	937	942	947	
agt cga gta aca tct cac aat cgc tcc ttt gat agg tcc ttg ttt gtc				3054
Ser Arg Val Thr Ser His Asn Arg Ser Phe Asp Arg Ser Leu Phe Val				
948	953	958	963	
gtg ctg gac agc ctg gcc tgc acg gat ggt gcc atc ggt gcg gca gcc				3102
Val Leu Asp Ser Leu Ala Cys Thr Asp Gly Ala Ile Gly Ala Ala Ala				
964	969	974	979	
cag ggc tgg ctg gtg cgt gcg ctc tcc ctc ggg gac gtg gct cgc atc				3150
Gln Gly Trp Leu Val Arg Ala Leu Ser Leu Gly Asp Val Ala Arg Ile				
980	985	990	995	

ctc gaa ccc gtg ctc ctg ctg ctg ctg cag cca aaa acc cag aga acc	3198
Leu Glu Pro Val Leu Leu Leu Leu Leu Gln Pro Lys Thr Gln Arg Thr	
996 1001 1006 1011	
tcc atc cac tgc ctc aag cag gag aac tcg gcc gat gac ttg cac cgt	3246
Ser Ile His Cys Leu Lys Gln Glu Asn Ser Ala Asp Asp Leu His Arg	
1012 1017 1022 1027	
tgg ttt aac agg aag aaa acc tct ttc aga gag gca tgc gca gtg ccc	3294
Trp Phe Asn Arg Lys Lys Thr Ser Phe Arg Glu Ala Cys Ala Val Pro	
1028 1033 1038 1043	
gag cct cag gag agc ggc tct gaa gag cac ctg cct ctg agc cag ttc	3342
Glu Pro Gln Glu Ser Gly Ser Glu Glu His Leu Pro Leu Ser Gln Phe	
1044 1049 1054 1059	
acc aca gtg gac cgt gaa gcc att tgg gcc gaa gtg gag aag gag ccc	3390
Thr Thr Val Asp Arg Glu Ala Ile Trp Ala Glu Val Glu Lys Glu Pro	
1060 1065 1070 1075	
gag aag tac ccg ctg cga ggc gag ctg agc gag gaa gag ctg ccc tac	3438
Glu Lys Tyr Pro Leu Arg Gly Glu Leu Ser Glu Glu Leu Pro Tyr	
1076 1081 1086 1091	
tac gtg gag ctt cca gac agg acg gcc cac ggc gcc ccg gac agc agc	3486
Tyr Val Glu Leu Pro Asp Arg Thr Ala His Gly Ala Pro Asp Ser Ser	
1092 1097 1102 1107	
gag cac acc gag tct gca gat aca agc tcc ggc cac acg gac agc gag	3534
Glu His Thr Glu Ser Ala Asp Thr Ser Ser Gly His Thr Asp Ser Glu	
1108 1113 1118 1123	
aac acg tcc tcc ttc tcc tcc cct tcc cac gac ctg cag gag ctg agc	3582
Asn Thr Ser Ser Phe Ser Ser Pro Ser His Asp Leu Gln Glu Leu Ser	
1124 1129 1134 1139	
aac gaa gag aac tgc tgt gca ccc atc cac atg ggg ggc agg gcg tac	3630
Asn Glu Glu Asn Cys Cys Ala Pro Ile His Met Gly Gly Arg Ala Tyr	
1140 1145 1150 1155	
ccc aag cgc tcg gcc ctg ctg gcg gcc ttc cag tca gaa agc ttc aag	3678
Pro Lys Arg Ser Ala Leu Leu Ala Ala Phe Gln Ser Glu Ser Phe Lys	
1156 1161 1166 1171	
gct ggg gcc aag tta agc ctg gtg cgg gtg gac tcg gac aag acg cag	3726
Ala Gly Ala Lys Leu Ser Leu Val Arg Val Asp Ser Asp Lys Thr Gln	
1172 1177 1182 1187	
gct tct gag tcg ttc tcc agc gac gag gag gcg gac ttg gag ctc cag	3774
Ala Ser Glu Ser Phe Ser Ser Asp Glu Glu Ala Asp Leu Glu Leu Gln	
1188 1193 1198 1203	
gcc ctc acc aca tcc agg ctg cta aag cag cag cgg gaa agg cag gag	3822
Ala Leu Thr Thr Ser Arg Leu Leu Lys Gln Gln Arg Glu Arg Gln Glu	
1204 1209 1214 1219	

gcc gtc gag gcc ttg ttc aag cac atc ctg ctc tac ctg cag ccc tac	3870
Ala Val Glu Ala Leu Phe Lys His Ile Leu Leu Tyr Leu Gln Pro Tyr	
1220 1225 1230 1235	
gac tct cgg cgg gtc ctc tat gcc ttc tcg gtg ctg gag gct gtg ctc	3918
Asp Ser Arg Arg Val Leu Tyr Ala Phe Ser Val Leu Glu Ala Val Leu	
1236 1241 1246 1251	
aaa acc aac cct aag gaa ttc atc gag gct gtg tcc agg act agc atg	3966
Lys Thr Asn Pro Lys Glu Phe Ile Glu Ala Val Ser Arg Thr Ser Met	
1252 1257 1262 1267	
gat acc agc tcc acc gcg cac ctc aac ctc atc tcc aac ctc ctc gct	4014
Asp Thr Ser Ser Thr Ala His Leu Asn Leu Ile Ser Asn Leu Leu Ala	
1268 1273 1278 1283	
cgc cac cag gag gcc ctc att ggc cag agt ttc tac gga aag ctc cag	4062
Arg His Gln Glu Ala Leu Ile Gly Gln Ser Phe Tyr Gly Lys Leu Gln	
1284 1289 1294 1299	
acc cag gtc ccc aac gtg tgc ccc cac tct ctg ctc ctg gag ctg ctc	4110
Thr Gln Val Pro Asn Val Cys Pro His Ser Leu Leu Leu Glu Leu Leu	
1300 1305 1310 1315	
acc tac ctc tgc ctg agc ttc ctg cgc tcc tac tac cct tgc tat ttg	4158
Thr Tyr Leu Cys Leu Ser Phe Leu Arg Ser Tyr Tyr Pro Cys Tyr Leu	
1316 1321 1326 1331	
aag gtc tcg cac cga gac att ctc ggc aac cgg gac gtg cag gtc aaa	4206
Lys Val Ser His Arg Asp Ile Leu Gly Asn Arg Asp Val Gln Val Lys	
1332 1337 1342 1347	
agt gtc gag gtt ttg atc agg ata atg atg cag ctg gtc tca gtg gcc	4254
Ser Val Glu Val Leu Ile Arg Ile Met Met Gln Leu Val Ser Val Ala	
1348 1353 1358 1363	
aag tct tcg gaa ggg aag aac gtg gag ttc atc cac agc ttg ctg cag	4302
Lys Ser Ser Glu Gly Lys Asn Val Glu Phe Ile His Ser Leu Leu Gln	
1364 1369 1374 1379	
agg tgc aaa gtt cag gag ttt gtc ctg ctc tcc ctg tcg gcg tcc atg	4350
Arg Cys Lys Val Gln Glu Phe Val Leu Leu Ser Leu Ser Ala Ser Met	
1380 1385 1390 1395	
tac acg agc cag aag cgc tac ggg ctg gcc acc gcc cac cac ggc agg	4398
Tyr Thr Ser Gln Lys Arg Tyr Gly Leu Ala Thr Ala His His Gly Arg	
1396 1401 1406 1411	
gcc ctg cca gag gac agc ctc ttt gag gag agt ctc att aac ttg ggt	4446
Ala Leu Pro Glu Asp Ser Leu Phe Glu Glu Ser Leu Ile Asn Leu Gly	
1412 1417 1422 1427	
cag gac cag atc tgg agt gag cac ccg ctg cag att gag ctg ctg aag	4494
Gln Asp Gln Ile Trp Ser Glu His Pro Leu Gln Ile Glu Leu Leu Lys	
1428 1433 1438 1443	
ctg ctg cag gtg ctg att gtc ttg gaa cac cac ctg ggt cgg gcc cat	4542

Leu	Leu	Gln	Val	Leu	Ile	Val	Leu	Glu	His	His	Leu	Gly	Arg	Ala	His	
1444					1449				1454						1459	
gag	gag	gag	gaa	aac	cag	ccc	gac	ctg	tcc	cgg	gag	tgg	cag	aga	gcc	4590
Glu	Glu	Ala	Glu	Asn	Gln	Pro	Asp	Leu	Ser	Arg	Glu	Trp	Gln	Arg	Ala	
1460				1465				1470							1475	
ctg	aac	ttc	cag	cag	gcc	atc	agc	gcc	ctg	cag	tac	gtg	cag	ccc	cac	4638
Leu	Asn	Phe	Gln	Gln	Ala	Ile	Ser	Ala	Leu	Gln	Tyr	Val	Gln	Pro	His	
1476				1481				1486							1491	
ccc	ctc	acc	tcc	cag	ggg	ctt	ctg	gtc	tct	gcg	gtg	gtg	agg	ggg	ctg	4686
Pro	Leu	Thr	Ser	Gln	Gly	Leu	Leu	Val	Ser	Ala	Val	Val	Arg	Gly	Leu	
1492				1497				1502							1507	
cag	ccc	gcc	tac	ggg	tac	ggc	atg	cat	ccg	gcc	tgg	gtg	agc	ttg	gtc	4734
Gln	Pro	Ala	Tyr	Gly	Tyr	Gly	Met	His	Pro	Ala	Trp	Val	Ser	Leu	Val	
1508				1513				1518							1523	
acg	cat	tcc	ttg	ccc	tac	ttc	gga	aag	tcc	ctg	ggc	tgg	acg	gtg	aca	4782
Thr	His	Ser	Leu	Pro	Tyr	Phe	Gly	Lys	Ser	Leu	Gly	Trp	Thr	Val	Thr	
1524				1529				1534							1539	
ccc	ttt	gtt	gtc	cag	att	tgc	aaa	aac	ttg	gat	gac	ttg	gtc	aag	cag	4830
Pro	Phe	Val	Val	Gln	Ile	Cys	Lys	Asn	Leu	Asp	Asp	Leu	Val	Lys	Gln	
1540				1545				1550							1555	
tat	gaa	agc	gaa	tct	gtg	aag	ctc	tct	gtc	agc	aca	acc	tcc	aag	agg	4878
Tyr	Glu	Ser	Glu	Ser	Val	Lys	Leu	Ser	Val	Ser	Thr	Thr	Ser	Lys	Arg	
1556				1561				1566							1571	
gaa	aac	att	tct	cca	gat	tat	cca	ctc	acc	ctt	cta	gaa	ggg	cta	acg	4926
Glu	Asn	Ile	Ser	Pro	Asp	Tyr	Pro	Leu	Thr	Leu	Leu	Glu	Gly	Leu	Thr	
1572				1577				1582							1587	
acc	att	agt	cat	ttt	tgt	ctt	ttg	gaa	caa	gcc	aac	caa	aac	aaa	aag	4974
Thr	Ile	Ser	His	Phe	Cys	Leu	Leu	Glu	Gln	Ala	Asn	Gln	Asn	Lys	Lys	
1588				1593				1598							1603	
acc	atg	gct	gca	ggg	gat	cct	gcc	aac	ttg	agg	aat	gcc	aga	aat	gcc	5022
Thr	Met	Ala	Ala	Gly	Asp	Pro	Ala	Asn	Leu	Arg	Asn	Ala	Arg	Asn	Ala	
1604				1609				1614							1619	
att	ttg	gaa	gag	ctg	cct	cga	act	gtt	aac	acc	atg	gcc	ctt	ctc	tgg	5070
Ile	Leu	Glu	Glu	Leu	Pro	Arg	Thr	Val	Asn	Thr	Met	Ala	Leu	Leu	Trp	
1620				1625				1630							1635	
aat	gtt	ctc	gga	aag	gag	gag	act	caa	aag	aga	cct	gtc	gat	ctc	cta	5118
Asn	Val	Leu	Gly	Lys	Glu	Glu	Thr	Gln	Lys	Arg	Pro	Val	Asp	Leu	Leu	
1636				1641				1646							1651	
ggg	gcc	gag	aag	gga	tcc	tct	tcc	gtt	tac	ttt	aaa	acc	acc	aaa	acc	5166
Gly	Ala	Ala	Lys	Gly	Ser	Ser	Ser	Val	Tyr	Phe	Lys	Thr	Thr	Lys	Thr	
1652				1657				1662							1667	
ata	aga	caa	aaa	att	tta	gac	ttc	tta	aac	ccc	ttg	acg	gcc	cat	ctt	5214
Ile	Arg	Gln	Lys	Ile	Leu	Asp	Phe	Leu	Asn	Pro	Leu	Thr	Ala	His	Leu	

1668	1673	1678	1683	
ggg gtt cag ttg aca gcg gct gtt gcg gca gtg tgg agc aga aag aaa				5262
Gly Val Gln Leu Thr Ala Ala Val Ala Ala Val Trp Ser Arg Lys Lys				
1684	1689	1694	1699	
gcc cag cgt cac agt aag atg aag att atc cca acg gca agt gca tcc				5310
Ala Gln Arg His Ser Lys Met Lys Ile Ile Pro Thr Ala Ser Ala Ser				
1700	1705	1710	1715	
cag cta acc ctt gtc gac ttg gtg tgt gca ctc agc acc ctg cag act				5358
Gln Leu Thr Leu Val Asp Leu Val Cys Ala Leu Ser Thr Leu Gln Thr				
1716	1721	1726	1731	
gac acg ctg ctg cac ctg gtg aag gag gtg gtg aag agg cca ccc caa				5406
Asp Thr Leu Leu His Leu Val Lys Glu Val Val Lys Arg Pro Pro Gln				
1732	1737	1742	1747	
gtc aaa ggg ggt gat gag aaa tcg ccc cta gtg gac att cct gtg ttg				5454
Val Lys Gly Gly Asp Glu Lys Ser Pro Leu Val Asp Ile Pro Val Leu				
1748	1753	1758	1763	
cag ttt tgc tat gct ttt ctc caa agg ctc cca gta cca gcc ttg caa				5502
Gln Phe Cys Tyr Ala Phe Leu Gln Arg Leu Pro Val Pro Ala Leu Gln				
1764	1769	1774	1779	
gag aac ttt tct tca ctg ttg gga gta ttg aaa gag tct gta cag ttg				5550
Glu Asn Phe Ser Ser Leu Leu Gly Val Leu Lys Glu Ser Val Gln Leu				
1780	1785	1790	1795	
aat cta gcc cca cct ggg tat ttt ctg ctt ctc agc atg ctg aat gac				5598
Asn Leu Ala Pro Pro Gly Tyr Phe Leu Leu Leu Ser Met Leu Asn Asp				
1796	1801	1806	1811	
ttt gta aca aga act ccc aac ctg gaa aac aag aag gac caa aaa gac				5646
Phe Val Thr Arg Thr Pro Asn Leu Glu Asn Lys Lys Asp Gln Lys Asp				
1812	1817	1822	1827	
ctg cag gaa atc act cag aaa atc cta gaa gct gtg ggg aac att gcc				5694
Leu Gln Glu Ile Thr Gln Lys Ile Leu Glu Ala Val Gly Asn Ile Ala				
1828	1833	1838	1843	
ggc tct tcc ttg gag caa acc agc tgg cta agc aga aac ctg gaa gtg				5742
Gly Ser Ser Leu Glu Gln Thr Ser Trp Leu Ser Arg Asn Leu Glu Val				
1844	1849	1854	1859	
aag gcc caa cct cag gcc tct cta gaa gaa tct gat gct gag gag gac				5790
Lys Ala Gln Pro Gln Ala Ser Leu Glu Glu Ser Asp Ala Glu Glu Asp				
1860	1865	1870	1875	
ctg tat gat gct gct gca gct tca gca atg gtg tct tca tcc gcc ccg				5838
Leu Tyr Asp Ala Ala Ala Ala Ser Ala Met Val Ser Ser Ser Ala Pro				
1876	1881	1886	1891	
tcg gtg tac agc gtg caa gcc ctc tct ctc ctg gca gag gta ctg gct				5886
Ser Val Tyr Ser Val Gln Ala Leu Ser Leu Leu Ala Glu Val Leu Ala				
1892	1897	1902	1907	

tcc ctc ctg gac atg gtt tat cga agt gat gag aag gag aaa gct gtg Ser Leu Leu Asp Met Val Tyr Arg Ser Asp Glu Lys Glu Lys Ala Val 1908 1913 1918 1923	5934
ccg tta atc tcc cgt ctg ctt tac tat gtt ttt cca tac tta cgc aac Pro Leu Ile Ser Arg Leu Leu Tyr Tyr Val Phe Pro Tyr Leu Arg Asn 1924 1929 1934 1939	5982
cac agt gcc tac aat gct ccc agc ttc cgg gct ggc gct cag ctg ctg His Ser Ala Tyr Asn Ala Pro Ser Phe Arg Ala Gly Ala Gln Leu Leu 1940 1945 1950 1955	6030
agc tcc ctg agt ggc tat gcc tac aca aag cga gcc tgg agg aag gag Ser Ser Leu Ser Gly Tyr Ala Tyr Thr Lys Arg Ala Trp Arg Lys Glu 1956 1961 1966 1971	6078
gtc ctg gag ctg ttt ctc gac ccc gct ttc ttt cag atg gat act tcc Val Leu Glu Leu Phe Leu Asp Pro Ala Phe Phe Gln Met Asp Thr Ser 1972 1977 1982 1987	6126
tgt gtt cat tgg aag tcc att att gac cat ctt ttg act cat gag aaa Cys Val His Trp Lys Ser Ile Ile Asp His Leu Leu Thr His Glu Lys 1988 1993 1998 2003	6174
aca atg ttt aag gat tta atg aac atg cag agc agt tct ttg aaa cta Thr Met Phe Lys Asp Leu Met Asn Met Gln Ser Ser Ser Leu Lys Leu 2004 2009 2014 2019	6222
ttc tca agt ttt gaa cag aaa gcc atg ctg tta aag cgc cag gct ttt Phe Ser Ser Phe Glu Gln Lys Ala Met Leu Leu Lys Arg Gln Ala Phe 2020 2025 2030 2035	6270
gct gtc ttc agt gga gaa ctt gat caa tac cac ctt tac ctt cca ctg Ala Val Phe Ser Gly Glu Leu Asp Gln Tyr His Leu Tyr Leu Pro Leu 2036 2041 2046 2051	6318
ata caa gaa cgc ctg aca gac aat ctc aga gtt gga cag aca tcc ata Ile Gln Glu Arg Leu Thr Asp Asn Leu Arg Val Gly Gln Thr Ser Ile 2052 2057 2062 2067	6366
gtt gct gct cag atg ttt ctt ttt ttc aga gtt ttg ctg cta aga ata Val Ala Ala Gln Met Phe Leu Phe Phe Arg Val Leu Leu Leu Arg Ile 2068 2073 2078 2083	6414
tct cct caa cat ttg act tca ttg tgg cca ata atg gtc tct gaa ttg Ser Pro Gln His Leu Thr Ser Leu Trp Pro Ile Met Val Ser Glu Leu 2084 2089 2094 2099	6462
att cag aca ttc aca cag ctt gaa gaa gat cta aaa gat gaa gat gag Ile Gln Thr Phe Thr Gln Leu Glu Glu Asp Leu Lys Asp Glu Asp Glu 2100 2105 2110 2115	6510
tca ttg aga agc acc aac aaa gta aac aga acg aaa gtt tca gtc ccg Ser Leu Arg Ser Thr Asn Lys Val Asn Arg Thr Lys Val Ser Val Pro 2116 2121 2126 2131	6558

gat gca aat gga ccc tca gtg ggg gag ata ccc cag agt gaa ctc atc	6606
Asp Ala Asn Gly Pro Ser Val Gly Glu Ile Pro Gln Ser Glu Leu Ile	
2132 2137 2142 2147	
ttg tat tta tca gct tgc aaa ttc ttg gac aca gcg ctt tct ttt cca	6654
Leu Tyr Leu Ser Ala Cys Lys Phe Leu Asp Thr Ala Leu Ser Phe Pro	
2148 2153 2158 2163	
cct gac aag atg cca tta ttt caa att tat agg tgg gca ttt att cca	6702
Pro Asp Lys Met Pro Leu Phe Gln Ile Tyr Arg Trp Ala Phe Ile Pro	
2164 2169 2174 2179	
gaa gtg gac aca gag ggc cct gcc ttc ctg tgc gat gta gag gag aat	6750
Glu Val Asp Thr Glu Gly Pro Ala Phe Leu Ser Asp Val Glu Glu Asn	
2180 2185 2190 2195	
cac caa gaa tgc aaa ccc cac act gtc agg att cta gaa ctt cta aaa	6798
His Gln Glu Cys Lys Pro His Thr Val Arg Ile Leu Glu Leu Leu Lys	
2196 2201 2206 2211	
tta aag ttt ggg gaa atc agt agc tct gat gag atc acc atg aag agt	6846
Leu Lys Phe Gly Glu Ile Ser Ser Ser Asp Glu Ile Thr Met Lys Ser	
2212 2217 2222 2227	
gaa ttc ccg ctt ctg cgc caa cat tct gtt tcc agc atc agg cag ttg	6894
Glu Phe Pro Leu Leu Arg Gln His Ser Val Ser Ser Ile Arg Gln Leu	
2228 2233 2238 2243	
atg cca ttc ttc atg act cta aat ggt gca ttt aag acc cag aga cag	6942
Met Pro Phe Phe Met Thr Leu Asn Gly Ala Phe Lys Thr Gln Arg Gln	
2244 2249 2254 2259	
ctg cct gct gat agc cca gga act cca ttc ttg gac ttt cct gtc aca	6990
Leu Pro Ala Asp Ser Pro Gly Thr Pro Phe Leu Asp Phe Pro Val Thr	
2260 2265 2270 2275	
gat agc cca agg atc tta aaa caa ctg gaa gaa tgc atc gaa tat gat	7038
Asp Ser Pro Arg Ile Leu Lys Gln Leu Glu Glu Cys Ile Glu Tyr Asp	
2276 2281 2286 2291	
ttt ctg gaa cat cca gaa tgt taa ccatgtgaga gagaatatgt ttaatccatg	7092
Phe Leu Glu His Pro Glu Cys *	
2292 2297	
tattggtact ttactgaaaa ccagggttata ttctaaagaa gaaagaaggc aggatagtgc	7152
ttttgaacaa gcctatattcc attttgaaag tagatttcag gctaggtgcg gtggctcaca	7212
cctgtaatct cagcactttg ggaggccaag gcaggcagat cacttgaggt caggagttcg	7272
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gtgtggtggc ggcgcctgta atcccageta cttgggaggc taaggcatga gaattgcttg	7392
aaccaggag gtggaggctg cagtgagccg agatcacgac actgcactcc agctgtgtga	7452
cagaatgaga ccatctccaa aaaaaaaaaa aagtagattt cagataattt actgttcagc	7512

aacaggacac acctccctaa atgccttgta atatatttga atctgattct gcatttcttc 7572
ctcaatttat gtaatgaaaa taaaattaat atatcatcta acagtagcac aaaatttgta 7632
atatgaagta aagtatgaag ataatgaaga agttgttttc tttgttgaag cagttatatg 7692
ggtctttctc agtatatttc tcttttctct aaaagtttaa acttattaaa agaattgtat 7752
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tcaccaaga tcattctcacc tcccatgaag ggaacggctc tctaa atg cag ttt 174
Met Gln Phe
1
tcc ttc cag cag ggt gga tgg gga gca tcg ctg gct gac agg ctg gtc 222
Ser Phe Gln Gln Gly Gly Trp Gly Ala Ser Leu Ala Asp Arg Leu Val
4 9 14 19
aga aaa tgt gat gtt ctg aat cgt gga ttt tca ggt tac aat acc agg 270
Arg Lys Cys Asp Val Leu Asn Arg Gly Phe Ser Gly Tyr Asn Thr Arg
20 25 30 35
tgg gcc aaa att atc ctt cca aga tta atc agg aaa gga aac agt ttg 318
Trp Ala Lys Ile Ile Leu Pro Arg Leu Ile Arg Lys Gly Asn Ser Leu
36 41 46 51
gac atc cca gta gca gtt aca att ttc ttt ggg gcc aat gac agt gca 366
Asp Ile Pro Val Ala Val Thr Ile Phe Phe Gly Ala Asn Asp Ser Ala
52 57 62 67
cta aaa gat gag aat ccc aag cag cac att ccc ctg gag gag tac gct 414
Leu Lys Asp Glu Asn Pro Lys Gln His Ile Pro Leu Glu Glu Tyr Ala
68 73 78 83

gcg aac cta aag agc atg gtg cag tac ctg aag tcc gtg gac atc cct	462
Ala Asn Leu Lys Ser Met Val Gln Tyr Leu Lys Ser Val Asp Ile Pro	
84 89 94 99	
gag aat cga gtc att ctc atc acg ccg acc cca ctt tgt gaa aca gcc	510
Glu Asn Arg Val Ile Leu Ile Thr Pro Thr Pro Leu Cys Glu Thr Ala	
100 105 110 115	
tgg gaa gaa cag tgc atc ata caa ggt tgc aaa cta aat cgc ctg aac	558
Trp Glu Glu Gln Cys Ile Ile Gln Gly Cys Lys Leu Asn Arg Leu Asn	
116 121 126 131	
tct gtt gtt ggt gaa tat gcc aat gcg tgt tta caa gtg gcc caa gac	606
Ser Val Val Gly Glu Tyr Ala Asn Ala Cys Leu Gln Val Ala Gln Asp	
132 137 142 147	
tgt ggg act gac gta ctt gac ctg tgg acc ctg atg cag gac agc cag	654
Cys Gly Thr Asp Val Leu Asp Leu Trp Thr Leu Met Gln Asp Ser Gln	
148 153 158 163	
gac ttc tca tct tat tta tca gat gga cta cat ttg tct cca aag ggg	702
Asp Phe Ser Ser Tyr Leu Ser Asp Gly Leu His Leu Ser Pro Lys Gly	
164 169 174 179	
aat gaa ttt ttg ttc tcg cat ctc tgg cct ttg ata gag aaa aag gtc	750
Asn Glu Phe Leu Phe Ser His Leu Trp Pro Leu Ile Glu Lys Lys Val	
180 185 190 195	
tct tct cta cct ttg ctg ctt cct tac tgg cgg gat gta gca gaa gca	798
Ser Ser Leu Pro Leu Leu Leu Pro Tyr Trp Arg Asp Val Ala Glu Ala	
196 201 206 211	
aaa cct gaa tta agt ctg ctg gga gat gga gac cat tag ccaatcacag	847
Lys Pro Glu Leu Ser Leu Leu Gly Asp Gly Asp His *	
212 217 222	
gagacccaaa tctgcttggt atctacagaa ctcaaagttg tcaatacgta gaggtacgct	907
tttttctca ggcttaaacc ttgccactg atattaataa taaaagtatt agatgatttt	967
tcagggaagt ttatactta ggtccattgt gtttcgacag tattttattaa tgcagatetc	1027
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tttctactcat acatacacc acacacccca ctcaaccttg tatcaaattc caaaagtgt	1207
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caagttccaa ggtattaggt ataacaaggt atctggggta accaaatgtc cttgggaatg	1327
gggggggtggg nggggtatat ggtaggtcc ccgggttggg ttaactgccc ntcaaattta	1387
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<210> 302
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 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> (1)...(1183)
 <223> n = a,t,c or g

<400> 302

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atg aat aga gca gct agg aac aaa tct gag aag agg tac tat tca gaa      165
Met Asn Arg Ala Ala Arg Asn Lys Ser Glu Lys Arg Tyr Tyr Ser Glu
   1             5             10             15

ttc ctc caa ata gct cat ctt ttt aat tat ggg ctt tca tcc ttc cta      213
Phe Leu Gln Ile Ala His Leu Phe Asn Tyr Gly Leu Ser Ser Phe Leu
   17             22             27             32

agg gag ttt att att ttt cta att aaa cta cta caa tga aggctattac      262
Arg Glu Phe Ile Ile Phe Leu Ile Lys Leu Leu Gln *
   33             38             43

ctttttgtct agctaaaaca atctttccta ttaatgaatt tattggcttc tctagtactc      322

ttcaaattgt cattgagctc tattcaagga ctacagccag ttttttccta atagaattag      382

gggtgaaaca aatcatgctt ctattatcac ttctggagtt agcccttcac ctgatcagct      442

tgtctagggt taagagtgcg ggggttttag cgccacaaag acgtgggcat gcggcagctt      502

cctgaacctc aggcattggt gtctaagcaa ctccaccatc cacacgtgtg acgttacagt      562

tctgggagat gcacgcacac tntctgtgcc tttctcaacc actagcttaa tcagcctcca      622

ccttcctagg cagcaacacg ggggtgcagga taaacaataa ctaaaagcat actgattatc      682

acatactcct gcaaagtgtt tgcaccaga aagcatgcag tcaactgcat catgaggggc      742

tcacaccttt ctttggtggt ctctgtcggg gggcacatgt tacctataaa agaggcccaa      802

gcattcgatt aaacagctct tctttataat tcagtttggc taagctgcct tcaaaaaact      862

tgtccccaat tcttcactta cccccccca cttttacaca cgcataatcc caacttacc      922

gggcccactt ggaaacacta catacatagc atgcttgcca aaagttcaca tagggattag      982

gattgcgaaa ggggtaccac aggtgggcca cagcgtcctg cgtctggacg taacacagtg     1042

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aggacgggct gtcattgcttc tgtgatcctc gtcacgccac gcctacgacg cgagtgccgt 1102
gagacggtcg gtacgctagg cattgggtcac catcgctacg acacgccata cagtgcgctt 1162
gccagcctct cgtgtcgcgc c 1183

<210> 303
<211> 1885
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<213> Homo sapiens

<220>
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<222> (1115)..(1744)

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gatgactggc tgctctacct tctttttgga cttcatcttt ttctttgcgg aggccttagg 180
gtcatcactt atggggatgt attccggagc ctcaactttg actggcttct ttttacttcc 240
tttcttaggg ctgctctcca tggacctgga gggcttggag tggcctggga gggcatctcc 300
ctcctgggtg attttttttt tcttcttcac cttccattg tgttctctgg ggctcttccg 360
cttccgtttc tgccccaagg ctgcctgttc ctcatccttc ttccccactg agcaagtgtc 420
cccaacatcc ctggcctccc tggcctcaca gaaccaaggg tcctggaccg agaaggctgt 480
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ttcctcctca ccctgtctag ggtctgggga ggttttcacc ccagaggcat gggacatggc 600
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cttctgagg ctgggtgact tctctgtccg tctagcaggc agcgtggtct caggttctac 720
atgctcctcg caaagggtgc tgacaccctt ctttttcttc ttctttttct tctactagagg 780
catctcaggt gcctgccccat gggccacact cttagagggg gatgtagctc ttaaaggaga 840
aacatcagca aagtaatcat cattgtttta aactgagtat cgagtctctg gttctttgac 900
cactttcttc ttctttttct tctctgggag cccaaggctt actttgtgtg tcttgggtgat 960
cattccgggtg ggcgaaattt ccccgctcc acgtgagagc cagctccgcc gtgaccggga 1020
agtccacttc gagtcgccgg cccacctct cgggttcggg cttcttcggg gtcgcgccct 1080
tccggcgaac gcggttaccg tggaaaccgc ggcc atg gcg gca ccg cgg caa 1132

Met Ala Ala Pro Arg Gln
1

atc ccc agc cac ata gtg cgc ctc aag ccc agc tgc tct aca gac tcg Ile Pro Ser His Ile Val Arg Leu Lys Pro Ser Cys Ser Thr Asp Ser 7 12 17 22	1180
tcg ttc acc cgg acg ccg gtg ccc acc gtg tct ctc gcg tcc cgc gag Ser Phe Thr Arg Thr Pro Val Pro Thr Val Ser Leu Ala Ser Arg Glu 23 28 33 38	1228
ctg cct gtc tcg tcg tgg cag gtc acc gag ccg tca agc aag aat ctg Leu Pro Val Ser Ser Trp Gln Val Thr Glu Pro Ser Ser Lys Asn Leu 39 44 49 54	1276
tgg gag cag atc tgc aag gag tat gaa gct gag cag cct ccc ttt cca Trp Glu Gln Ile Cys Lys Glu Tyr Glu Ala Glu Gln Pro Pro Phe Pro 55 60 65 70	1324
gaa gga tat aaa gtc aaa cag gag cct gtg att acg gtt gcg cca gta Glu Gly Tyr Lys Val Lys Gln Glu Pro Val Ile Thr Val Ala Pro Val 71 76 81 86	1372
gag gaa atg ctt ttt cat ggc ttc agt gca gag cac tat ttt ccg gtt Glu Glu Met Leu Phe His Gly Phe Ser Ala Glu His Tyr Phe Pro Val 87 92 97 102	1420
tcc cat ttc acc atg atc tca cgt aca ccc tgt cct caa gat aaa tcg Ser His Phe Thr Met Ile Ser Arg Thr Pro Cys Pro Gln Asp Lys Ser 103 108 113 118	1468
gaa aca atc aac cca aaa aca tgt tct ccc aaa gaa tat ttg gaa act Glu Thr Ile Asn Pro Lys Thr Cys Ser Pro Lys Glu Tyr Leu Glu Thr 119 124 129 134	1516
ttc atc ttt cct gtt ctg ctt ccc gga atg gct agc ctg ctt cac caa Phe Ile Phe Pro Val Leu Leu Pro Gly Met Ala Ser Leu Leu His Gln 135 140 145 150	1564
gcg aag aaa gaa aaa tgt ttt gag gtt cgc tgt gat cct gag att caa Ala Lys Lys Glu Lys Cys Phe Glu Val Arg Cys Asp Pro Glu Ile Gln 151 156 161 166	1612
gaa ctg cgt cag tgg cag aag aaa ctt cgc gag gcc aag cac att cac Glu Leu Arg Gln Trp Gln Lys Lys Leu Arg Glu Ala Lys His Ile His 167 172 177 182	1660
cag caa gtc aaa att ttc tgg gcc aag caa gaa caa aaa gtg aaa tgc Gln Gln Val Lys Ile Phe Trp Ala Lys Gln Glu Gln Lys Val Lys Cys 183 188 193 198	1708
aaa atg gag gac gat cag tac ctg cag cca aga tga aaat tccatcatct Lys Met Glu Asp Asp Gln Tyr Leu Gln Pro Arg *	1758
199 204 209	
taaccatagc taagacgtat ctttgcccat tcgacacaag ttaccttgtg caaggaaaat	1818

gtccaaatga tgctctctct cttgtgattt ctttaacaag acttgaaca tgtgcaaaaa 1878
 aaaaaaa 1885

<210> 304
 <211> 635
 <212> DNA
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 <222> (115)..(363)

<400> 304
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 Met
 1
 gat tcc ttt ggg caa ccc aga cca gaa gat aat cag tca gta gtc aga 165
 Asp Ser Phe Gly Gln Pro Arg Pro Glu Asp Asn Gln Ser Val Val Arg
 2 7 12 17
 aga atg caa aag aaa tac tgg aaa act aaa cag gtc ttt atc aaa gca 213
 Arg Met Gln Lys Lys Tyr Trp Lys Thr Lys Gln Val Phe Ile Lys Ala
 18 23 28 33
 aca gga aaa aaa gag gat gag cac ttg gtg gcg tct gat gct gaa ctg 261
 Thr Gly Lys Lys Glu Asp Glu His Leu Val Ala Ser Asp Ala Glu Leu
 34 39 44 49
 gat gct aaa ctt gag gtt ttt cac tct gtt caa gag aca tgc act gaa 309
 Asp Ala Lys Leu Glu Val Phe His Ser Val Gln Glu Thr Cys Thr Glu
 50 55 60 65
 ctt ctg aag ata atc gag aaa tac cag cta aga ctc aat ggt atg aaa 357
 Leu Leu Lys Ile Ile Glu Lys Tyr Gln Leu Arg Leu Asn Gly Met Lys
 66 71 76 81
 tca tag ttatctatct gataattccc atttaaaata aatattagca ttttttaaaa 413
 Ser *
 82
 tgaaagattt aatgtaaaaa caattttgtg aatagcttct tatggcaaaa tatgaatatt 473
 tacagctacc tggtctcaaa ggccccagta ttctctcttc tttcctcagt taatcaaadc 533
 ctctgaccca gatttatattt ttgctgatat tttttttctt tgagacaggg tctttctctg 593
 cactccagcc taggcaacag agcaagactc cgtctcaaaa aa 635

<210> 305
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (407)..(2746)

<400> 305

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tctgggacat ccagcacagt gagcggcccc tgggcaccac cagaaaacat ttgtgggtga	180
acgtggagtg atgaccatgt ggacactgtc ttccagggtt ttcttgagc ctctgcagag	240
tctggggggc aggtttctta gtggaaactg caggatcttc cttctgacct ctgcttgctt	300
cgccccagca gctccggttg agtccacaga tgccagctca gcttccagct tggggaagag	360
tggggttgtc agcaggagag cctgaggggt gaggcccagc gtgaac atg gca gct	415
	Met Ala Ala
	1
aat ggg gac tct ccc cca tgg tcc ccg gcc ctg gct gca gag gga cgt	463
Asn Gly Asp Ser Pro Pro Trp Ser Pro Ala Leu Ala Ala Glu Gly Arg	
4 9 14 19	
ggc agc tca tgt gag gct tca gtg tca ttt gag gac gtg act gtg gac	511
Gly Ser Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val Thr Val Asp	
20 25 30 35	
ttc agc aag gag gag tgg cag cac ttg gac cct gcc cag aga cgc ctg	559
Phe Ser Lys Glu Glu Trp Gln His Leu Asp Pro Ala Gln Arg Arg Leu	
36 41 46 51	
tac tgg gat gtg aca cta gag aac tac agc cac ctg ctc tca gtg ggg	607
Tyr Trp Asp Val Thr Leu Glu Asn Tyr Ser His Leu Leu Ser Val Gly	
52 57 62 67	
tac caa att ccc aag tca gag gct gcc ttc aag ttg gag caa gga gag	655
Tyr Gln Ile Pro Lys Ser Glu Ala Ala Phe Lys Leu Glu Gln Gly Glu	
68 73 78 83	
ggg cca tgg atg ctg gag ggg gaa gcc cca cat cag agc tgt tca ggt	703
Gly Pro Trp Met Leu Glu Gly Glu Ala Pro His Gln Ser Cys Ser Gly	
84 89 94 99	
gag gct att ggg aaa atg cag caa cag gga att cct gga gga att ttc	751
Glu Ala Ile Gly Lys Met Gln Gln Gln Gly Ile Pro Gly Gly Ile Phe	
100 105 110 115	
ttc cac tgt gag aga ttt gat caa ccc ata gga gaa gat tca tta tgt	799
Phe His Cys Glu Arg Phe Asp Gln Pro Ile Gly Glu Asp Ser Leu Cys	

116	121	126	131	
tct att tta gaa gaa ctg tgg caa gat aat gac cag cta gag caa cgt				847
Ser Ile Leu Glu Glu Leu Trp Gln Asp Asn Asp Gln Leu Glu Gln Arg				
132	137	142	147	
cag gaa aac cag aat aac ctt tta agt cat gtg aaa gta ttg att aag				895
Gln Glu Asn Gln Asn Asn Leu Leu Ser His Val Lys Val Leu Ile Lys				
148	153	158	163	
gag agg ggc tat gaa cat aaa aac att gaa aaa ata att cat gtg act				943
Glu Arg Gly Tyr Glu His Lys Asn Ile Glu Lys Ile Ile His Val Thr				
164	169	174	179	
acc aag ctt gtt cct tca att aaa aga ctc cat aac tgt gac aca att				991
Thr Lys Leu Val Pro Ser Ile Lys Arg Leu His Asn Cys Asp Thr Ile				
180	185	190	195	
ttg aag cat act tta aac tca cat aat cat aat aga aac agt gca aca				1039
Leu Lys His Thr Leu Asn Ser His Asn His Asn Arg Asn Ser Ala Thr				
196	201	206	211	
aag aac ctt ggc aag att ttt gga aat ggt aac aat ttc ccc cat agc				1087
Lys Asn Leu Gly Lys Ile Phe Gly Asn Gly Asn Asn Phe Pro His Ser				
212	217	222	227	
cct tcc tct act aag aat gag aat gct aaa aca gga gca aat tcc tgt				1135
Pro Ser Ser Thr Lys Asn Glu Asn Ala Lys Thr Gly Ala Asn Ser Cys				
228	233	238	243	
gaa cat gac cac tat gaa aaa cat ctc agc cac aaa caa gct ccc acc				1183
Glu His Asp His Tyr Glu Lys His Leu Ser His Lys Gln Ala Pro Thr				
244	249	254	259	
cac cat cag aaa att cat cct gag gag aag ctt tat gtg tgt act gaa				1231
His His Gln Lys Ile His Pro Glu Glu Lys Leu Tyr Val Cys Thr Glu				
260	265	270	275	
tgt gta atg ggc ttc act cag aag tca cat ctg ttt gag cat cag aga				1279
Cys Val Met Gly Phe Thr Gln Lys Ser His Leu Phe Glu His Gln Arg				
276	281	286	291	
att cat gct gga gaa aag tcc cgt gaa tgt gac aaa agc aac aaa gtc				1327
Ile His Ala Gly Glu Lys Ser Arg Glu Cys Asp Lys Ser Asn Lys Val				
292	297	302	307	
ttc ccc cag aaa ccc cag gtt gat gta cat cca agt gtt tat aca gga				1375
Phe Pro Gln Lys Pro Gln Val Asp Val His Pro Ser Val Tyr Thr Gly				
308	313	318	323	
gaa aaa ccc tat ctg tgt act caa tgt ggg aaa gtc ttt acc ctc aaa				1423
Glu Lys Pro Tyr Leu Cys Thr Gln Cys Gly Lys Val Phe Thr Leu Lys				
324	329	334	339	
tca aac ctc att aca cat caa aaa att cat acc ggg cag aaa ccc tac				1471
Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Gly Gln Lys Pro Tyr				
340	345	350	355	

aaa tgc agt gaa tgt gga aaa gcc ttt ttc cag aga tca gac ctc ttt	1519
Lys Cys Ser Glu Cys Gly Lys Ala Phe Phe Gln Arg Ser Asp Leu Phe	
356 361 366 371	
aga cat ctg aga att cat aca gga gaa aaa cct tat gaa tgc agt gaa	1567
Arg His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu	
372 377 382 387	
tgt gga aaa ggc ttc tcc cag aac tca gac ctc agt ata cat cag aaa	1615
Cys Gly Lys Gly Phe Ser Gln Asn Ser Asp Leu Ser Ile His Gln Lys	
388 393 398 403	
act cat acc gga gag aaa cac tat gaa tgc aat gaa tgt ggg aag gct	1663
Thr His Thr Gly Glu Lys His Tyr Glu Cys Asn Glu Cys Gly Lys Ala	
404 409 414 419	
ttc aca aga aaa tca gca ctc agg atg cat cag aga atc cac acg gga	1711
Phe Thr Arg Lys Ser Ala Leu Arg Met His Gln Arg Ile His Thr Gly	
420 425 430 435	
gag aaa cct tat gta tgc gct gac tgt ggg aag gcc ttc atc cag aaa	1759
Glu Lys Pro Tyr Val Cys Ala Asp Cys Gly Lys Ala Phe Ile Gln Lys	
436 441 446 451	
tca cat ttc aac aca cat cag aga att cat act gga gaa aag ccg tat	1807
Ser His Phe Asn Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr	
452 457 462 467	
gaa tgc agt gac tgt ggg aaa tcc ttc act aag aag tca caa ctc cat	1855
Glu Cys Ser Asp Cys Gly Lys Ser Phe Thr Lys Lys Ser Gln Leu His	
468 473 478 483	
gtg cat caa aga att cac acc gga gag aaa ccc tat ata tgt aca gaa	1903
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Thr Glu	
484 489 494 499	
tgt gga aag gtc ttc act cac agg aca aac ctc acc aca cat cag aaa	1951
Cys Gly Lys Val Phe Thr His Arg Thr Asn Leu Thr Thr His Gln Lys	
500 505 510 515	
act cat act ggg gaa aaa ccc tat atg tgt gct gaa tgt gga aag gct	1999
Thr His Thr Gly Glu Lys Pro Tyr Met Cys Ala Glu Cys Gly Lys Ala	
516 521 526 531	
ttt act gac cag tca aat ctc att aaa cac cag aaa act cac act gga	2047
Phe Thr Asp Gln Ser Asn Leu Ile Lys His Gln Lys Thr His Thr Gly	
532 537 542 547	
gag aaa ccc tat aag tgc aat ggc tgt gga aaa gcc ttc ata tgg aag	2095
Glu Lys Pro Tyr Lys Cys Asn Gly Cys Gly Lys Ala Phe Ile Trp Lys	
548 553 558 563	
tcg cgc ctc aaa ata cat cag aaa tct cat att gga gag aga cac tat	2143
Ser Arg Leu Lys Ile His Gln Lys Ser His Ile Gly Glu Arg His Tyr	
564 569 574 579	

gaa tgc aag gac tgc ggg aaa gcc ttc atc cag aaa tca aca cta agc	2191
Glu Cys Lys Asp Cys Gly Lys Ala Phe Ile Gln Lys Ser Thr Leu Ser	
580 585 590 595	
gtg cat cag aga atc cat aca gga gag aaa ccg tac gtt tgt cct gaa	2239
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Glu	
596 601 606 611	
tgc ggg aag gcc ttt atc cag aaa tcg cac ttc att gcg cat cat aga	2287
Cys Gly Lys Ala Phe Ile Gln Lys Ser His Phe Ile Ala His His Arg	
612 617 622 627	
atc cat act gga gag aag cct tat gaa tgc agc gac tgt ggg aaa tgc	2335
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Cys	
628 633 638 643	
ttc act aag aag tca caa ctc cgt gtg cat cag aaa atc cac aca ggt	2383
Phe Thr Lys Lys Ser Gln Leu Arg Val His Gln Lys Ile His Thr Gly	
644 649 654 659	
gag aag ccc aat ata tgt gct gaa tgt gga aag gcc ttc act gac cga	2431
Glu Lys Pro Asn Ile Cys Ala Glu Cys Gly Lys Ala Phe Thr Asp Arg	
660 665 670 675	
tca aat ctc ata aca cat cag aaa atc cac act agg gag aaa ccc tat	2479
Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Arg Glu Lys Pro Tyr	
676 681 686 691	
gaa tgt ggt gac tgc ggg aaa acc ttc acc tgg aag tca cgc ctc aat	2527
Glu Cys Gly Asp Cys Gly Lys Thr Phe Thr Trp Lys Ser Arg Leu Asn	
692 697 702 707	
ata cat cag aag tct cat act gga gaa aga cac tat gaa tgt agt aaa	2575
Ile His Gln Lys Ser His Thr Gly Glu Arg His Tyr Glu Cys Ser Lys	
708 713 718 723	
tgt ggg aaa gct ttc atc cag aaa gcc aca cta agt atg cat cag ata	2623
Cys Gly Lys Ala Phe Ile Gln Lys Ala Thr Leu Ser Met His Gln Ile	
724 729 734 739	
att cat aca gga aag aaa cct tat gct tgt aca gaa tgt cag aag gcc	2671
Ile His Thr Gly Lys Lys Pro Tyr Ala Cys Thr Glu Cys Gln Lys Ala	
740 745 750 755	
ttt act gac aga tcg aat ctc att aaa cac cag aaa atg cat agt gga	2719
Phe Thr Asp Arg Ser Asn Leu Ile Lys His Gln Lys Met His Ser Gly	
756 761 766 771	
gaa aaa cgc tat aaa gcc agt gac tga gaaag tcttcacctg gaaatcaca	2771
Glu Lys Arg Tyr Lys Ala Ser Asp *	
772 777	
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 <222> (148)..(459)

<400> 306

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ctgctgagta ggcgctgtga tttcaga      atg tct ggg cga ggt aaa ggt ggc      171
                                   Met Ser Gly Arg Gly Lys Gly Gly
                                   1                               5

aag ggg ctg ggt aag gga ggc gcc aag cgc cac cgg aag gtg ctg cgg      219
Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His Arg Lys Val Leu Arg
  9                               14                               19                               24

gac aat atc caa ggc att aca aag ccg gcg att cgc cgt ctc gcc cga      267
Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Arg Leu Ala Arg
 25                               30                               35                               40

cgt ggg ggc gtc aag cgc att tct ggt ctc atc tac gag gag acc cgg      315
Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu Thr Arg
 41                               46                               51                               56

gga gtc ctc aaa gtc ttc ctg gag aac gtg atc cgt gac gcg gtg act      363
Gly Val Leu Lys Val Phe Leu Glu Asn Val Ile Arg Asp Ala Val Thr
 57                               62                               67                               72

tac acg gag cac gcc aag cgc aag acc gtc acg gcc atg gat gtg gtg      411
Tyr Thr Glu His Ala Lys Arg Lys Thr Val Thr Ala Met Asp Val Val
 73                               78                               83                               88

tac gcg ctg aaa cgc cag ggt cgc acc ctt tat ggt ttc ggc ggt tga      459
Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr Gly Phe Gly Gly *
 89                               94                               99                               104

gctgtcccca cagcttctct acagactcca aaaggccctt ttcagggccc ccaaactgtc      519
acagaaagag ctgttaacac ttcctagata acggaccaag tctagctctg ccaccgaggc      579
tggagtgcag tggcacgata tcgcctccgc ctcccggggt caagcgattc acctgcctca      639
gcttcccag tagctgggat tacaggcctg cgccaccacg cctggctaata ttttgtattt      699
tttttttttt ttgggaaaaa acgggggttt cccttgtggg ccgggggggt tttgaactcc      759
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Glu Ala Lys Leu Met Gly Phe Thr Gln Gly Cys Val Thr Phe Glu Asp	
17 22 27 32	
gtg gcc att tac ttc tcc cag gaa gaa tgg ggg ctc ctt gat gag gct	144
Val Ala Ile Tyr Phe Ser Gln Glu Glu Trp Gly Leu Leu Asp Glu Ala	
33 38 43 48	
cag agg ctc ctg tac cgc gat gtg atg ctg gag aac ttt gca ctt ata	192
Gln Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Ile	
49 54 59 64	
act gcg ctg gtt tgt tgg cat ggg atg gag gat gaa gag aca cct gag	240
Thr Ala Leu Val Cys Trp His Gly Met Glu Asp Glu Glu Thr Pro Glu	
65 70 75 80	
caa agt gtt tct gta gaa gga gta cct cag gtc agg act cca gag gcc	288
Gln Ser Val Ser Val Glu Gly Val Pro Gln Val Arg Thr Pro Glu Ala	
81 86 91 96	
agt cca tcc acc cag aag att caa tcc tgt gac atg tgt gtc cca ttc	336
Ser Pro Ser Thr Gln Lys Ile Gln Ser Cys Asp Met Cys Val Pro Phe	
97 102 107 112	
ctg acc gac att ttg cac ctg acc gat ttg cct ggg cag gaa cta tac	384
Leu Thr Asp Ile Leu His Leu Thr Asp Leu Pro Gly Gln Glu Leu Tyr	
113 118 123 128	
ttg act ggg gca tgt gcg gtc ttt cac cag gac cag aag cat cat agt	432
Leu Thr Gly Ala Cys Ala Val Phe His Gln Asp Gln Lys His His Ser	
129 134 139 144	
gca gag aaa ccc ttg gaa agt gac atg gac aag gcc tca ttt gtg cag	480
Ala Glu Lys Pro Leu Glu Ser Asp Met Asp Lys Ala Ser Phe Val Gln	
145 150 155 160	
tgc tgc ctg ttc cat gag tca gga atg cct ttc acc agc agt gag gtt	528
Cys Cys Leu Phe His Glu Ser Gly Met Pro Phe Thr Ser Ser Glu Val	
161 166 171 176	
ggg aag gac ttc cta gcc cca ttg ggc att ctt cag ccg caa gct att	576

Gly	Lys	Asp	Phe	Leu	Ala	Pro	Leu	Gly	Ile	Leu	Gln	Pro	Gln	Ala	Ile	
177					182					187					192	
gct	aac	tat	gag	aag	cca	aac	aaa	atc	agc	aaa	tgt	gag	gag	gcc	ttt	624
Ala	Asn	Tyr	Glu	Lys	Pro	Asn	Lys	Ile	Ser	Lys	Cys	Glu	Glu	Ala	Phe	
193					198					203					208	
cat	gtt	gga	ata	agt	cat	tac	aag	tgg	agt	caa	tgc	agg	aga	gag	tcc	672
His	Val	Gly	Ile	Ser	His	Tyr	Lys	Trp	Ser	Gln	Cys	Arg	Arg	Glu	Ser	
209					214					219					224	
agc	cac	aaa	cac	act	ttt	ttt	cac	cct	aga	gtc	tgc	act	gga	aaa	agg	720
Ser	His	Lys	His	Thr	Phe	Phe	His	Pro	Arg	Val	Cys	Thr	Gly	Lys	Arg	
225					230					235					240	
ctt	tat	gaa	tct	agc	aaa	tgt	ggg	aaa	gcc	tgc	tgc	tgt	gag	tgc	tcc	768
Leu	Tyr	Glu	Ser	Ser	Lys	Cys	Gly	Lys	Ala	Cys	Cys	Cys	Glu	Cys	Ser	
241					246					251					256	
ctt	gtt	cag	ctg	caa	aga	gtc	cac	cct	gga	gaa	agg	cct	tat	gag	tgc	816
Leu	Val	Gln	Leu	Gln	Arg	Val	His	Pro	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	
257					262					267					272	
agt	gaa	tgt	ggg	aaa	tct	ttt	agc	caa	acc	tct	cat	ctg	aat	gat	cat	864
Ser	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Thr	Ser	His	Leu	Asn	Asp	His	
273					278					283					288	
cgg	aga	atc	cac	act	gga	gaa	agg	cct	tat	gtg	tgt	ggg	cag	tgt	ggg	912
Arg	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Val	Cys	Gly	Gln	Cys	Gly	
289					294					299					304	
aaa	tca	ttt	agc	caa	aga	gcc	acc	ctc	att	aaa	cat	cac	aga	gtt	cac	960
Lys	Ser	Phe	Ser	Gln	Arg	Ala	Thr	Leu	Ile	Lys	His	His	Arg	Val	His	
305					310					315					320	
act	gga	gaa	agg	cct	tac	gag	tgt	ggg	gaa	tgt	ggg	aaa	tct	ttt	agc	1008
Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Gly	Glu	Cys	Gly	Lys	Ser	Phe	Ser	
321					326					331					336	
caa	agt	tcc	aac	ctt	att	gaa	cat	tgc	aga	att	cac	act	gga	gaa	agg	1056
Gln	Ser	Ser	Asn	Leu	Ile	Glu	His	Cys	Arg	Ile	His	Thr	Gly	Glu	Arg	
337					342					347					352	
cct	tat	gag	tgt	gat	gaa	tgt	gga	aaa	gcc	ttt	ggg	tcc	aaa	tcc	act	1104
Pro	Tyr	Glu	Cys	Asp	Glu	Cys	Gly	Lys	Ala	Phe	Gly	Ser	Lys	Ser	Thr	
353					358					363					368	
ctt	gtt	cga	cac	cag	aga	act	cac	aca	gga	gaa	aag	cca	tat	gag	tgt	1152
Leu	Val	Arg	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	
369					374					379					384	
ggg	gaa	tgt	ggg	aaa	tta	ttc	aga	caa	agc	ttc	agc	ctt	gtt	gta	cac	1200
Gly	Glu	Cys	Gly	Lys	Leu	Phe	Arg	Gln	Ser	Phe	Ser	Leu	Val	Val	His	
385					390					395					400	
cag	aga	att	cac	act	aca	gca	agg	cct	tat	gag	tgt	ggc	cag	tgt	ggg	1248
Gln	Arg	Ile	His	Thr	Thr	Ala	Arg	Pro	Tyr	Glu	Cys	Gly	Gln	Cys	Gly	

401	406	411	416	
aaa tca ttt agc cta aag tgt ggc ctc att cag cac cag tta att cac				1296
Lys Ser Phe Ser Leu Lys Cys Gly Leu Ile Gln His Gln Leu Ile His				
417	422	427	432	
agt gga gct agg ccc ttt gag tgt gat gag tgc gga aaa tcc ttt agc				1344
Ser Gly Ala Arg Pro Phe Glu Cys Asp Glu Cys Gly Lys Ser Phe Ser				
433	438	443	448	
caa aga acc acc ctc aat aaa cac cac aaa gtt cac act gca gaa agg				1392
Gln Arg Thr Thr Leu Asn Lys His His Lys Val His Thr Ala Glu Arg				
449	454	459	464	
cct tat gta tgt ggg gaa tgt ggg aaa gct ttt atg ttc aaa tct aaa				1440
Pro Tyr Val Cys Gly Glu Cys Gly Lys Ala Phe Met Phe Lys Ser Lys				
465	470	475	480	
ctt gtt agg cac cag aga act cac act gga gaa agg cct ttt gag tgc				1488
Leu Val Arg His Gln Arg Thr His Thr Gly Glu Arg Pro Phe Glu Cys				
481	486	491	496	
agt gaa tgt ggg aaa ttt ttt aga caa agc tat acc ctc gtt gaa cac				1536
Ser Glu Cys Gly Lys Phe Phe Arg Gln Ser Tyr Thr Leu Val Glu His				
497	502	507	512	
cag aaa att cac act gga tta agg cct tac gac tgt gga cag tgc ggg				1584
Gln Lys Ile His Thr Gly Leu Arg Pro Tyr Asp Cys Gly Gln Cys Gly				
513	518	523	528	
aaa tcc ttt atc caa aag tct agc ctc att caa cac caa gtg gtt cac				1632
Lys Ser Phe Ile Gln Lys Ser Ser Leu Ile Gln His Gln Val Val His				
529	534	539	544	
aca gga gaa agg cca tat gag tgt ggc aaa tgt ggg aag tcc ttt aca				1680
Thr Gly Glu Arg Pro Tyr Glu Cys Gly Lys Cys Gly Lys Ser Phe Thr				
545	550	555	560	
caa cac tct ggc ctc att ctc cac cga aaa tct cac act gtg gag agg				1728
Gln His Ser Gly Leu Ile Leu His Arg Lys Ser His Thr Val Glu Arg				
561	566	571	576	
cct cgt gac agc agc aaa tgt gga aaa ccc tac agc cca aga tct aac				1776
Pro Arg Asp Ser Ser Lys Cys Gly Lys Pro Tyr Ser Pro Arg Ser Asn				
577	582	587	592	
att gtt taa ctcttga aactccaaac ctgagaaaag ccttagacct gcaggggaatg				1832
Ile Val *				
593				
tgccatgtct ttcttcagtg ttatg				1857

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cgggtcccagc gtccagagcgc cgggcccttc ggctttcttct aggcc      atg gca ggg      174
                                   Met Ala Gly
                                   1

ccg ggc cca ggc ccg ggg gac ccg gac gag cag tac gat ttc ctg ttc      222
Pro Gly Pro Gly Pro Gly Asp Pro Asp Glu Gln Tyr Asp Phe Leu Phe
   4                               9                               14                               19

aag ctg gtg ctg gtg ggc gac gca agc gtg ggc aag acg tgc gtg gtg      270
Lys Leu Val Leu Val Gly Asp Ala Ser Val Gly Lys Thr Cys Val Val
  20                               25                               30                               35

cag cgc ttc aag acc ggc gcc ttc tcg gag cgc cag gga agc acc atc      318
Gln Arg Phe Lys Thr Gly Ala Phe Ser Glu Arg Gln Gly Ser Thr Ile
  36                               41                               46                               51

ggc gtc gac ttc acc atg aag acg ctg gag atc cag ggc aag cgg gtc      366
Gly Val Asp Phe Thr Met Lys Thr Leu Glu Ile Gln Gly Lys Arg Val
  52                               57                               62                               67

aag ctg cag atc tgg gac acg gcc ggc cag gag cgg ttc cgc acc atc      414
Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
  68                               73                               78                               83

acc cag agc tac tac cgc agt gcc aat ggg gcc atc ctt gcc tac gac      462
Thr Gln Ser Tyr Tyr Arg Ser Ala Asn Gly Ala Ile Leu Ala Tyr Asp
  84                               89                               94                               99

atc acc aag agg agc tcc ttc ctg tcg gtg cct cac tgg att gag gat      510
Ile Thr Lys Arg Ser Ser Phe Leu Ser Val Pro His Trp Ile Glu Asp
 100                               105                               110                               115

gtg agg aag tat gcg ggc tcc aac att gtg cag ctg ctg atc ggg aac      558
Val Arg Lys Tyr Ala Gly Ser Asn Ile Val Gln Leu Leu Ile Gly Asn
 116                               121                               126                               131

aag tca gac ctc agc gag ctt cgg gag gtc tcc ttg gct gag gca cag      606
Lys Ser Asp Leu Ser Glu Leu Arg Glu Val Ser Leu Ala Glu Ala Gln
 132                               137                               142                               147

agc ctg gct gag cac tat gac atc ctg tgt gcc att gag acg tct gcc      654
Ser Leu Ala Glu His Tyr Asp Ile Leu Cys Ala Ile Glu Thr Ser Ala
 148                               153                               158                               163

aag gac tcg agc aac gtg gag gag gcc ttc ctg agg gtg gcc acg gag      702
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Lys	Asp	Ser	Ser	Asn	Val	Glu	Glu	Ala	Phe	Leu	Arg	Val	Ala	Thr	Glu	
164					169					174					179	
ctc	atc	atg	cgg	cac	ggg	ggc	ccc	ttg	ttc	agc	gag	aag	agc	ccc	gac	750
Leu	Ile	Met	Arg	His	Gly	Gly	Pro	Leu	Phe	Ser	Glu	Lys	Ser	Pro	Asp	
180					185					190					195	
cac	atc	cag	ctg	aac	agc	aag	gac	atc	gga	gaa	ggc	tgg	ggc	tgc	ggg	798
His	Ile	Gln	Leu	Asn	Ser	Lys	Asp	Ile	Gly	Glu	Gly	Trp	Gly	Cys	Gly	
196					201					206					211	
tgc	tga	ccagggggccg	ggccggcaga	ctggggggttc	cccacctcct	tgctctcccc										854
Cys	*															
212																
agcctgccaa	gcccagccct	ccagagccag	ccctcctggg	taccggcaac	tacagcagcc											914
gggtgaagct	ctggagctct	gcatacctgtg	gcctggctgc	gggatggagg	ctctccttga											974
ggaaggggaa	gcaggatacc	ctggcggggc	accctgccag	ccagcagctg	gccctccacc											1034
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cagtcctccc	tgtcccatg															1113

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aaaaaaaaaa	aaaattcaa	ctaatacttt	agtcattgtg	actttaagaa	agagacttgg											240
tcacctttac	tgtaacactc	agacatcatt	tacttcagtt	gatggagatt	tcaaaattcc											300
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ctggctagag	tttaataaca	agaatgagta	aactctggga	attctgaaaa	atcacacaca											480
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 gaatccataa aatgtcagca atgctgatgt gcaactggact gaaacatctt gatcatcttc 780
 tgatagaagt aatattccat acaaaaagat tcttagattc cattttttgc ttcattattg 840
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 cgatac atg cac aca act gct tca aat ggt agg atg ctc ttc atg aag 948
 Met His Thr Thr Ala Ser Asn Gly Arg Met Leu Phe Met Lys
 1 5 10
 gtc acg atg tac atg agg cgg gga gtg cag atc atg ggc tgg tca gtg 996
 Val Thr Met Tyr Met Arg Arg Gly Val Gln Ile Met Gly Trp Ser Val
 15 20 25 30
 agg atg gcc ttc atg gcc tgc ttc aca cag taa tcaggctt cagaggtggc 1047
 Arg Met Ala Phe Met Ala Cys Phe Thr Gln *
 31 36 41
 agaaaaggct caatttcttt cctgaaagtt atttattcaa aaacaaaatg aaaaattaac 1107
 tcaatagaaa agactggaaa tacatatcaa aacattaaca gtgatgttat ctgagtgatg 1167
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 gtctgctttt ccataagatg aaaaagtcac gtttttaaga tgccttaaaa gtatttcaaa 1347
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 Met Ala Trp Gln Val Ser Leu Leu Glu Leu Glu Asp
 1 5 10
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 Arg Leu Gln Cys Pro Ile Cys Leu Glu Val Phe Lys Glu Ser Leu Met
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 Leu Gln Cys Gly His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser
 29 34 39 44
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 Tyr His Leu Asp Thr Lys Val Arg Cys Pro Met Cys Trp Gln Val Val
 45 50 55 60
 gac ggc agc agc tcc ttg ccc aac gtc tcc ctg gcc tgg gtg atc gaa 602
 Asp Gly Ser Ser Ser Leu Pro Asn Val Ser Leu Ala Trp Val Ile Glu
 61 66 71 76
 gcc ctg agg ctc cct ggg gac ccg gag ccc aag gtc tgc gtg cac cac 650
 Ala Leu Arg Leu Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His
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 cgg aac ccg ctc agc ctt ttc tgc gag aag gac cag gag ctc atc tgt 698
 Arg Asn Pro Leu Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys
 93 98 103 108
 ggc ctc tgc ggt ctg ctg ggc tcc cac caa cac cac ccg gtc acg ccc 746
 Gly Leu Cys Gly Leu Leu Gly Ser His Gln His His Pro Val Thr Pro
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 Val Ser Thr Val Cys Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Phe
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 tct gag ctg aag cag gag cag aag aag gtg gat gag ctc atc gcc aaa 842
 Ser Glu Leu Lys Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys
 141 146 151 156
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 Leu Val Lys Asn Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser
 157 162 167 172
 tgg gtg atc cgc cgc gag ttc cag gag ctg cgc cac ccg gtg gac gag 938
 Trp Val Ile Arg Arg Glu Phe Gln Glu Leu Arg His Pro Val Asp Glu
 173 178 183 188
 gag cag gcc cgc tgc ctg gag ggg ata ggg ggt cac acc cgt ggc ctg 986
 Glu Gln Ala Arg Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu
 189 194 199 204
 gtg gcc tcc ctg gac atg cag ctg gag cag gcc cag gga acc cgg gag 1034
 Val Ala Ser Leu Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu

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Arg Leu Ala Gln Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp				
221	226	231	236	
cac cat gag ttc atc tgg aag ttc cac tcc atg gcc tcc agg taa taa				1130
His His Glu Phe Ile Trp Lys Phe His Ser Met Ala Ser Arg *				
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gttcctccat tcagcttaac cagcgctcc caagcagctg cctatagctg gctctataac				1250
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	Met Ala Pro Leu Asp Leu Asp Lys Tyr Val Glu Ile Ala			
	1 5 10			
cgg ctg tgc aag tac ctg cca gag aac gac ctg aag cgg cta tgt gac				157
Arg Leu Cys Lys Tyr Leu Pro Glu Asn Asp Leu Lys Arg Leu Cys Asp				
14 19 24 29				
tac gtt tgt gac ctc ctc tta gaa gag tca aat gtt cag cca gta tca				205
Tyr Val Cys Asp Leu Leu Leu Glu Glu Ser Asn Val Gln Pro Val Ser				
30 35 40 45				
aca cca gta aca gtg tgt gga gat atc cat gga cag ttt tat gac ctt				253
Thr Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu				
46 51 56 61				
tgt gaa ctg ttc aga act gga ggt cag gtt cct gac aca aac tac ata				301
Cys Glu Leu Phe Arg Thr Gly Gly Gln Val Pro Asp Thr Asn Tyr Ile				

62	67	72	77	
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Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Tyr Ser Leu Glu Thr Phe				
78	83	88	93	
act tac ctt ctt gca tta aag gct aaa tgg cct gat cgt att aca ctt				397
Thr Tyr Leu Leu Ala Leu Lys Ala Lys Trp Pro Asp Arg Ile Thr Leu				
94	99	104	109	
ttg cga gga aat cat gag agt aga cag ata aca cag gtc tat gga ttt				445
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe				
110	115	120	125	
tat gat gag tgc caa acc aaa tat gga aat gct aat gcc tgg aga tac				493
Tyr Asp Glu Cys Gln Thr Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr				
126	131	136	141	
tgt acc aaa gtt ttt gac atg ctc aca gta gca gct tta ata gat gag				541
Cys Thr Lys Val Phe Asp Met Leu Thr Val Ala Ala Leu Ile Asp Glu				
142	147	152	157	
cag att ttg tgt gtc cat ggt ggt tta tct cct gat atc aaa aca ctg				589
Gln Ile Leu Cys Val His Gly Gly Leu Ser Pro Asp Ile Lys Thr Leu				
158	163	168	173	
gat caa att cga acc atc gaa cgg aat cag gaa att cct cat aaa gga				637
Asp Gln Ile Arg Thr Ile Glu Arg Asn Gln Glu Ile Pro His Lys Gly				
174	179	184	189	
gca ttt tgt gat ctg gtt tgg tca gat cct gaa gat gtg gat acc tgg				685
Ala Phe Cys Asp Leu Val Trp Ser Asp Pro Glu Asp Val Asp Thr Trp				
190	195	200	205	
gct atc agt ccc cga gga gca ggt tgg ctt ttt gga gca aag gtc aca				733
Ala Ile Ser Pro Arg Gly Ala Gly Trp Leu Phe Gly Ala Lys Val Thr				
206	211	216	221	
aat gag ttt gtt cat atc aac aac tta aaa ctc atc tgc aga gca cat				781
Asn Glu Phe Val His Ile Asn Asn Leu Lys Leu Ile Cys Arg Ala His				
222	227	232	237	
caa cta gtg cac gaa ggc tat aaa ttt atg ttt gat gag aag ctg gtg				829
Gln Leu Val His Glu Gly Tyr Lys Phe Met Phe Asp Glu Lys Leu Val				
238	243	248	253	
aca gta tgg tct gct cct aat tac tgc tat cgt tgt gga aat att gct				877
Thr Val Trp Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Ile Ala				
254	259	264	269	
tcg atc atg gtc ttc aaa gat gta aat aca aga gaa cca aag tta ttc				925
Ser Ile Met Val Phe Lys Asp Val Asn Thr Arg Glu Pro Lys Leu Phe				
270	275	280	285	
cgg gca gtt cca gat tca gaa cgt gtt att cct ccc aga acg aca acg				973
Arg Ala Val Pro Asp Ser Glu Arg Val Ile Pro Pro Arg Thr Thr Thr				
286	291	296	301	

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Pro Tyr Phe Leu *	
302	
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tgaaatgctg cctcttgcc tttttttttt aaatttttaa ttatctaaat ttattgtttg	1148
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gaccctttgg ttattgagtt taaaacttca attgaaattc aatagtattt attttttaa	1808
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taaagcttgg atgggggttg acctctgcag ggcagcgccc agctatagga gttcccctgc 180

tgagcagaga ag atg act gca gaa ttg aga gaa gcc atg gcc cta gcc 228
Met Thr Ala Glu Leu Arg Glu Ala Met Ala Leu Ala
1 5 10

cca tgg ggc cca gtg aag gtg aaa aag gag gag gaa gaa gaa gaa aac 276
Pro Trp Gly Pro Val Lys Val Lys Lys Glu Glu Glu Glu Glu Glu Asn
13 18 23 28

ttc cca ggt cag gca tcc agc caa caa gtg cac tcc gag aac atc aaa 324
Phe Pro Gly Gln Ala Ser Ser Gln Gln Val His Ser Glu Asn Ile Lys
29 34 39 44

gtc tgg gcc cca gtg cag ggt ctt cag aca ggc ctt gat gga tca gaa 372
Val Trp Ala Pro Val Gln Gly Leu Gln Thr Gly Leu Asp Gly Ser Glu
45 50 55 60

gag gaa gaa aag ggt cag aac ata tcc tgg gat atg gcg gta gtc ctg 420
Glu Glu Glu Lys Gly Gln Asn Ile Ser Trp Asp Met Ala Val Val Leu
61 66 71 76

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Lys Ala Thr Gln Glu Ala Pro Ala Ala Ser Thr Leu Gly Ser Tyr Ser
77 82 87 92

tta cca ggg act ctg gcc aag agt gag ata ctg gag act cat ggg acc 516
Leu Pro Gly Thr Leu Ala Lys Ser Glu Ile Leu Glu Thr His Gly Thr
93 98 103 108

atg aac ttt cta ggt gct gaa acc aag aac cta cag tta ctg gtt cca 564
Met Asn Phe Leu Gly Ala Glu Thr Lys Asn Leu Gln Leu Leu Val Pro
109 114 119 124

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Lys Thr Glu Ile Cys Glu Glu Ala Glu Lys Pro Leu Ile Ile Ser Glu
125 130 135 140

aga atc cag aaa gct gat cct caa gga cct gag tta gga gaa gct tgt 660
Arg Ile Gln Lys Ala Asp Pro Gln Gly Pro Glu Leu Gly Glu Ala Cys
141 146 151 156

gaa aag gga aac atg tta aag agg cag aga ata aag aga gaa aag aaa 708
Glu Lys Gly Asn Met Leu Lys Arg Gln Arg Ile Lys Arg Glu Lys Lys
157 162 167 172

gat ttc aga caa gtg ata gtg aat gac tgt cac tta cct gaa agc ttc 756
Asp Phe Arg Gln Val Ile Val Asn Asp Cys His Leu Pro Glu Ser Phe
173 178 183 188

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Leu Asn Ser Gly Ala Val Lys Asn Pro Lys Thr Gln Leu Gly Gln Lys				
205	210	215	220	
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Pro Phe Thr Cys Ser Val Cys Gly Lys Gly Phe Ser Gln Ser Ala Asn				
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ctc gtt gtg cat cag cga atc cac act gga gag aaa ccc ttt gaa tgt				948
Leu Val Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys				
237	242	247	252	
cat gag tgt ggg aag gcc ttc att cag agt gca aac ctc gtt gtg cat				996
His Glu Cys Gly Lys Ala Phe Ile Gln Ser Ala Asn Leu Val Val His				
253	258	263	268	
cag aga atc cac act gga cag aaa cct tat gtt tgc tca aaa tgt ggg				1044
Gln Arg Ile His Thr Gly Gln Lys Pro Tyr Val Cys Ser Lys Cys Gly				
269	274	279	284	
aaa gcc ttc act cag agt tca aat ctg act gta cat caa aaa atc cac				1092
Lys Ala Phe Thr Gln Ser Ser Asn Leu Thr Val His Gln Lys Ile His				
285	290	295	300	
tcc tta gaa aaa act ttt aag tgc aat gaa tgt gag aaa gcc ttt agt				1140
Ser Leu Glu Lys Thr Phe Lys Cys Asn Glu Cys Glu Lys Ala Phe Ser				
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tac agc tca caa ctt gct cgg cac cag aaa gtc cac att acg gaa aaa				1188
Tyr Ser Ser Gln Leu Ala Arg His Gln Lys Val His Ile Thr Glu Lys				
317	322	327	332	
tgc tat gaa tgt aat gaa tgt ggg aaa aca ttt act agg agc tca aac				1236
Cys Tyr Glu Cys Asn Glu Cys Gly Lys Thr Phe Thr Arg Ser Ser Asn				
333	338	343	348	
ctc att gtc cac cag agg atc cac act ggg gag aag ccc ttt gcc tgt				1284
Leu Ile Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Ala Cys				
349	354	359	364	
aac gac tgt ggc aaa gcc ttt acc cag agt gca aat ctt att gta cat				1332
Asn Asp Cys Gly Lys Ala Phe Thr Gln Ser Ala Asn Leu Ile Val His				
365	370	375	380	
cag cga agc cat act ggt gag aag cca tat gag tgt aaa gag tgt ggg				1380
Gln Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly				
381	386	391	396	
aaa gcc ttt agt tgt ttt tca cac ctt att gtg cac cag aga att cac				1428
Lys Ala Phe Ser Cys Phe Ser His Leu Ile Val His Gln Arg Ile His				
397	402	407	412	
act gca gag aaa cct tac gac tgc agc gaa tgt ggg aaa gcc ttc agt				1476
Thr Ala Glu Lys Pro Tyr Asp Cys Ser Glu Cys Gly Lys Ala Phe Ser				
413	418	423	428	

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Gln Leu Ser Cys Leu Ile Val His Gln Arg Ile His Ser Gly Asp Leu	
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cct tac gtg tgt aat gaa tgt ggg aag gcc ttc aca tgt agc tca tac	1572
Pro Tyr Val Cys Asn Glu Cys Gly Lys Ala Phe Thr Cys Ser Ser Tyr	
445 450 455 460	
cta ctt att cat cag aga att cat aat gga gaa aaa cct tac aca tgt	1620
Leu Leu Ile His Gln Arg Ile His Asn Gly Glu Lys Pro Tyr Thr Cys	
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aat gag tgt ggg aag gcc ttc aga cag agg tcg agc ctc acc gtg cac	1668
Asn Glu Cys Gly Lys Ala Phe Arg Gln Arg Ser Ser Leu Thr Val His	
477 482 487 492	
cag aga acc cac act ggg gag aag ccc tat gaa tgt gag aag tgt ggt	1716
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Glu Lys Cys Gly	
493 498 503 508	
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Ala Ala Phe Ile Ser Asn Ser His Leu Met Arg His His Arg Thr His	
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Leu Val Glu *	
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 Ala Glu Ala Ala Leu Val Asn Thr Pro Gln Ile Pro Met Val Thr Glu
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 gag ttt gtg aaa cca tca cag ggc cat gtg acc ttt gag gat att gct 391
 Glu Phe Val Lys Pro Ser Gln Gly His Val Thr Phe Glu Asp Ile Ala
 18 23 28 33
 gtg tac ttc tcc cag gag gag tgg ggc ctc ctt gat gaa gct caa agg 439
 Val Tyr Phe Ser Gln Glu Glu Trp Gly Leu Leu Asp Glu Ala Gln Arg
 34 39 44 49
 tgc ctg tat cat gat gtg atg ctg gag aac ttt tcg ctt atg gcc tca 487
 Cys Leu Tyr His Asp Val Met Leu Glu Asn Phe Ser Leu Met Ala Ser
 50 55 60 65
 gta ggt tgt ttg cat gga ata gag gct gag gag gcc cct tct gag cag 535
 Val Gly Cys Leu His Gly Ile Glu Ala Glu Glu Ala Pro Ser Glu Gln
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 Thr Leu Ser Ala Gln Gly Val Ser Gln Ala Arg Thr Pro Lys Leu Gly
 82 87 92 97
 cct tcc atc cca aat gct cat tct tgt gag atg tgt atc ctg gtc atg 631
 Pro Ser Ile Pro Asn Ala His Ser Cys Glu Met Cys Ile Leu Val Met
 98 103 108 113
 aaa gac att ttg tac ctc agt gag cat cag ggg aca ctt ccc tgg cag 679
 Lys Asp Ile Leu Tyr Leu Ser Glu His Gln Gly Thr Leu Pro Trp Gln
 114 119 124 129

aaa cct tat acg tct gtg gcc agt ggg aaa tgg ttt tca ttt ggt tct	727
Lys Pro Tyr Thr Ser Val Ala Ser Gly Lys Trp Phe Ser Phe Gly Ser	
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aac ctg caa cag cac cag aac cag gac agt gga gag aaa cac atc aga	775
Asn Leu Gln Gln His Gln Asn Gln Asp Ser Gly Glu Lys His Ile Arg	
146 151 156 161	
aag gag gag agc agt gcc ttg ctt ctg aat agc tgc aaa att cct ctg	823
Lys Glu Glu Ser Ser Ala Leu Leu Leu Asn Ser Cys Lys Ile Pro Leu	
162 167 172 177	
tca gac aat ctt ttc cca tgc aaa gat gtt gag aag gat ttt cca acc	871
Ser Asp Asn Leu Phe Pro Cys Lys Asp Val Glu Lys Asp Phe Pro Thr	
178 183 188 193	
atc ctg ggc ctt ctc caa cac cag acc acc cac agc aga caa gag tat	919
Ile Leu Gly Leu Leu Gln His Gln Thr Thr His Ser Arg Gln Glu Tyr	
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gca cat aga agc agg gag acc ttt caa caa aga cgt tac aaa tgt gag	967
Ala His Arg Ser Arg Glu Thr Phe Gln Gln Arg Arg Tyr Lys Cys Glu	
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caa gtt ttc aat gag aaa gtt cat gtt act gag cat cag aga gtc cac	1015
Gln Val Phe Asn Glu Lys Val His Val Thr Glu His Gln Arg Val His	
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242 247 252 257	
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Ser Lys Tyr Leu Phe Val Glu His Gln Arg Thr His Asn Ala Glu Lys	
258 263 268 273	
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Pro Tyr Val Cys Asn Ile Cys Gly Lys Ser Phe Leu His Lys Gln Thr	
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Leu Val Gly His Gln Gln Arg Ile His Thr Arg Glu Arg Ser Tyr Val	
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Cys Ile Glu Cys Gly Lys Ser Leu Ser Ser Lys Tyr Ser Leu Val Glu	
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cac cag aga acc cat aat gga gaa aag cct tat gtg tgc aat gta tgt	1303
His Gln Arg Thr His Asn Gly Glu Lys Pro Tyr Val Cys Asn Val Cys	
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ggg aaa tca ttc cgc cac aaa caa aca ttt gtt ggc cat cag cag aga	1351
Gly Lys Ser Phe Arg His Lys Gln Thr Phe Val Gly His Gln Gln Arg	
338 343 348 353	
atc cac act gga gag agg cct tat gtg tgt atg gaa tgt ggg aaa tct	1399

Ile His Thr Gly Glu Arg Pro Tyr Val Cys Met Glu Cys Gly Lys Ser	
354 359 364 369	
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Phe Ile His Ser Tyr Asp Arg Ile Arg His Gln Arg Val His Thr Gly	
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Trp Phe Cys Val Gly Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys	
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agg ctc gtg atg gtc aag gtt gtg ccc acg tgc ctc agg gcc ttg gta	1335
Arg Leu Val Met Val Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val	
361 366 371 376	
 gaa atg gcc cgg gta ggg ggt gcc tcc tcc ctg gag aat act gtg gac	1383
Glu Met Ala Arg Val Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp	
377 382 387 392	
 ctg cac att tcc aac agc cac cca ctc tcc ctc acc tcc gac cag tac	1431
Leu His Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln Tyr	
393 398 403 408	
 aag gcc tac ctg cag gac ttg gtg gag ggc atg gat ttc cag ggc cct	1479
Lys Ala Tyr Leu Gln Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro	
409 414 419 424	
 ggg gag agc tga gcc ctcgctcctc atggtgtgcc tccaaccccc ctgttcccca	1534
Gly Glu Ser *	
425	
 ccacctcaac caataaactg gttcctgcta tgaaaaaaaa aaaa	1578

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	Met Ala Arg Val Leu
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	53
 aag gct gca gcc gcg aat gcc gta ggg ctt ttt tcc aga ctt caa gct	101
Lys Ala Ala Ala Ala Asn Ala Val Gly Leu Phe Ser Arg Leu Gln Ala	
6 11 16 21	
 ccc att cca aca gta aga gct tct tcc aca tca cag ccc ttg gat caa	149
Pro Ile Pro Thr Val Arg Ala Ser Ser Thr Ser Gln Pro Leu Asp Gln	
22 27 32 37	
 gtg aca ggt tct gtg tgg aac ctg ggt cga ctc aac cat gta gcc ata	197
Val Thr Gly Ser Val Trp Asn Leu Gly Arg Leu Asn His Val Ala Ile	
38 43 48 53	
 gca gtg cca gat ttg gaa aag gct gca gca ttt tat aag aat att ctg	245
Ala Val Pro Asp Leu Glu Lys Ala Ala Ala Phe Tyr Lys Asn Ile Leu	
54 59 64 69	
 ggg gcc cag gta agt gaa gcg gtc cct ctt cct gaa cat gga gta tct	293
Gly Ala Gln Val Ser Glu Ala Val Pro Leu Pro Glu His Gly Val Ser	

70	75	80	85	
gtt gtt ttt gtc aac ctg gga aat acc aag atg gaa ctg ctt cat cca				341
Val Val Phe Val Asn Leu Gly Asn Thr Lys Met Glu Leu Leu His Pro				
86	91	96	101	
ttg gga cgt gac agt cca att gca ggt ttt ctg cag aaa aac aag gct				389
Leu Gly Arg Asp Ser Pro Ile Ala Gly Phe Leu Gln Lys Asn Lys Ala				
102	107	112	117	
gga gga atg cat cac atc tgc atc gag gtg gat aat att aat gca gct				437
Gly Gly Met His His Ile Cys Ile Glu Val Asp Asn Ile Asn Ala Ala				
118	123	128	133	
gtg atg gat ttg aaa aaa aag aag atc cgc agt cta agt gaa gag gtc				485
Val Met Asp Leu Lys Lys Lys Lys Ile Arg Ser Leu Ser Glu Glu Val				
134	139	144	149	
aaa ata gga gca cat gga aaa cca gtg att ttt ctc cat cct aaa gac				533
Lys Ile Gly Ala His Gly Lys Pro Val Ile Phe Leu His Pro Lys Asp				
150	155	160	165	
tgt ggt gga gtc ctt gtg gaa ctg gag caa gct tga ttta tatttgcaag				583
Cys Gly Gly Val Leu Val Glu Leu Glu Gln Ala *				
166	171	176		
caactaaatt aattgacctg aaaaagccta tcaaatacta tcaaaatgta ctatgacatt				643
gagtccttca ctgcttccat catgtaaaag ttcacagtta aagactgaat tacagaaaga				703
ttaaaatata tacatatata aatacataaa tatgtatatt atttagatta acaaacatat				763
ttgttaattt gaatttgaag aaaatcttga ttactaatta cttagggaac attattaaaa				823
tcatatagaa ataaattatt cctcttctac aatgggggtaa aaaaaaaaaa				873

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<220>
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Met Ala Asp Val Thr Ala Arg Ser Leu Gln Tyr Glu Tyr Lys Ala Asn				
1	5	10		
tcg aat ctt gtg ctc caa gct gac cgt tct ctc att gac cgg acc cgc				96
Ser Asn Leu Val Leu Gln Ala Asp Arg Ser Leu Ile Asp Arg Thr Arg				
17	22	27	32	

cgg gat gaa ccc aca gga gag gtg ctg tcc ctt gtt ggg aag ctg gag	144
Arg Asp Glu Pro Thr Gly Glu Val Leu Ser Leu Val Gly Lys Leu Glu	
33 38 43 48	
ggc acc cgt atg gga gac aag gct caa cgg acc aaa ccg cag atg cag	192
Gly Thr Arg Met Gly Asp Lys Ala Gln Arg Thr Lys Pro Gln Met Gln	
49 54 59 64	
gag gaa aga aga gcc aag cga aga aag cgt gat gag gac cgg cat gac	240
Glu Glu Arg Arg Ala Lys Arg Arg Lys Arg Asp Glu Asp Arg His Asp	
65 70 75 80	
atc aac aag atg aag ggt tat act ctg ctg tcg gag ggc att gat gag	288
Ile Asn Lys Met Lys Gly Tyr Thr Leu Leu Ser Glu Gly Ile Asp Glu	
81 86 91 96	
atg gtg ggc atc atc tac aag ccc aaa act aaa gag act cgg gag acc	336
Met Val Gly Ile Ile Tyr Lys Pro Lys Thr Lys Glu Thr Arg Glu Thr	
97 102 107 112	
tat gag gtg cta ctc agc ttc atc cag gct gct ctt ggg gac cag cca	384
Tyr Glu Val Leu Leu Ser Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro	
113 118 123 128	
cgt gat atc ctt tgt ggg gca gct gat gaa gtt cta gct gtt cta aag	432
Arg Asp Ile Leu Cys Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys	
129 134 139 144	
aat gaa aag ctg cgg gac aag gaa agg cga aag gag att gac ctg ctg	480
Asn Glu Lys Leu Arg Asp Lys Glu Arg Arg Lys Glu Ile Asp Leu Leu	
145 150 155 160	
ctg ggt caa aca gat gat acc aga tac cat gtg cta gtg aac ctg ggc	528
Leu Gly Gln Thr Asp Asp Thr Arg Tyr His Val Leu Val Asn Leu Gly	
161 166 171 176	
aaa aag atc aca gac tat ggt gga gat aag gaa atc caa aat atg gat	576
Lys Lys Ile Thr Asp Tyr Gly Gly Asp Lys Glu Ile Gln Asn Met Asp	
177 182 187 192	
gac aac att gat gag aca tac ggt gtg aat gtg cag ttt gag tct gat	624
Asp Asn Ile Asp Glu Thr Tyr Gly Val Asn Val Gln Phe Glu Ser Asp	
193 198 203 208	
gag gag gaa ggt gat gaa gac gta tac ggg gag gtt cga gaa gag gca	672
Glu Glu Glu Gly Asp Glu Asp Val Tyr Gly Glu Val Arg Glu Glu Ala	
209 214 219 224	
tct gat gat gac atg gaa ggg gac gag gct gtc gtg cgc tgc acc ctc	720
Ser Asp Asp Asp Met Glu Gly Asp Glu Ala Val Val Arg Cys Thr Leu	
225 230 235 240	
tcg gct aat atg tat gtt gat gaa atc tta gtc tgg tgt gct tct gaa	768
Ser Ala Asn Met Tyr Val Asp Glu Ile Leu Val Trp Cys Ala Ser Glu	
241 246 251 256	
ctc aat att cca gag ttt ttt cct ctg gaa agt cct cac aag aag gtg	816

Leu Asn Ile Pro Glu Phe Phe Pro Leu Glu Ser Pro His Lys Lys Val	
257 262 267 272	
ggc tat gga ttg tca agt aga act tgg ttg cag ggt ggt ggc aaa gtg	864
Gly Tyr Gly Leu Ser Ser Arg Thr Trp Leu Gln Gly Gly Gly Lys Val	
273 278 283 288	
atc gag gct ggc aga gac ctg ctc gta gcc tca ggt gaa ctg atg agt	912
Ile Glu Ala Gly Arg Asp Leu Leu Val Ala Ser Gly Glu Leu Met Ser	
289 294 299 304	
tcc aag aag aag gat ttg cac cct cgg gat att gat gca ttt tgg ctg	960
Ser Lys Lys Lys Asp Leu His Pro Arg Asp Ile Asp Ala Phe Trp Leu	
305 310 315 320	
cag cgg cag ctc agt cgt ttc tat gat gat gcc atc gtg tcg cag aag	1008
Gln Arg Gln Leu Ser Arg Phe Tyr Asp Asp Ala Ile Val Ser Gln Lys	
321 326 331 336	
aag gca gat gaa gta ttg gag att ttg aag acg gcc agt gat gat cgg	1056
Lys Ala Asp Glu Val Leu Glu Ile Leu Lys Thr Ala Ser Asp Asp Arg	
337 342 347 352	
gaa tgt gaa aat cag ctg gtt ctg ctg ctt ggt ttc aac acc ttt gat	1104
Glu Cys Glu Asn Gln Leu Val Leu Leu Leu Gly Phe Asn Thr Phe Asp	
353 358 363 368	
ttc att aaa gtg ttg cgg cag cac agg atg atg att tta tac tgt acc	1152
Phe Ile Lys Val Leu Arg Gln His Arg Met Met Ile Leu Tyr Cys Thr	
369 374 379 384	
ttg ctg gcc agt gca caa agt gaa gct gaa aag gaa agg att atg gga	1200
Leu Leu Ala Ser Ala Gln Ser Glu Ala Glu Lys Glu Arg Ile Met Gly	
385 390 395 400	
aag atg gaa gct gac cca gag cta tcc aag ttc ctc tac cag ctt cat	1248
Lys Met Glu Ala Asp Pro Glu Leu Ser Lys Phe Leu Tyr Gln Leu His	
401 406 411 416	
gaa acc gag aag gag gat ctg atc cga gag gaa agg tcc cgg aga gag	1296
Glu Thr Glu Lys Glu Asp Leu Ile Arg Glu Glu Arg Ser Arg Arg Glu	
417 422 427 432	
cga gtg cgt cag tct cga atg gac aca gat ctg gaa acc atg gat ctc	1344
Arg Val Arg Gln Ser Arg Met Asp Thr Asp Leu Glu Thr Met Asp Leu	
433 438 443 448	
gac cag ggt gga gag gca ctg gct cca cgg cag gtt ctg gac ttg gag	1392
Asp Gln Gly Gly Glu Ala Leu Ala Pro Arg Gln Val Leu Asp Leu Glu	
449 454 459 464	
gac ctg gtt ttt acc caa ggg agc cac ttt atg gcc aat aaa cgc tgt	1440
Asp Leu Val Phe Thr Gln Gly Ser His Phe Met Ala Asn Lys Arg Cys	
465 470 475 480	
cag ctt cct gat gga tcc ttc cgt cgc cag cgt aag ggc tat gaa gag	1488
Gln Leu Pro Asp Gly Ser Phe Arg Arg Gln Arg Lys Gly Tyr Glu Glu	

481	486	491	496	
gtg cat gtg cct gct ctg aag ccc aag ccc ttt ggc tca gaa gaa caa				1536
Val His Val Pro Ala Leu Lys Pro Lys Pro Phe Gly Ser Glu Glu Gln				
497	502	507	512	
ctg ctt cca gtg gaa aag ctg cca aag tat gcc cag gct ggg ttt gag				1584
Leu Leu Pro Val Glu Lys Leu Pro Lys Tyr Ala Gln Ala Gly Phe Glu				
513	518	523	528	
ggc ttc aaa aca ctg aat cgg atc cag agt aag ctc tac cgt gct gcc				1632
Gly Phe Lys Thr Leu Asn Arg Ile Gln Ser Lys Leu Tyr Arg Ala Ala				
529	534	539	544	
ctt gag acg gat gag aat ctg ctg ctg tgt gct cct act ggt gct ggg				1680
Leu Glu Thr Asp Glu Asn Leu Leu Leu Cys Ala Pro Thr Gly Ala Gly				
545	550	555	560	
aag acc aac gtg gcc ctg atg tgc atg ctc cga gag att ggg aaa cac				1728
Lys Thr Asn Val Ala Leu Met Cys Met Leu Arg Glu Ile Gly Lys His				
561	566	571	576	
ata aac atg gac ggc acc atc aat gtg gat gac ttc aag att atc tac				1776
Ile Asn Met Asp Gly Thr Ile Asn Val Asp Asp Phe Lys Ile Ile Tyr				
577	582	587	592	
att gcc ccc atg cgc tcc ttg gtg cag gag atg gtg ggc agc ttt gga				1824
Ile Ala Pro Met Arg Ser Leu Val Gln Glu Met Val Gly Ser Phe Gly				
593	598	603	608	
aag cgc ctg gcc act tat ggc atc act gtt gct gaa ctg act ggg gac				1872
Lys Arg Leu Ala Thr Tyr Gly Ile Thr Val Ala Glu Leu Thr Gly Asp				
609	614	619	624	
cac cag ctg tgc aaa gaa gag atc agt gcc act cag atc atc gtc tgc				1920
His Gln Leu Cys Lys Glu Glu Ile Ser Ala Thr Gln Ile Ile Val Cys				
625	630	635	640	
acc ccc gag aag tgg gac atc atc acc cgc aag ggt ggt gag cgc acc				1968
Thr Pro Glu Lys Trp Asp Ile Ile Thr Arg Lys Gly Gly Glu Arg Thr				
641	646	651	656	
tac acc cag ctg gtg cgg ctc atc att ctg gat gag att cat ctt ctc				2016
Tyr Thr Gln Leu Val Arg Leu Ile Ile Leu Asp Glu Ile His Leu Leu				
657	662	667	672	
cac gat gac aga ggt cct gtc tta gaa gct tta gtg gcc agg gcc atc				2064
His Asp Asp Arg Gly Pro Val Leu Glu Ala Leu Val Ala Arg Ala Ile				
673	678	683	688	
cga aac att gag atg acc caa gag gat gtc cga ctc att ggt ctc agt				2112
Arg Asn Ile Glu Met Thr Gln Glu Asp Val Arg Leu Ile Gly Leu Ser				
689	694	699	704	
gcc acc cta ccc aac tat gaa gat gta gcc acc ttt cta cgt gtt gac				2160
Ala Thr Leu Pro Asn Tyr Glu Asp Val Ala Thr Phe Leu Arg Val Asp				
705	710	715	720	

cct gcc aag ggt ctc ttt tac ttt gac aac agc ttc cgt cca gtg cct	2208
Pro Ala Lys Gly Leu Phe Tyr Phe Asp Asn Ser Phe Arg Pro Val Pro	
721 726 731 736	
ctg gaa cag aca tat gtg ggt atc aca gag aaa aaa gct atc aag cgt	2256
Leu Glu Gln Thr Tyr Val Gly Ile Thr Glu Lys Lys Ala Ile Lys Arg	
737 742 747 752	
ttc cag atc atg aat gaa ata gtc tat gaa aaa atc atg gaa cat gct	2304
Phe Gln Ile Met Asn Glu Ile Val Tyr Glu Lys Ile Met Glu His Ala	
753 758 763 768	
gga aaa aat cag gtg ctc gtg ttt gtc cat tct cgc aaa gaa act ggg	2352
Gly Lys Asn Gln Val Leu Val Phe Val His Ser Arg Lys Glu Thr Gly	
769 774 779 784	
aag aca gca agg gca atc cgt gac atg tgt ctg gag aag gac act ttg	2400
Lys Thr Ala Arg Ala Ile Arg Asp Met Cys Leu Glu Lys Asp Thr Leu	
785 790 795 800	
ggc ctg ttt ctt cgc gag ggt tct gcc tcc act gaa gtc ctt cgt aca	2448
Gly Leu Phe Leu Arg Glu Gly Ser Ala Ser Thr Glu Val Leu Arg Thr	
801 806 811 816	
gaa gca gag cag tgc aag aac ttg gag ctg aag gat ctt ttg ccc tat	2496
Glu Ala Glu Gln Cys Lys Asn Leu Glu Leu Lys Asp Leu Leu Pro Tyr	
817 822 827 832	
ggc ttt gct att cat cat gca ggc atg act aga gtt gac cga aca ctt	2544
Gly Phe Ala Ile His His Ala Gly Met Thr Arg Val Asp Arg Thr Leu	
833 838 843 848	
gta gaa gat ctt ttt ggt gac aag cat att cag gtt tta gtt tcc acc	2592
Val Glu Asp Leu Phe Gly Asp Lys His Ile Gln Val Leu Val Ser Thr	
849 854 859 864	
gca act ctg gcg tgg ggt gta aat ctt cct gca cat aca gtc atc att	2640
Ala Thr Leu Ala Trp Gly Val Asn Leu Pro Ala His Thr Val Ile Ile	
865 870 875 880	
aaa ggt acc caa gtg tac agt cca gag aag ggg cgt tgg aca gag ctg	2688
Lys Gly Thr Gln Val Tyr Ser Pro Glu Lys Gly Arg Trp Thr Glu Leu	
881 886 891 896	
gga gca ctg gat atc ctg cag atg ctg ggc cgt gct gga cgg ccg cag	2736
Gly Ala Leu Asp Ile Leu Gln Met Leu Gly Arg Ala Gly Arg Pro Gln	
897 902 907 912	
tat gac acc aag ggt gaa ggc atc ctc atc aca tcc cat ggg gag ctc	2784
Tyr Asp Thr Lys Gly Glu Gly Ile Leu Ile Thr Ser His Gly Glu Leu	
913 918 923 928	
cag tac tac ctc tcc ctc ctc aac cag cag ctg cct atc gag agc cag	2832
Gln Tyr Tyr Leu Ser Leu Leu Asn Gln Gln Leu Pro Ile Glu Ser Gln	
929 934 939 944	

atg gtc tcc aag ctg cct gac atg ctc aat gcg gaa att gtt ctg ggc	2880
Met Val Ser Lys Leu Pro Asp Met Leu Asn Ala Glu Ile Val Leu Gly	
945 950 955 960	
aat gtc cag aat gca aag gat gca gtg aac tgg ctg ggc tat gcc tac	2928
Asn Val Gln Asn Ala Lys Asp Ala Val Asn Trp Leu Gly Tyr Ala Tyr	
961 966 971 976	
cta tac atc cga atg ctc cgg tcc cct acc ctc tat ggc att tct cat	2976
Leu Tyr Ile Arg Met Leu Arg Ser Pro Thr Leu Tyr Gly Ile Ser His	
977 982 987 992	
gat gac ctc aag gga gat ccc ttg ctg gac cag cgc cga ctc gat ctt	3024
Asp Asp Leu Lys Gly Asp Pro Leu Leu Asp Gln Arg Arg Leu Asp Leu	
993 998 1003 1008	
gtt cac act gct gcc ttg atg ctg gac aag aac aat ctg gtc aag tac	3072
Val His Thr Ala Ala Leu Met Leu Asp Lys Asn Asn Leu Val Lys Tyr	
1009 1014 1019 1024	
gac aag aag aca ggc aac ttc cag gtg aca gaa ctt ggc cgg ata gca	3120
Asp Lys Lys Thr Gly Asn Phe Gln Val Thr Glu Leu Gly Arg Ile Ala	
1025 1030 1035 1040	
agt cac tac tat atc acc aat gat act gtg cag acc tac aac cag ctg	3168
Ser His Tyr Tyr Ile Thr Asn Asp Thr Val Gln Thr Tyr Asn Gln Leu	
1041 1046 1051 1056	
ctg aag cct act ctg agt gag att gag ctt ttc cga gtg ttc tcc ttg	3216
Leu Lys Pro Thr Leu Ser Glu Ile Glu Leu Phe Arg Val Phe Ser Leu	
1057 1062 1067 1072	
tcc tca gag ttc aag aac atc act gta aga gag gag gag aag ctg gag	3264
Ser Ser Glu Phe Lys Asn Ile Thr Val Arg Glu Glu Glu Lys Leu Glu	
1073 1078 1083 1088	
ctg cag aag ttg ctg gag aga gtg ccc atc cct gta aag gag agc att	3312
Leu Gln Lys Leu Leu Glu Arg Val Pro Ile Pro Val Lys Glu Ser Ile	
1089 1094 1099 1104	
gag gaa ccc agc gct aag atc aac gtg ctt ctc caa gcc ttc atc tca	3360
Glu Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Phe Ile Ser	
1105 1110 1115 1120	
cag ctg aaa ctc gaa ggc ttt gcg ctg atg gct gac atg gtg tat gtg	3408
Gln Leu Lys Leu Glu Gly Phe Ala Leu Met Ala Asp Met Val Tyr Val	
1121 1126 1131 1136	
acc cag tcg gct ggc cgg ttg atg cgt gca atc ttc gaa att gtc ctg	3456
Thr Gln Ser Ala Gly Arg Leu Met Arg Ala Ile Phe Glu Ile Val Leu	
1137 1142 1147 1152	
aac cga ggt tgg gca cag ctt aca gat aag acc ctg aat ctc tgc aag	3504
Asn Arg Gly Trp Ala Gln Leu Thr Asp Lys Thr Leu Asn Leu Cys Lys	
1153 1158 1163 1168	
atg att gac aag cgc atg tgg cag tcc atg tgt cct ctt cgc cag ttc	3552

Met Ile Asp Lys Arg Met Trp Gln Ser Met Cys Pro Leu Arg Gln Phe	
1169 1174 1179 1184	
cga aaa ctt cct gag gaa gta gtg aag aag att gag aag aaa aac ttc	3600
Arg Lys Leu Pro Glu Glu Val Val Lys Lys Ile Glu Lys Lys Asn Phe	
1185 1190 1195 1200	
ccc ttt gag cgg ctg tat gac ttg aat cat aat gag ata ggt gaa ctt	3648
Pro Phe Glu Arg Leu Tyr Asp Leu Asn His Asn Glu Ile Gly Glu Leu	
1201 1206 1211 1216	
att cga atg ccg aag atg ggg aag acc atc cac aag tat gtc cat ctt	3696
Ile Arg Met Pro Lys Met Gly Lys Thr Ile His Lys Tyr Val His Leu	
1217 1222 1227 1232	
ttc ccc aag ttg gag ttg tca gtg cac ctg cag cct att aca cgc tct	3744
Phe Pro Lys Leu Glu Leu Ser Val His Leu Gln Pro Ile Thr Arg Ser	
1233 1238 1243 1248	
acg ctg aaa gta gag ctg act atc aca cca gat ttc cag tgg gat gaa	3792
Thr Leu Lys Val Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Glu	
1249 1254 1259 1264	
aag gtc cat ggt tgc tca gag gca ttt tgg att ctg gtg gag gat gtg	3840
Lys Val His Gly Ser Ser Glu Ala Phe Trp Ile Leu Val Glu Asp Val	
1265 1270 1275 1280	
gac agc gag gtg att ctg cac cat gaa tat ttt ctg ctg aag gcc aag	3888
Asp Ser Glu Val Ile Leu His His Glu Tyr Phe Leu Leu Lys Ala Lys	
1281 1286 1291 1296	
tat gcc cag gat gag cac ctc atc aca ttc ttt gtt cca gtc ttt gaa	3936
Tyr Ala Gln Asp Glu His Leu Ile Thr Phe Phe Val Pro Val Phe Glu	
1297 1302 1307 1312	
cca cta cct cct cag tac ttc att cga gta gtg tct gat cgc tgg ctc	3984
Pro Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Arg Trp Leu	
1313 1318 1323 1328	
tct tgt gag acg cag cta cct gtc tcc ttc cgg cat ctg atc cta cca	4032
Ser Cys Glu Thr Gln Leu Pro Val Ser Phe Arg His Leu Ile Leu Pro	
1329 1334 1339 1344	
gag aag tac cca cct cca act gaa ctg ttg gac ctg cag cca ttg cct	4080
Glu Lys Tyr Pro Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro	
1345 1350 1355 1360	
gtg tct gct ctg aga aac agt gct ttt gag agc ctt tac caa gat aaa	4128
Val Ser Ala Leu Arg Asn Ser Ala Phe Glu Ser Leu Tyr Gln Asp Lys	
1361 1366 1371 1376	
ttt cct ttc ttc aat ccc atc cag act caa gta ttt aat acc gtg tac	4176
Phe Pro Phe Phe Asn Pro Ile Gln Thr Gln Val Phe Asn Thr Val Tyr	
1377 1382 1387 1392	
aac agt gat gat aac gtg ttt gtg ggg gcc ccc acg ggc agc ggg aag	4224
Asn Ser Asp Asp Asn Val Phe Val Gly Ala Pro Thr Gly Ser Gly Lys	

1393	1398	1403	1408	
act atc tgc gcg gag ttt gcc atc ctt cgg atg ctg ctg cag aat tct				4272
Thr Ile Cys Ala Glu Phe Ala Ile Leu Arg Met Leu Leu Gln Asn Ser				
1409	1414	1419	1424	
gag gga cgc tgt gtc tac att acc cct atg agg ctc tgg cag gag cag				4320
Glu Gly Arg Cys Val Tyr Ile Thr Pro Met Arg Leu Trp Gln Glu Gln				
1425	1430	1435	1440	
gta tac atg gac tgg tat gag aag ttt cag gac agg ctc aac aag aag				4368
Val Tyr Met Asp Trp Tyr Glu Lys Phe Gln Asp Arg Leu Asn Lys Lys				
1441	1446	1451	1456	
gtc gtg ctg ctg acg ggg gag acc agc aca gac ctg aag ctc ctg ggc				4416
Val Val Leu Leu Thr Gly Glu Thr Ser Thr Asp Leu Lys Leu Leu Gly				
1457	1462	1467	1472	
aaa ggc aac atc atc atc agt acc cct gag aag tgg gac atc ctc tct				4464
Lys Gly Asn Ile Ile Ile Ser Thr Pro Glu Lys Trp Asp Ile Leu Ser				
1473	1478	1483	1488	
cgg agg tgg aag cag cgc aag aac gtc cag aac att aac ctc ttt gtg				4512
Arg Arg Trp Lys Gln Arg Lys Asn Val Gln Asn Ile Asn Leu Phe Val				
1489	1494	1499	1504	
gtg gat gag gtc cac ctt att ggg ggc gag aat ggg cct gtc ttg gaa				4560
Val Asp Glu Val His Leu Ile Gly Gly Glu Asn Gly Pro Val Leu Glu				
1505	1510	1515	1520	
gtg atc tgc tcc cgg atg cgc tac atc tcc tcc cag att gag cgg ccc				4608
Val Ile Cys Ser Arg Met Arg Tyr Ile Ser Ser Gln Ile Glu Arg Pro				
1521	1526	1531	1536	
att cgc att gtg gca ctt agc tcc tca ctc tcc aat gcc aag gat gtg				4656
Ile Arg Ile Val Ala Leu Ser Ser Ser Leu Ser Asn Ala Lys Asp Val				
1537	1542	1547	1552	
gct cac tgg ctg ggc tgc agt gcc acc tcc acc ttc aac ttc cat cct				4704
Ala His Trp Leu Gly Cys Ser Ala Thr Ser Thr Phe Asn Phe His Pro				
1553	1558	1563	1568	
aat gtg cgc cct gta cct ttg gaa ctg cac atc cag ggc ttc aac atc				4752
Asn Val Arg Pro Val Pro Leu Glu Leu His Ile Gln Gly Phe Asn Ile				
1569	1574	1579	1584	
agt cac aca cag act cgc ctg ctc tct atg gcc aag cct gtg ttc cat				4800
Ser His Thr Gln Thr Arg Leu Leu Ser Met Ala Lys Pro Val Phe His				
1585	1590	1595	1600	
gct atc acc aaa cac tca ccc aag aag cct gtc atc gtt ttt gtc cca				4848
Ala Ile Thr Lys His Ser Pro Lys Lys Pro Val Ile Val Phe Val Pro				
1601	1606	1611	1616	
tct cgt aag cag acc cgc ctc act gca ata gac atc ctc act acc tgt				4896
Ser Arg Lys Gln Thr Arg Leu Thr Ala Ile Asp Ile Leu Thr Thr Cys				
1617	1622	1627	1632	

gca gca gac atc cag cgg cag agg ttc ctg cac tgc acc gag aag gac	4944
Ala Ala Asp Ile Gln Arg Gln Arg Phe Leu His Cys Thr Glu Lys Asp	
1633 1638 1643 1648	
ctg atc cct tac ctg gag aag ctc agt gac agc aca ctc aaa gag acc	4992
Leu Ile Pro Tyr Leu Glu Lys Leu Ser Asp Ser Thr Leu Lys Glu Thr	
1649 1654 1659 1664	
ctg tta aat ggg gtg ggc tac ctg cat gaa ggc ctg agc ccc atg gag	5040
Leu Leu Asn Gly Val Gly Tyr Leu His Glu Gly Leu Ser Pro Met Glu	
1665 1670 1675 1680	
agg cgc ctg gta gag cag ctc ttc agc tcc ggg gct atc cag gtg gtg	5088
Arg Arg Leu Val Glu Gln Leu Phe Ser Ser Gly Ala Ile Gln Val Val	
1681 1686 1691 1696	
gta gct tct cgg agt ctc tgc tgg ggc atg aat gtt gct gct cat cta	5136
Val Ala Ser Arg Ser Leu Cys Trp Gly Met Asn Val Ala Ala His Leu	
1697 1702 1707 1712	
gtg atc atc atg gat act ctg tac tac aat ggc aag atc cat gcc tat	5184
Val Ile Ile Met Asp Thr Leu Tyr Tyr Asn Gly Lys Ile His Ala Tyr	
1713 1718 1723 1728	
gtg gat tac ccc atc tat gat gtg ctt cag atg gtg ggc cat gcc aac	5232
Val Asp Tyr Pro Ile Tyr Asp Val Leu Gln Met Val Gly His Ala Asn	
1729 1734 1739 1744	
cgg ccc ctg cag gat gat gag ggg cgc tgt gtc atc atg tgt cag ggt	5280
Arg Pro Leu Gln Asp Asp Glu Gly Arg Cys Val Ile Met Cys Gln Gly	
1745 1750 1755 1760	
tct aaa aag gat ttt ttc aaa aaa ttt ttg tat gag cca ttg cca gta	5328
Ser Lys Lys Asp Phe Phe Lys Lys Phe Leu Tyr Glu Pro Leu Pro Val	
1761 1766 1771 1776	
gag tct cac ctg gac cac tgt atg cat gac cac ttc aat gct gag att	5376
Glu Ser His Leu Asp His Cys Met His Asp His Phe Asn Ala Glu Ile	
1777 1782 1787 1792	
gtc acc aag acc att gag aac aag cag gat gct gtg gac tac ctc acc	5424
Val Thr Lys Thr Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr Leu Thr	
1793 1798 1803 1808	
tgg acc ttt ctg tat cgc aga atg aca cag aac ccc aat tac tac aac	5472
Trp Thr Phe Leu Tyr Arg Arg Met Thr Gln Asn Pro Asn Tyr Tyr Asn	
1809 1814 1819 1824	
ctg cag ggg ata tcc cat cgt cat ctg tct gac cac ctg tca gag ctg	5520
Leu Gln Gly Ile Ser His Arg His Leu Ser Asp His Leu Ser Glu Leu	
1825 1830 1835 1840	
gtg gag cag acc ctc agt gac ctg gag cag tcc aaa tgc atc agt att	5568
Val Glu Gln Thr Leu Ser Asp Leu Glu Gln Ser Lys Cys Ile Ser Ile	
1841 1846 1851 1856	

gag gac gag atg gat gtg gcc cct ctg aac ctg ggc atg att gct gcc	5616
Glu Asp Glu Met Asp Val Ala Pro Leu Asn Leu Gly Met Ile Ala Ala	
1857 1862 1867 1872	
tac tat tac ata aac tac acc acc att gag ctc ttc agc atg tct ctg	5664
Tyr Tyr Tyr Ile Asn Tyr Thr Thr Ile Glu Leu Phe Ser Met Ser Leu	
1873 1878 1883 1888	
aat gct aaa acc aag gtt cga gga ctt att gag atc att tcc aat gca	5712
Asn Ala Lys Thr Lys Val Arg Gly Leu Ile Glu Ile Ile Ser Asn Ala	
1889 1894 1899 1904	
gca gag tat gag aac att cca atc agg cat cat gaa gac aac ctc ctg	5760
Ala Glu Tyr Glu Asn Ile Pro Ile Arg His His Glu Asp Asn Leu Leu	
1905 1910 1915 1920	
cgc cag ttg gct cag aag gtc ccc cac aag ctg aat aac ccc aag ttc	5808
Arg Gln Leu Ala Gln Lys Val Pro His Lys Leu Asn Asn Pro Lys Phe	
1921 1926 1931 1936	
aat gat cca cat gtg aag acc aat ctg ctg ctg cag gct cac ctg tcc	5856
Asn Asp Pro His Val Lys Thr Asn Leu Leu Gln Ala His Leu Ser	
1937 1942 1947 1952	
cgc atg cag cta agt gct gaa cta cag tca gac aca gag gag atc ctt	5904
Arg Met Gln Leu Ser Ala Glu Leu Gln Ser Asp Thr Glu Glu Ile Leu	
1953 1958 1963 1968	
agt aag gca atc cgg cta att cag gcc tgt gtg gat gta ctc tcc agt	5952
Ser Lys Ala Ile Arg Leu Ile Gln Ala Cys Val Asp Val Leu Ser Ser	
1969 1974 1979 1984	
aat ggg tgg ctt agt cct gct ctg gca gcc atg gaa ctg gcc cag atg	6000
Asn Gly Trp Leu Ser Pro Ala Leu Ala Ala Met Glu Leu Ala Gln Met	
1985 1990 1995 2000	
gtc acc caa gcc atg tgg tct gag gac tct tac ctg agg cgg ttg ccc	6048
Val Thr Gln Ala Met Trp Ser Glu Asp Ser Tyr Leu Arg Arg Leu Pro	
2001 2006 2011 2016	
cct ttc cct tcg ggg ctt ttc aaa cgt tgc aca gat aag gga gtg gag	6096
Pro Phe Pro Ser Gly Leu Phe Lys Arg Cys Thr Asp Lys Gly Val Glu	
2017 2022 2027 2032	
agt gtt ttt gac atc atg gag atg gag gat gaa gaa cgg aat gca ttg	6144
Ser Val Phe Asp Ile Met Glu Met Glu Asp Glu Glu Arg Asn Ala Leu	
2033 2038 2043 2048	
ctt cag ttg act gac agc cag att gca gat gtg gcc cgc ttc tgt aac	6192
Leu Gln Leu Thr Asp Ser Gln Ile Ala Asp Val Ala Arg Phe Cys Asn	
2049 2054 2059 2064	
cgc tac ccg aat att gaa ctg tcc tat gaa gtg gtg gat aaa gac agc	6240
Arg Tyr Pro Asn Ile Glu Leu Ser Tyr Glu Val Val Asp Lys Asp Ser	
2065 2070 2075 2080	
atc cgc agt ggc gga cca gtt gtg gtg cta gtg caa ctg gag cga gag	6288

gag gaa aga aga gcc aag cga aga aag cgt gat gag gac cgg cat gac	240
Glu Glu Arg Arg Ala Lys Arg Arg Lys Arg Asp Glu Asp Arg His Asp	
65 70 75 80	
atc aac aag atg aag ggt tat act ctg ctg tcg gag ggc att gat gag	288
Ile Asn Lys Met Lys Gly Tyr Thr Leu Leu Ser Glu Gly Ile Asp Glu	
81 86 91 96	
atg gtg ggc atc atc tac aag ccc aaa act aaa gag act cgg gag acc	336
Met Val Gly Ile Ile Tyr Lys Pro Lys Thr Lys Glu Thr Arg Glu Thr	
97 102 107 112	
tat gag gtg cta ctc agc ttc atc cag gct gct ctt ggg gac cag cca	384
Tyr Glu Val Leu Leu Ser Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro	
113 118 123 128	
cgt gat atc ctt tgt ggg gca gct gat gaa gtt cta gct gtt cta aag	432
Arg Asp Ile Leu Cys Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys	
129 134 139 144	
aat gaa aag ctg cgg gac aag gaa agg cga aag gag att gac ctg ctg	480
Asn Glu Lys Leu Arg Asp Lys Glu Arg Arg Lys Glu Ile Asp Leu Leu	
145 150 155 160	
ctg ggt caa aca gat gat acc aga tac cat gtg cta gtg aac ctg ggc	528
Leu Gly Gln Thr Asp Asp Thr Arg Tyr His Val Leu Val Asn Leu Gly	
161 166 171 176	
aaa aag atc aca gac tat ggt gga gat aag gaa atc caa aat atg gat	576
Lys Lys Ile Thr Asp Tyr Gly Gly Asp Lys Glu Ile Gln Asn Met Asp	
177 182 187 192	
gac aac att gat gag aca tac ggt gtg aat gtg cag ttt gag tct gat	624
Asp Asn Ile Asp Glu Thr Tyr Gly Val Asn Val Gln Phe Glu Ser Asp	
193 198 203 208	
gag gag gaa ggt gat gaa gac gta tac ggg gag gtt cga gaa gag gca	672
Glu Glu Glu Gly Asp Glu Asp Val Tyr Gly Glu Val Arg Glu Glu Ala	
209 214 219 224	
tct gat gat gac atg gaa ggg gac gag gct gtc gtg cgc tgc acc ctc	720
Ser Asp Asp Asp Met Glu Gly Asp Glu Ala Val Val Arg Cys Thr Leu	
225 230 235 240	
tcg gct aat atg tat gtt gat gaa atc tta gtc tgg tgt gct tct gaa	768
Ser Ala Asn Met Tyr Val Asp Glu Ile Leu Val Trp Cys Ala Ser Glu	
241 246 251 256	
ctc aat att cca gag ttt ttt cct ctg gaa agt cct cac aag aag gtg	816
Leu Asn Ile Pro Glu Phe Phe Pro Leu Glu Ser Pro His Lys Lys Val	
257 262 267 272	
ggc tat gga ttg tca agt aga act tgg ttg cag ggt ggt ggc aaa gtg	864
Gly Tyr Gly Leu Ser Ser Arg Thr Trp Leu Gln Gly Gly Gly Lys Val	
273 278 283 288	
atc gag gct ggc aga gac ctg ctc gta gcc tca ggt gaa ctg atg agt	912

Ile Glu Ala Gly Arg Asp Leu Leu Val Ala Ser Gly Glu Leu Met Ser	
289 294 299 304	
tcc aag aag aag gat ttg cac cct cgg gat att gat gca ttt tgg ctg	960
Ser Lys Lys Lys Asp Leu His Pro Arg Asp Ile Asp Ala Phe Trp Leu	
305 310 315 320	
cag cgg cag ctc agt cgt ttc tat gat gat gcc atc gtg tcg cag aag	1008
Gln Arg Gln Leu Ser Arg Phe Tyr Asp Asp Ala Ile Val Ser Gln Lys	
321 326 331 336	
aag gca gat gaa gta ttg gag att ttg aag acg gcc agt gat gat cgg	1056
Lys Ala Asp Glu Val Leu Glu Ile Leu Lys Thr Ala Ser Asp Asp Arg	
337 342 347 352	
gaa tgt gaa aat cag ctg gtt ctg ctg ctt ggt ttc aac acc ttt gat	1104
Glu Cys Glu Asn Gln Leu Val Leu Leu Leu Gly Phe Asn Thr Phe Asp	
353 358 363 368	
ttc att aaa gtg ttg cgg cag cac agg atg atg att tta tac tgt acc	1152
Phe Ile Lys Val Leu Arg Gln His Arg Met Met Ile Leu Tyr Cys Thr	
369 374 379 384	
ttg ctg gcc agt gca caa agt gaa gct gaa aag gaa agg att atg gga	1200
Leu Leu Ala Ser Ala Gln Ser Glu Ala Glu Lys Glu Arg Ile Met Gly	
385 390 395 400	
aag atg gaa gct gac cca gag cta tcc aag ttc ctc tac cag ctt cat	1248
Lys Met Glu Ala Asp Pro Glu Leu Ser Lys Phe Leu Tyr Gln Leu His	
401 406 411 416	
gaa acc gag aag gag gat ctg atc cga gag gaa agg tcc cgg aga gag	1296
Glu Thr Glu Lys Glu Asp Leu Ile Arg Glu Glu Arg Ser Arg Arg Glu	
417 422 427 432	
cga gtg cgt cag tct cga atg gac aca gat ctg gaa acc atg gat ctc	1344
Arg Val Arg Gln Ser Arg Met Asp Thr Asp Leu Glu Thr Met Asp Leu	
433 438 443 448	
gac cag ggt gga gag gca ctg gct cca cgg cag gtt ctg gac ttg gag	1392
Asp Gln Gly Gly Glu Ala Leu Ala Pro Arg Gln Val Leu Asp Leu Glu	
449 454 459 464	
gac ctg gtt ttt acc caa ggg agc cac ttt atg gcc aat aaa cgc tgt	1440
Asp Leu Val Phe Thr Gln Gly Ser His Phe Met Ala Asn Lys Arg Cys	
465 470 475 480	
cag ctt cct gat gga tcc ttc cgt cgc cag cgt aag ggc tat gaa gag	1488
Gln Leu Pro Asp Gly Ser Phe Arg Arg Gln Arg Lys Gly Tyr Glu Glu	
481 486 491 496	
gtg cat gtg cct gct ctg aag ccc aag ccc ttt ggc tca gaa gaa caa	1536
Val His Val Pro Ala Leu Lys Pro Lys Pro Phe Gly Ser Glu Glu Gln	
497 502 507 512	
ctg ctt cca gtg gaa aag ctg cca aag tat gcc cag gct ggg ttt gag	1584
Leu Leu Pro Val Glu Lys Leu Pro Lys Tyr Ala Gln Ala Gly Phe Glu	

513	518	523	528	
ggc ttc aaa aca ctg aat cgg atc cag agt aag ctc tac cgt gct gcc				1632
Gly Phe Lys Thr Leu Asn Arg Ile Gln Ser Lys Leu Tyr Arg Ala Ala				
529	534	539	544	
ctt gag acg gat gag aat ctg ctg ctg tgt gct cct act ggt gct ggg				1680
Leu Glu Thr Asp Glu Asn Leu Leu Leu Cys Ala Pro Thr Gly Ala Gly				
545	550	555	560	
aag acc aac gtg gcc ctg atg tgc atg ctc cga gag att ggg aaa cac				1728
Lys Thr Asn Val Ala Leu Met Cys Met Leu Arg Glu Ile Gly Lys His				
561	566	571	576	
ata aac atg gac ggc acc atc aat gtg gat gac ttc aag att atc tac				1776
Ile Asn Met Asp Gly Thr Ile Asn Val Asp Asp Phe Lys Ile Ile Tyr				
577	582	587	592	
att gcc ccc atg cgc tcc ttg gtg cag gag atg gtg ggc agc ttt gga				1824
Ile Ala Pro Met Arg Ser Leu Val Gln Glu Met Val Gly Ser Phe Gly				
593	598	603	608	
aag cgc ctg gcc act tat ggc atc act gtt gct gaa ctg act ggg gac				1872
Lys Arg Leu Ala Thr Tyr Gly Ile Thr Val Ala Glu Leu Thr Gly Asp				
609	614	619	624	
cac cag ctg tgc aaa gaa gag atc agt gcc act cag atc atc gtc tgc				1920
His Gln Leu Cys Lys Glu Glu Ile Ser Ala Thr Gln Ile Ile Val Cys				
625	630	635	640	
acc ccc gag aag tgg gac atc atc acc cgc aag gtg gat gag att cat				1968
Thr Pro Glu Lys Trp Asp Ile Ile Thr Arg Lys Val Asp Glu Ile His				
641	646	651	656	
ctt ctc cac gat gac aga ggt cct gtc tta gaa gct tta gtg gcc agg				2016
Leu Leu His Asp Asp Arg Gly Pro Val Leu Glu Ala Leu Val Ala Arg				
657	662	667	672	
gcc atc cga aac att gag atg acc caa gag gat gtc cga ctc att ggt				2064
Ala Ile Arg Asn Ile Glu Met Thr Gln Glu Asp Val Arg Leu Ile Gly				
673	678	683	688	
ctc agt gcc acc cta ccc aac tat gaa gat gta gcc acc ttt cta cgt				2112
Leu Ser Ala Thr Leu Pro Asn Tyr Glu Asp Val Ala Thr Phe Leu Arg				
689	694	699	704	
gtt gac cct gcc aag ggt ctc ttt tac ttt gac aac agc ttc cgt cca				2160
Val Asp Pro Ala Lys Gly Leu Phe Tyr Phe Asp Asn Ser Phe Arg Pro				
705	710	715	720	
gtg cct ctg gaa cag aca tat gtg ggt atc aca gag aaa aaa gct atc				2208
Val Pro Leu Glu Gln Thr Tyr Val Gly Ile Thr Glu Lys Lys Ala Ile				
721	726	731	736	
aag cgt ttc cag atc atg aat gaa atc gtc tat gaa aaa atc atg gaa				2256
Lys Arg Phe Gln Ile Met Asn Glu Ile Val Tyr Glu Lys Ile Met Glu				
737	742	747	752	

cat gct gga aaa aat cag gtg ctg gtg ttt gtc cac tcc cgg aag gag	2304
His Ala Gly Lys Asn Gln Val Leu Val Phe Val His Ser Arg Lys Glu	
753 758 763 768	
act gga aag aca gcc agg gcc atc cgg gac atg tgc cta gaa aag gac	2352
Thr Gly Lys Thr Ala Arg Ala Ile Arg Asp Met Cys Leu Glu Lys Asp	
769 774 779 784	
act ctg ggt ctg ttt ctg agg gag ggc tca gcc tcc aca gaa gtc ctg	2400
Thr Leu Gly Leu Phe Leu Arg Glu Gly Ser Ala Ser Thr Glu Val Leu	
785 790 795 800	
cga aca gaa gct gag cag tgc aag aac cta gag ctg aag gat ctt ctg	2448
Arg Thr Glu Ala Glu Gln Cys Lys Asn Leu Glu Leu Lys Asp Leu Leu	
801 806 811 816	
cct tat ggc ttt gct att cat cac gca ggc atg acc agg gtt gac cga	2496
Pro Tyr Gly Phe Ala Ile His His Ala Gly Met Thr Arg Val Asp Arg	
817 822 827 832	
aca ctc gtg gag gat ctt ttt gct gat aaa cat att cag gtt tta gtt	2544
Thr Leu Val Glu Asp Leu Phe Ala Asp Lys His Ile Gln Val Leu Val	
833 838 843 848	
tcc aca gca act cta gct tgg ggt gtg aat ctc cct gca cat aca gtc	2592
Ser Thr Ala Thr Leu Ala Trp Gly Val Asn Leu Pro Ala His Thr Val	
849 854 859 864	
atc atc aaa ggc acc cag gtg tac agt cca gag aag ggg cgt tgg aca	2640
Ile Ile Lys Gly Thr Gln Val Tyr Ser Pro Glu Lys Gly Arg Trp Thr	
865 870 875 880	
gaa ctg gga gca ctg gac att ctg cag atg ctg gga cgt gcc gga aga	2688
Glu Leu Gly Ala Leu Asp Ile Leu Gln Met Leu Gly Arg Ala Gly Arg	
881 886 891 896	
ccc cag tat gac acc aag ggt gaa ggc ata ctc atc aca tct cat ggg	2736
Pro Gln Tyr Asp Thr Lys Gly Glu Gly Ile Leu Ile Thr Ser His Gly	
897 902 907 912	
gag cta cag tac tac ctg tcc ctc ctc aat caa caa ctt cct att gaa	2784
Glu Leu Gln Tyr Tyr Leu Ser Leu Leu Asn Gln Gln Leu Pro Ile Glu	
913 918 923 928	
agc cag atg gtt tca aag ctt cct gac atg ctc aat gca gaa atc gtg	2832
Ser Gln Met Val Ser Lys Leu Pro Asp Met Leu Asn Ala Glu Ile Val	
929 934 939 944	
cta gga aat gtc cag aat gcc aag gat gcg gtg aac tgg ctg ggc tat	2880
Leu Gly Asn Val Gln Asn Ala Lys Asp Ala Val Asn Trp Leu Gly Tyr	
945 950 955 960	
gcc tac ctc tat atc cga atg ctg cga tcc cca acc ctc tat ggc atc	2928
Ala Tyr Leu Tyr Ile Arg Met Leu Arg Ser Pro Thr Leu Tyr Gly Ile	
961 966 971 976	

tct cat gat gac ctc aag gga gat ccc ctg ctg gac cag cgc cga cta	2976
Ser His Asp Asp Leu Lys Gly Asp Pro Leu Leu Asp Gln Arg Arg Leu	
977 982 987 992	
gat ctg gtt cat aca gct gcc ctg atg ctg gac aag aac aat ctg gtc	3024
Asp Leu Val His Thr Ala Ala Leu Met Leu Asp Lys Asn Asn Leu Val	
993 998 1003 1008	
aag tac gac aag aag acg ggc aac ttc cag gtg aca gaa ctg ggc cgt	3072
Lys Tyr Asp Lys Lys Thr Gly Asn Phe Gln Val Thr Glu Leu Gly Arg	
1009 1014 1019 1024	
ata gcc agc cac tac tac atc acc aat gat aca gtg cag act tac aac	3120
Ile Ala Ser His Tyr Tyr Ile Thr Asn Asp Thr Val Gln Thr Tyr Asn	
1025 1030 1035 1040	
cag ctg ctg aag ccc acc ctg agt gag att gag ctt ttc agg gtc ttc	3168
Gln Leu Leu Lys Pro Thr Leu Ser Glu Ile Glu Leu Phe Arg Val Phe	
1041 1046 1051 1056	
tca ttg tcc tct gag ttc aag aac atc aca gtg aga gag gag gag aag	3216
Ser Leu Ser Ser Glu Phe Lys Asn Ile Thr Val Arg Glu Glu Glu Lys	
1057 1062 1067 1072	
ctg gag ctg cag aag ttg ctg gag agg gtg cct atc cct gta aag gag	3264
Leu Glu Leu Gln Lys Leu Leu Glu Arg Val Pro Ile Pro Val Lys Glu	
1073 1078 1083 1088	
agc att gag gaa ccc agt gct aag atc aac gtt ctt ctg caa gcc ttc	3312
Ser Ile Glu Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Phe	
1089 1094 1099 1104	
atc tca cag ctg aaa ttg gag ggc ttt gca ctg atg gct gac atg gtg	3360
Ile Ser Gln Leu Lys Leu Glu Gly Phe Ala Leu Met Ala Asp Met Val	
1105 1110 1115 1120	
tat gtc aca cag tcg gct ggc cgg ttg atg cga gcg ata ttt gaa att	3408
Tyr Val Thr Gln Ser Ala Gly Arg Leu Met Arg Ala Ile Phe Glu Ile	
1121 1126 1131 1136	
gtc ctg aac cga ggt tgg gca cag ctt aca gac aag acc ctg aac ctc	3456
Val Leu Asn Arg Gly Trp Ala Gln Leu Thr Asp Lys Thr Leu Asn Leu	
1137 1142 1147 1152	
tgc aag atg atc gac aaa cgc atg tgg cag tcc atg tgt cct ctg cgc	3504
Cys Lys Met Ile Asp Lys Arg Met Trp Gln Ser Met Cys Pro Leu Arg	
1153 1158 1163 1168	
cag ttc cgg aaa ctc cct gag gaa gta gtg aag aag att gag aag aag	3552
Gln Phe Arg Lys Leu Pro Glu Glu Val Val Lys Lys Ile Glu Lys Lys	
1169 1174 1179 1184	
aat ttc ccc ttt gag cgt ctg tac gac ctg aat cat aat gag att ggg	3600
Asn Phe Pro Phe Glu Arg Leu Tyr Asp Leu Asn His Asn Glu Ile Gly	
1185 1190 1195 1200	
gag ctt atc cgc atg cca aag atg ggg aag acc atc cac aaa tat gtc	3648

Glu Leu Ile Arg Met Pro Lys Met Gly Lys Thr Ile His Lys Tyr Val	
1201	1206 1211 1216
cat ctg ttt ccc aag ttg gag ttg tca gtg cac ctg cag cct atc aca	3696
His Leu Phe Pro Lys Leu Glu Leu Ser Val His Leu Gln Pro Ile Thr	
1217	1222 1227 1232
cgc tcc acc ctg aag gtg gag ctg acc atc acg cca gac ttc cag tgg	3744
Arg Ser Thr Leu Lys Val Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp	
1233	1238 1243 1248
gat gaa aag gtg cat ggt tca tcc gag gct ttt tgg att ctg gtg gag	3792
Asp Glu Lys Val His Gly Ser Ser Glu Ala Phe Trp Ile Leu Val Glu	
1249	1254 1259 1264
gat gtg gac agc gag gtg att ctg cac cat gag tat ttt ctc ctc aag	3840
Asp Val Asp Ser Glu Val Ile Leu His His Glu Tyr Phe Leu Leu Lys	
1265	1270 1275 1280
gcc aag tac gcc cag gac gag cac ctc att aca ttc ttc gtg cct gtc	3888
Ala Lys Tyr Ala Gln Asp Glu His Leu Ile Thr Phe Phe Val Pro Val	
1281	1286 1291 1296
ttt gaa ccg ctg ccc cct cag tac ttc atc cga gtg gtg tct gac cgc	3936
Phe Glu Pro Leu Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Arg	
1297	1302 1307 1312
tgg ctc tct tgt gag acc cag ctg cct gtc tcc ttc cgg cac ctg atc	3984
Trp Leu Ser Cys Glu Thr Gln Leu Pro Val Ser Phe Arg His Leu Ile	
1313	1318 1323 1328
ttg ccg gag aag tac ccc cct cca acc gaa ctt ttg gac ctg cag ccc	4032
Leu Pro Glu Lys Tyr Pro Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro	
1329	1334 1339 1344
ttg ccc gtg tct gct ctg aga aac agt gcc ttt gag agt ctt tac caa	4080
Leu Pro Val Ser Ala Leu Arg Asn Ser Ala Phe Glu Ser Leu Tyr Gln	
1345	1350 1355 1360
gat aaa ttt cct ttc ttc aat ccc atc cag acc cag gtg ttt aac act	4128
Asp Lys Phe Pro Phe Phe Asn Pro Ile Gln Thr Gln Val Phe Asn Thr	
1361	1366 1371 1376
gta tac aac agt gac gac aac gtg ttt gtg ggg gcc ccc acg ggc agc	4176
Val Tyr Asn Ser Asp Asp Asn Val Phe Val Gly Ala Pro Thr Gly Ser	
1377	1382 1387 1392
ggg aag act att tgt gca gag ttt gcc atc ctg cga atg ctg ctg cag	4224
Gly Lys Thr Ile Cys Ala Glu Phe Ala Ile Leu Arg Met Leu Leu Gln	
1393	1398 1403 1408
agc tcg gag ggg cgc tgt gtg tac atc acc ccc atg gag gcc ctg gca	4272
Ser Ser Glu Gly Arg Cys Val Tyr Ile Thr Pro Met Glu Ala Leu Ala	
1409	1414 1419 1424
gag cag gta tac atg gac tgg tac gag aag ttc cag gac agg ctc aac	4320
Glu Gln Val Tyr Met Asp Trp Tyr Glu Lys Phe Gln Asp Arg Leu Asn	

1425	1430	1435	1440	
aag aag gtg gta ctc ctg	aca ggc gag acc agc	aca gac ctg aag ctg		4368
Lys Lys Val Val Leu Leu	Thr Gly Glu Thr Ser Thr	Asp Leu Lys Leu		
1441	1446	1451	1456	
ctg ggc aaa ggg aac att	atc atc agc acc cct	gag aag tgg gac ata		4416
Leu Gly Lys Gly Asn Ile	Ile Ile Ser Thr Pro	Glu Lys Trp Asp Ile		
1457	1462	1467	1472	
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Leu Ser Arg Arg Trp Lys	Gln Arg Lys Asn Val	Gln Asn Ile Asn Leu		
1473	1478	1483	1488	
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Phe Val Val Asp Glu Val	His Leu Ile Gly Gly	Glu Asn Gly Pro Val		
1489	1494	1499	1504	
tta gaa gtg atc tgc tcc	cga atg cgc tac atc	tcc tcc cag att gag		4560
Leu Glu Val Ile Cys Ser	Arg Met Arg Tyr Ile	Ser Ser Gln Ile Glu		
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cgg ccc att cgc att gtg	gca ctc agc tct tgc	ctc tcc aat gcc aag		4608
Arg Pro Ile Arg Ile Val	Ala Leu Ser Ser Leu	Ser Asn Ala Lys		
1521	1526	1531	1536	
gat gtg gcc cac tgg ctg	ggc tgc agt gcc acc	tcc acc ttc aac ttc		4656
Asp Val Ala His Trp Leu	Gly Cys Ser Ala Thr	Ser Thr Phe Asn Phe		
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cat ccc aat gtg cgt ccc	gtc ccc ttg gag ctg	cac atc cag ggc ttc		4704
His Pro Asn Val Arg Pro	Val Pro Leu Glu Leu	His Ile Gln Gly Phe		
1553	1558	1563	1568	
aac atc agc cat aca caa	acc cgc ctg ctc tcc	atg gcc aag cct gtg		4752
Asn Ile Ser His Thr Gln	Thr Arg Leu Leu Ser	Met Ala Lys Pro Val		
1569	1574	1579	1584	
tac cat gct atc acc aag	cac tgc ccc aag aag	cct gtc att gtc ttt		4800
Tyr His Ala Ile Thr Lys	His Ser Pro Lys Lys	Pro Val Ile Val Phe		
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gtg ccg tct cgc aag cag	acc cgc ctc act gcc	att gac atc ctc acc		4848
Val Pro Ser Arg Lys Gln	Thr Arg Leu Thr Ala	Ile Asp Ile Leu Thr		
1601	1606	1611	1616	
acc tgt gca gca gac atc	caa cgg cag agg ttc	ttg cac tgc acc gag		4896
Thr Cys Ala Ala Asp Ile	Gln Arg Gln Arg Phe	Leu His Cys Thr Glu		
1617	1622	1627	1632	
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Lys Asp Leu Ile Pro Tyr	Leu Glu Lys Leu Ser	Asp Ser Thr Leu Lys		
1633	1638	1643	1648	
gaa acg ctg cta aat ggg	gtg ggc tac ctg cat	gag ggg ctc agc ccc		4992
Glu Thr Leu Leu Asn Gly	Val Gly Tyr Leu His	Glu Gly Leu Ser Pro		
1649	1654	1659	1664	

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Met Glu Arg Arg Leu Val Glu Gln Leu Phe Ser Ser Gly Ala Ile Gln	
1665 1670 1675 1680	
gtg gtg gtg gct tct cgg agt ctc tgc tgg ggc atg aac gtg gct gcc	5088
Val Val Val Ala Ser Arg Ser Leu Cys Trp Gly Met Asn Val Ala Ala	
1681 1686 1691 1696	
cac ctg gta atc atc atg gat acc cag tac tac aat ggc aag atc cac	5136
His Leu Val Ile Ile Met Asp Thr Gln Tyr Tyr Asn Gly Lys Ile His	
1697 1702 1707 1712	
gcc tat gtg gat tac ccc atc tat gac gtg ctt cag atg gtg ggc cac	5184
Ala Tyr Val Asp Tyr Pro Ile Tyr Asp Val Leu Gln Met Val Gly His	
1713 1718 1723 1728	
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Ala Asn Arg Pro Leu Gln Asp Asp Glu Gly Arg Cys Val Ile Met Cys	
1729 1734 1739 1744	
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Gln Gly Ser Lys Lys Asp Phe Phe Lys Lys Phe Leu Tyr Glu Pro Leu	
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cca gta gaa tct cac ctg gac cac tgt atg cat gac cac ttc aat gct	5328
Pro Val Glu Ser His Leu Asp His Cys Met His Asp His Phe Asn Ala	
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Glu Ile Val Thr Lys Thr Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr	
1777 1782 1787 1792	
ctc acc tgg acc ttt ctg tac cgc cgc atg aca cag aac ccc aat tac	5424
Leu Thr Trp Thr Phe Leu Tyr Arg Arg Met Thr Gln Asn Pro Asn Tyr	
1793 1798 1803 1808	
tac aac ctg cag ggc atc tcc cat cgt cac ttg tcg gac cac ttg tca	5472
Tyr Asn Leu Gln Gly Ile Ser His Arg His Leu Ser Asp His Leu Ser	
1809 1814 1819 1824	
gag ctg gtg gag cag acc ctg agt gac ctg gag cag tcc aag tgc atc	5520
Glu Leu Val Glu Gln Thr Leu Ser Asp Leu Glu Gln Ser Lys Cys Ile	
1825 1830 1835 1840	
agc atc gag gac gag atg gac gtg gcg cct ctg aac cta ggc atg atc	5568
Ser Ile Glu Asp Glu Met Asp Val Ala Pro Leu Asn Leu Gly Met Ile	
1841 1846 1851 1856	
gcc gcc tac tat tac atc aac tac acc acc att gag ctc ttc agc atg	5616
Ala Ala Tyr Tyr Tyr Ile Asn Tyr Thr Thr Ile Glu Leu Phe Ser Met	
1857 1862 1867 1872	
tcc ctc aat gcc aag acc aag gtg cga ggg ctt atc gag atc atc tcc	5664
Ser Leu Asn Ala Lys Thr Lys Val Arg Gly Leu Ile Glu Ile Ile Ser	
1873 1878 1883 1888	

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ctc ctg agg cag ttg gct cag aag gtc ccc cac aag ctg aat aac cct Leu Leu Arg Gln Leu Ala Gln Lys Val Pro His Lys Leu Asn Asn Pro 1905 1910 1915 1920	5760
aag ttc aat gat ccg cac gtc aag acc aac ctg ctc ctg cag gct cac Lys Phe Asn Asp Pro His Val Lys Thr Asn Leu Leu Leu Gln Ala His 1921 1926 1931 1936	5808
ttg tct cgc atg cag ctg agt gct gag ttg cag tca gat acg gag gaa Leu Ser Arg Met Gln Leu Ser Ala Glu Leu Gln Ser Asp Thr Glu Glu 1937 1942 1947 1952	5856
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gtg gag agt gtt ttc gac atc atg gag atg gag gat gaa gaa cgg aac Val Glu Ser Val Phe Asp Ile Met Glu Met Glu Asp Glu Glu Arg Asn 2017 2022 2027 2032	6096
gcg ttg ctt cag ctg act gac agc cag att gca gat gtg gct cgc ttt Ala Leu Leu Gln Leu Thr Asp Ser Gln Ile Ala Asp Val Ala Arg Phe 2033 2038 2043 2048	6144
tgt aac cgc tac cct aat atc gaa cta tct tat gag gtg gta gat aag Cys Asn Arg Tyr Pro Asn Ile Glu Leu Ser Tyr Glu Val Val Asp Lys 2049 2054 2059 2064	6192
gac agc atc cgc agt ggc ggg cca gtt gtg gtg ctg gtg cag ctg gag Asp Ser Ile Arg Ser Gly Gly Pro Val Val Val Leu Val Gln Leu Glu 2065 2070 2075 2080	6240
cga gag gag gaa gtc aca ggc cct gtc att gcg cct ctc ttc ccg cag Arg Glu Glu Glu Val Thr Gly Pro Val Ile Ala Pro Leu Phe Pro Gln 2081 2086 2091 2096	6288
aaa cgt gaa gag ggc tgg tgg gtg gtg att gga gat gcc aag tcc aat Lys Arg Glu Glu Gly Trp Trp Val Val Ile Gly Asp Ala Lys Ser Asn 2097 2102 2107 2112	6336
agc ctc atc tcc atc aag agg ctg acc ttg cag cag aag gcc aag gtg	6384

Ser	Leu	Ile	Ser	Ile	Lys	Arg	Leu	Thr	Leu	Gln	Gln	Lys	Ala	Lys	Val	
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Lys	Leu	Asp	Phe	Val	Ala	Pro	Ala	Thr	Gly	Ala	His	Asn	Tyr	Thr	Leu	
2129					2134					2139					2144	
tac	ttc	atg	agt	gac	gct	tac	atg	gga	tgt	gac	cag	gag	tac	aaa	ttc	6480
Tyr	Phe	Met	Ser	Asp	Ala	Tyr	Met	Gly	Cys	Asp	Gln	Glu	Tyr	Lys	Phe	
2145					2150					2155					2160	
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Val	Arg	Thr	Arg	Ile	Lys	Ala	Phe	Leu	Ile	Trp	Ala	Tyr	Phe	Asp	Lys	
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Glu	Phe	Ser	Ile	Thr	Glu	Phe	Ser	Glu	Gly	Ala	Lys	Gln	Ala	Phe	Ala	
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cat	gta	tcc	aag	ttg	ctg	tca	cag	tgt	aaa	ttt	gat	ctg	ttg	gaa	gaa	493
His	Val	Ser	Lys	Leu	Leu	Ser	Gln	Cys	Lys	Phe	Asp	Leu	Leu	Glu	Glu	
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ctt	gtg	gcc	aaa	gag	gtg	cta	cat	gca	ttg	aaa	gaa	aag	gtt	act	tca	541
Leu	Val	Ala	Lys	Glu	Val	Leu	His	Ala	Leu	Lys	Glu	Lys	Val	Thr	Ser	

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cta cct gac aac cat aaa aat gcc ctt gct gct aac ata gat gaa att				589
Leu Pro Asp Asn His Lys Asn Ala Leu Ala Ala Asn Ile Asp Glu Ile				
77	82	87	92	
gta ttt aca tca aca gga gac atc tcc att tac tat gat gag aaa gga				637
Val Phe Thr Ser Thr Gly Asp Ile Ser Ile Tyr Tyr Asp Glu Lys Gly				
93	98	103	108	
agg aag ttt gtt aac atc ctg atg tgc ttt tgg tat cta acc agt gcc				685
Arg Lys Phe Val Asn Ile Leu Met Cys Phe Trp Tyr Leu Thr Ser Ala				
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aac atc ccc agt gaa act tta aga gga gcc agt gta ttc cag gtt aag				733
Asn Ile Pro Ser Glu Thr Leu Arg Gly Ala Ser Val Phe Gln Val Lys				
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Leu Gly Asn Gln Asn Val Glu Thr Lys Gln Leu Leu Ser Ala Ser Tyr				
141	146	151	156	
gag ttt cag agg gag ttc aca caa gga gta aag cct gac tgg acc att				829
Glu Phe Gln Arg Glu Phe Thr Gln Gly Val Lys Pro Asp Trp Thr Ile				
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Ala Arg Ile Glu His Ser Lys Leu Leu Glu *				
173	178	183		
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aag aag gac ggg agt gga gga gct tct gga act ttg cag ccg tca tcg	218
Lys Lys Asp Gly Ser Gly Gly Ala Ser Gly Thr Leu Gln Pro Ser Ser	
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Gly Gly Gly Ser Ser Asn Ser Arg Glu Arg His Arg Leu Val Ser Lys	
26 31 36 41	
cac aag cgg cat aag tcc aaa cac tcc aaa gac atg ggg ttg gtg acc	314
His Lys Arg His Lys Ser Lys His Ser Lys Asp Met Gly Leu Val Thr	
42 47 52 57	
ccc gaa gca gca tcc ctg ggc aca gtt atc aaa cct ttg gtg gag tat	362
Pro Glu Ala Ala Ser Leu Gly Thr Val Ile Lys Pro Leu Val Glu Tyr	
58 63 68 73	
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Asp Asp Ile Ser Ser Asp Ser Asp Thr Phe Ser Asp Asp Met Ala Phe	
74 79 84 89	
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Lys Leu Asp Arg Arg Glu Asn Asp Glu Arg Arg Gly Ser Asp Arg Ser	
90 95 100 105	
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Asp Arg Leu His Lys His Arg His His Gln His Arg Arg Ser Arg Asp	
106 111 116 121	
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Leu Leu Lys Ala Lys Gln Thr Glu Lys Glu Lys Ser Gln Glu Val Ser	
122 127 132 137	
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Ser Lys Ser Gly Ser Met Lys Asp Arg Ile Ser Gly Ser Ser Lys Arg	
138 143 148 153	
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Ser Asn Glu Glu Thr Asp Asp Tyr Gly Lys Ala Gln Val Ala Lys Ser	
154 159 164 169	
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Ser Ser Lys Glu Ser Arg Ser Ser Lys Leu His Lys Glu Lys Thr Arg	
170 175 180 185	
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Lys Glu Arg Glu Leu Lys Ser Gly His Lys Asp Arg Ser Lys Ser His	
186 191 196 201	
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Arg Lys Arg Glu Thr Pro Lys Ser Tyr Lys Thr Val Asp Ser Pro Lys	
202 207 212 217	

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Arg Arg Ser Arg Ser Pro His Arg Lys Trp Ser Asp Ser Ser Lys Gln	
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Asp Asp Ser Pro Ser Gly Ala Ser Tyr Gly Gln Asp Tyr Asp Leu Ser	
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Pro Ser Arg Ser His Thr Ser Ser Asn Tyr Asp Ser Tyr Lys Lys Ser	
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Pro Gly Ser Thr Ser Arg Arg Gln Ser Val Ser Pro Pro Tyr Lys Glu	
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Pro Ser Ala Tyr Gln Ser Ser Thr Arg Ser Pro Ser Pro Tyr Ser Arg	
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Pro Leu Pro Ser Arg Lys Ser Met Lys Ser Arg Ser Arg Ser Pro Ala	
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Tyr Ser Arg His Ser Ser Ser His Ser Lys Lys Lys Arg Ser Ser Ser	
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Ser Leu Gly Ala Glu Leu Ser Lys Lys Lys Lys Lys Lys Ala Ala Ala	
394 399 404 409	
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Phe Leu Pro Arg Lys Glu Asn Ser Ser Val Glu Ala Lys Asp Ser Gly	
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Pro Asp Thr Glu Leu Val Asn Val Thr His Leu Asn Thr Glu Val Lys	
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Asn Ser Ser Asp Thr Gly Lys Val Lys Leu Asp Glu Asn Ser Glu Lys	
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His Leu Val Lys Asp Leu Lys Ala Gln Gly Thr Arg Asp Ser Lys Pro	
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Ile Ala Leu Lys Glu Glu Ile Val Thr Pro Lys Glu Thr Glu Thr Ser	
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Glu Lys Glu Thr Pro Pro Pro Leu Pro Thr Ile Ala Ser Pro Pro Pro	
522 527 532 537	
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Pro Leu Pro Thr Thr Thr Pro Pro Pro Gln Thr Pro Pro Leu Pro Pro	
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Gln Pro Ala Phe Ser Gln Val Pro Ala Ser Ser Thr Ser Thr Leu Pro	
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Pro Ser Thr His Ser Lys Thr Ser Ala Val Ser Ser Gln Ala Asn Ser	
586 591 596 601	
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Gln Pro Pro Val Gln Val Ser Val Lys Thr Gln Val Ser Val Thr Ala	
602 607 612 617	
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Ala Ile Pro His Leu Lys Thr Ser Thr Leu Pro Pro Leu Pro Leu Pro	
618 623 628 633	
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Pro Leu Leu Pro Gly Gly Asp Asp Met Asp Ser Pro Lys Glu Thr Leu	
634 639 644 649	
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Pro Ser Lys Pro Val Lys Lys Glu Lys Glu Gln Arg Thr Arg His Leu	
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Pro Pro Asp Ser Pro Glu Pro Lys Ala Ile Thr Pro Pro Gln Gln Pro	
682 687 692 697	
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Tyr Lys Lys Arg Pro Lys Ile Cys Cys Pro Arg Tyr Gly Glu Arg Arg	
698 703 708 713	
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Gln Thr Glu Ser Asp Trp Gly Lys Arg Cys Val Asp Lys Phe Asp Ile	
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Tyr Leu Val Phe Glu Tyr Met Asp His Asp Leu Met Gly Leu Leu Glu	
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Ser Gly Leu Val His Phe Ser Glu Asp His Ile Lys Ser Phe Met Lys	
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Gln Leu Met Glu Gly Leu Glu Tyr Cys His Lys Lys Asn Phe Leu His	
842 847 852 857	
cgg gat att aag tgt tct aac att ttg ctg aat aac agt ggg caa atc	2762
Arg Asp Ile Lys Cys Ser Asn Ile Leu Leu Asn Asn Ser Gly Gln Ile	
858 863 868 873	
aaa cta gca gat ttt gga ctt gct cgg ctc tat aac tct gaa gag agt	2810
Lys Leu Ala Asp Phe Gly Leu Ala Arg Leu Tyr Asn Ser Glu Glu Ser	
874 879 884 889	
cgc cct tac aca aac aaa gtc att act ttg tgg tac cga cct cca gaa	2858
Arg Pro Tyr Thr Asn Lys Val Ile Thr Leu Trp Tyr Arg Pro Pro Glu	

890	895	900	905	
cta ctg cta gga gag gaa cgt tac aca cca gcc ata gat gtt tgg agc				2906
Leu Leu Leu Gly Glu Glu Arg Tyr Thr Pro Ala Ile Asp Val Trp Ser				
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Cys Gly Cys Ile Leu Gly Glu Leu Phe Thr Lys Lys Pro Ile Phe Gln				
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gcc aat ctg gaa ctg gct cag cta gaa ctg atc agc cga ctt tgt ggt				3002
Ala Asn Leu Glu Leu Ala Gln Leu Glu Leu Ile Ser Arg Leu Cys Gly				
938	943	948	953	
agc cct tgt cca gct gtg tgg cct gat gtt atc aaa ctg ccc tac ttc				3050
Ser Pro Cys Pro Ala Val Trp Pro Asp Val Ile Lys Leu Pro Tyr Phe				
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aac acc atg aaa ccg aag aag caa tat cga agg cgt cta cga gaa gaa				3098
Asn Thr Met Lys Pro Lys Lys Gln Tyr Arg Arg Arg Leu Arg Glu Glu				
970	975	980	985	
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Phe Ser Phe Ile Pro Ser Ala Ala Leu Asp Leu Leu Asp His Met Leu				
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aca cta gat cct agt aag cgg tgc aca gct gaa cag acc cta cag agc				3194
Thr Leu Asp Pro Ser Lys Arg Cys Thr Ala Glu Gln Thr Leu Gln Ser				
1002	1007	1012	1017	
gac ttc ctt aaa gat gtc gaa ctc agc aaa atg gct cct cca gac ctc				3242
Asp Phe Leu Lys Asp Val Glu Leu Ser Lys Met Ala Pro Pro Asp Leu				
1018	1023	1028	1033	
ccc cac tgg cag gat tgc cat gag ttg tgg agt aag aaa cgg cga cgt				3290
Pro His Trp Gln Asp Cys His Glu Leu Trp Ser Lys Lys Arg Arg Arg				
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Gln Arg Gln Ser Gly Val Val Val Glu Glu Pro Pro Pro Ser Lys Thr				
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tct cga aaa gaa act acc tca ggg aca agt act gag cct gtg aag aac				3386
Ser Arg Lys Glu Thr Thr Ser Gly Thr Ser Thr Glu Pro Val Lys Asn				
1066	1071	1076	1081	
agc agc cca gca cca cct cag cct gct cct ggc aag gtg gag tct ggg				3434
Ser Ser Pro Ala Pro Pro Gln Pro Ala Pro Gly Lys Val Glu Ser Gly				
1082	1087	1092	1097	
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Ala Gly Asp Ala Ile Gly Leu Ala Asp Ile Thr Gln Gln Leu Asn Gln				
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agt gaa ttg gca gtg tta tta aac ctg ctg cag agc caa acc gac ctg				3530
Ser Glu Leu Ala Val Leu Leu Asn Leu Leu Gln Ser Gln Thr Asp Leu				
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Ser Ile Pro Gln Met Ala Gln Leu Leu Asn Ile His Ser Asn Pro Glu	
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Met Gln Gln Gln Leu Glu Ala Leu Asn Gln Ser Ile Ser Ala Leu Thr	
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Glu Ala Thr Ser Gln Gln Gln Asp Ser Glu Thr Met Ala Pro Glu Glu	
1162 1167 1172 1177	
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Ser Leu Lys Glu Ala Pro Ser Ala Pro Val Ile Leu Pro Ser Ala Glu	
1178 1183 1188 1193	
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Gln Met Thr Leu Glu Ala Ser Ser Thr Pro Ala Asp Met Gln Asn Ile	
1194 1199 1204 1209	
ttg gca gtt ctc ttg agt cag ctg atg aaa acc caa gag cca gca ggc	3818
Leu Ala Val Leu Leu Ser Gln Leu Met Lys Thr Gln Glu Pro Ala Gly	
1210 1215 1220 1225	
agt ctg gag gaa aac aac agt gac aag aac agt ggg cca cag ggg ccc	3866
Ser Leu Glu Glu Asn Asn Ser Asp Lys Asn Ser Gly Pro Gln Gly Pro	
1226 1231 1236 1241	
cga aga act ccc aca atg cca cag gag gag gca gca gca tgt cct cct	3914
Arg Arg Thr Pro Thr Met Pro Gln Glu Glu Ala Ala Ala Cys Pro Pro	
1242 1247 1252 1257	
cac att ctt cca cca gag aag agg ccc cct gag ccc ccc gga cct cca	3962
His Ile Leu Pro Pro Glu Lys Arg Pro Pro Glu Pro Pro Gly Pro Pro	
1258 1263 1268 1273	
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Pro Pro Pro Pro Pro Pro Pro Leu Val Glu Gly Asp Leu Ser Ser Ala	
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Pro Gln Glu Leu Asn Pro Ala Val Thr Ala Ala Leu Leu Gln Leu Leu	
1290 1295 1300 1305	
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Ser Gln Pro Glu Ala Glu Pro Pro Gly His Leu Pro His Glu His Gln	
1306 1311 1316 1321	
gcc ttg aga cca atg gag tac tcc acc cga ccc cgt cca aac agg act	4154
Ala Leu Arg Pro Met Glu Tyr Ser Thr Arg Pro Arg Pro Asn Arg Thr	
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tat gga aac act gat ggg cct gaa aca ggg ttc agt gcc att gac act	4202
Tyr Gly Asn Thr Asp Gly Pro Glu Thr Gly Phe Ser Ala Ile Asp Thr	
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 Met Pro His Gln Arg Pro Arg Thr Cys Ala Met Asn Pro Glu Leu Thr
 1 5 10 15

atg gaa agt ctg ggc act ttg cac ggc gcg cgc ggc ggc ggc agt ggc 154
 Met Glu Ser Leu Gly Thr Leu His Gly Ala Arg Gly Gly Gly Ser Gly
 17 22 27 32

ggg ggc ggc ggc ggg ggc ggc ggg ggc ggc ggc ggg ggc ccg ggc cat 202
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Gly His
 33 38 43 48

gag cag gag ctg ctg gcc agc ccc agc ccc cac cac gcg cgc cgc ggc 250
 Glu Gln Glu Leu Leu Ala Ser Pro Ser Pro His His Ala Arg Arg Gly
 49 54 59 64

ccg cgt ggc tcg ctg cgg ggc cct ccg ccg cct cca acc gcg cac cag 298
 Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro Pro Pro Thr Ala His Gln
 65 70 75 80

gag ctg ggc acg gcg gca gcg gcg gca gcg gcg gcg tcg cgc tcg gcc 346
 Glu Leu Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ser Arg Ser Ala
 81 86 91 96

atg gtc acc agc atg gcc tcg atc ctg gac ggc ggc gac tac cgg ccc 394
 Met Val Thr Ser Met Ala Ser Ile Leu Asp Gly Gly Asp Tyr Arg Pro
 97 102 107 112

gag ctc tcc atc ccg ctg cac cac gcc atg agc atg tcc tgc gac tcg 442
 Glu Leu Ser Ile Pro Leu His His Ala Met Ser Met Ser Cys Asp Ser
 113 118 123 128

tct ccg cct ggc atg ggc atg agc aac acc tac acc acg ctg aca ccg 490
 Ser Pro Pro Gly Met Gly Met Ser Asn Thr Tyr Thr Thr Leu Thr Pro

129		134		139		144	
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Leu Gln Pro Leu Pro Pro Ile Ser Thr Val Ser Asp Lys Phe His His							
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cct cac ccg cac cac cat ccg cac cac cac cac cac cac cac cag	586						
Pro His Pro His His His Pro His His His His His His His His Gln							
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cgc ctg tcc ggc aac gtc agc ggc agc ttc acc ctc atg cgc gac gag	634						
Arg Leu Ser Gly Asn Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu							
177		182		187		192	
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Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr Ser Pro Tyr Lys Glu Met							
193		198		203		208	
ccc ggc atg agc cag agc ctg tcc ccg ctg gcc gcc acg ccg ctg ggc	730						
Pro Gly Met Ser Gln Ser Leu Ser Pro Leu Ala Ala Thr Pro Leu Gly							
209		214		219		224	
aac ggg cta ggc ggc ctc cac aac gcg cag cag agt ctg ccc aac tac	778						
Asn Gly Leu Gly Gly Leu His Asn Ala Gln Gln Ser Leu Pro Asn Tyr							
225		230		235		240	
ggc ccg ccg ggc cac gac aaa atg ctc agc ccc aac ttc gac gcg cac	826						
Gly Pro Pro Gly His Asp Lys Met Leu Ser Pro Asn Phe Asp Ala His							
241		246		251		256	
cac act gcc atg ctg acc cgc ggt gag caa cac ctg tcc cgc ggc ctg	874						
His Thr Ala Met Leu Thr Arg Gly Glu Gln His Leu Ser Arg Gly Leu							
257		262		267		272	
ggc acc cca cct gcg gcc atg atg tcg cac ctg aac ggc ctg cac cac	922						
Gly Thr Pro Pro Ala Ala Met Met Ser His Leu Asn Gly Leu His His							
273		278		283		288	
ccg ggc cac act cag tct cac ggg ccg gtg ctg gca ccc agt cgc gag	970						
Pro Gly His Thr Gln Ser His Gly Pro Val Leu Ala Pro Ser Arg Glu							
289		294		299		304	
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Arg Pro Pro Ser Ser Ser Ser Gly Ser Gln Val Ala Thr Ser Gly Gln							
305		310		315		320	
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Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Val Leu							
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Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro							
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Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys	
369 374 379 384	
tgg ctt cag gag ccc gag ttc cag cgc atg tcc gcc tta cgc ctg gca	1258
Trp Leu Gln Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala	
385 390 395 400	
gcg tgc aaa cgc aaa gag caa gaa cca aac aaa gac agg aac aat tcc	1306
Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn Lys Asp Arg Asn Asn Ser	
401 406 411 416	
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Gln Lys Lys Ser Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu	
417 422 427 432	
ttc gcc atc ttc aag gag aac aaa cgc ccg tca aag gag atg cag atc	1402
Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Ile	
433 438 443 448	
acc att tcc cag cag ctg ggc ctg gag ctc aca acc gtc agc aac ttc	1450
Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu Thr Thr Val Ser Asn Phe	
449 454 459 464	
ttc atg aac gcc cgg cgc cgc agc ctg gag aag tgg caa gac gat ctg	1498
Phe Met Asn Ala Arg Arg Arg Ser Leu Glu Lys Trp Gln Asp Asp Leu	
465 470 475 480	
agc aca ggg ggc tcc tcg tcc acc tcc agc acg tgt acc aaa gca tga	1546
Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser Thr Cys Thr Lys Ala *	
481 486 491 496	
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caattctctt gcaaagaaac ttatattcta gctgtaatca taggccaggt gttcttcttt	1726
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cttggttccc cctccctcag cttccgcccc aaaagcagaa gtagaaagta atgaaaagga	180
caacagacct gaggaagaag agcaagtaat acatgaagat gatgaaagac cttctgagaa	240
aaatgaatth tctagacgaa aacgtttctaa atcagaagac atg gac aat gta cag	295
Met Asp Asn Val Gln	
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tct aaa cgt cgt cga tat atg gaa gaa gaa tat gag gca gaa ttt caa	343
Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu Tyr Glu Ala Glu Phe Gln	
6 11 16 21	
gta aag att aca gcc aaa gga gac att aac cag aaa ctt caa aag gtt	391
Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln Lys Leu Gln Lys Val	
22 27 32 37	
ata cag tgg ttg ctg gaa gaa aaa ttg tgt gcg ctg cag tgt gct gta	439
Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala Leu Gln Cys Ala Val	
38 43 48 53	
ttt gat aag act ttg gca gaa ttg aaa aca cga gtg gaa aag att gaa	487
Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg Val Glu Lys Ile Glu	
54 59 64 69	
tgt aac aag agg cat aaa aca gtt ctc act gaa cta cag gcc aag ata	535
Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu Leu Gln Ala Lys Ile	
70 75 80 85	
gcc agg tta acc aaa cgc ttt gaa gca gcc aaa gaa gat ctt aag aaa	583
Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys Glu Asp Leu Lys Lys	
86 91 96 101	
aga cat gaa cat cca ccc aac cca cca gta tca cca gga aaa act gta	631
Arg His Glu His Pro Asn Pro Pro Val Ser Pro Gly Lys Thr Val	
102 107 112 117	
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Asn Asp Val Asn Ser Asn Asn Asn Met Ser Tyr Arg Asn Ala Gly Thr	
118 123 128 133	
gtg aga cag atg ctg gag tcc aaa aga aat gta agc gag agt gca cca	727
Val Arg Gln Met Leu Glu Ser Lys Arg Asn Val Ser Glu Ser Ala Pro	
134 139 144 149	
cca tcc ttt caa act cct gtg aat aca gta tct tca acc aat ctt gtc	775
Pro Ser Phe Gln Thr Pro Val Asn Thr Val Ser Ser Thr Asn Leu Val	
150 155 160 165	
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Thr	Pro	Pro	Ala	Val	Val	Ser	Ser	Gln	Pro	Lys	Leu	Gln	Thr	Pro	Val	
166					171					176					181	
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Thr	Ser	Gly	Ser	Leu	Thr	Ala	Thr	Ser	Val	Leu	Pro	Ala	Pro	Asn	Thr	
182					187					192					197	
gct	act	gta	gtt	gct	act	act	cag	gtg	cct	agt	gga	aat	ccc	cag	cct	919
Ala	Thr	Val	Val	Ala	Thr	Thr	Gln	Val	Pro	Ser	Gly	Asn	Pro	Gln	Pro	
198					203					208					213	
aca	atc	tct	tta	cag	cct	ttg	cca	gtg	att	ttg	cat	gta	cct	gtt	gca	967
Thr	Ile	Ser	Leu	Gln	Pro	Leu	Pro	Val	Ile	Leu	His	Val	Pro	Val	Ala	
214					219					224					229	
gta	tcc	tcc	cag	cct	cag	ctt	cta	cag	agc	cat	cca	ggg	act	ttg	gtg	1015
Val	Ser	Ser	Gln	Pro	Gln	Leu	Leu	Gln	Ser	His	Pro	Gly	Thr	Leu	Val	
230					235					240					245	
act	aat	caa	cca	tct	ggc	aat	gtt	gaa	ttc	att	tct	gtg	caa	agc	cca	1063
Thr	Asn	Gln	Pro	Ser	Gly	Asn	Val	Glu	Phe	Ile	Ser	Val	Gln	Ser	Pro	
246					251					256					261	
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Pro	Thr	Val	Ser	Gly	Leu	Thr	Lys	Asn	Pro	Val	Ser	Leu	Pro	Ser	Leu	
262					267					272					277	
cca	aat	ccc	act	aaa	cca	aac	aac	gtt	cct	tct	gtg	ccc	agt	cct	agt	1159
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Ile	Gln	Arg	Asn	Pro	Thr	Ala	Ser	Ala	Ala	Pro	Leu	Gly	Thr	Thr	Leu	
294					299					304					309	
gct	gtg	cag	gct	gtt	cca	aca	gca	cac	tct	att	gta	caa	gcc	aca	agg	1255
Ala	Val	Gln	Ala	Val	Pro	Thr	Ala	His	Ser	Ile	Val	Gln	Ala	Thr	Arg	
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Thr	Ser	Leu	Pro	Thr	Val	Gly	Pro	Ser	Gly	Leu	Tyr	Ser	Pro	Ser	Thr	
326					331					336					341	
aat	cga	ggt	cct	ata	cag	atg	aaa	att	cca	att	tct	gca	ttt	agt	act	1351
Asn	Arg	Gly	Pro	Ile	Gln	Met	Lys	Ile	Pro	Ile	Ser	Ala	Phe	Ser	Thr	
342					347					352					357	
tcg	tct	gct	gca	gaa	cag	aac	agc	aat	acc	acc	cca	aga	att	gaa	aac	1399
Ser	Ser	Ala	Ala	Glu	Gln	Asn	Ser	Asn	Thr	Thr	Pro	Arg	Ile	Glu	Asn	
358					363					368					373	
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Gln	Thr	Asn	Lys	Thr	Ile	Asp	Ala	Ser	Val	Ser	Lys	Lys	Ala	Ala	Asp	
374					379					384					389	
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Ser	Thr	Ser	Gln	Cys	Gly	Lys	Ala	Thr	Gly	Ser	Asp	Ser	Ser	Gly	Val	

390	395	400	405	
att gat ctc aca atg gat gat gaa gag agt gga gct tca caa gac ccc				1543
Ile Asp Leu Thr Met Asp Asp Glu Glu Ser Gly Ala Ser Gln Asp Pro				
406	411	416	421	
aaa aaa cta aat cac act cct gta tca acc atg agt tct tct cag cct				1591
Lys Lys Leu Asn His Thr Pro Val Ser Thr Met Ser Ser Ser Gln Pro				
422	427	432	437	
gtg tca cga cca ttg caa ccc ata caa cca gca ccg cct ctt caa cca				1639
Val Ser Arg Pro Leu Gln Pro Ile Gln Pro Ala Pro Pro Leu Gln Pro				
438	443	448	453	
tct ggg gtg cca aca agt gga cca tct cag acc acc ata cac tta cta				1687
Ser Gly Val Pro Thr Ser Gly Pro Ser Gln Thr Thr Ile His Leu Leu				
454	459	464	469	
cct aca gct cca act acc gtg aat gta aca cat cgt cca gta act cag				1735
Pro Thr Ala Pro Thr Thr Val Asn Val Thr His Arg Pro Val Thr Gln				
470	475	480	485	
gtg acc aca aga ctc cct gta cca aga gct cct gca aac cac cag gtg				1783
Val Thr Thr Arg Leu Pro Val Pro Arg Ala Pro Ala Asn His Gln Val				
486	491	496	501	
gtt tat aca act ctt cct gca cca cca gct cag gct ccc ttg cga gga				1831
Val Tyr Thr Thr Leu Pro Ala Pro Pro Ala Gln Ala Pro Leu Arg Gly				
502	507	512	517	
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Thr Val Met Gln Ala Pro Ala Val Arg Gln Val Asn Pro Gln Asn Ser				
518	523	528	533	
gtt aca gtt cga gtg cct caa aca acc aca tat gtt gta aac aat gga				1927
Val Thr Val Arg Val Pro Gln Thr Thr Thr Tyr Val Val Asn Asn Gly				
534	539	544	549	
cta acc ctg gga tca aca gga cct cag ctc aca gtg cat cac cga cca				1975
Leu Thr Leu Gly Ser Thr Gly Pro Gln Leu Thr Val His His Arg Pro				
550	555	560	565	
cca caa gtg cat act gag ccc cca cgc ccc gtg cac cca gca ccc tta				2023
Pro Gln Val His Thr Glu Pro Pro Arg Pro Val His Pro Ala Pro Leu				
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cca gaa gct cca caa cca cag cgt ctg ccc cca gaa gct gcc agc aca				2071
Pro Glu Ala Pro Gln Pro Gln Arg Leu Pro Pro Glu Ala Ala Ser Thr				
582	587	592	597	
tct ctg cct cag aag cca cac ttg aag tta gca cgc gtt cag agt caa				2119
Ser Leu Pro Gln Lys Pro His Leu Lys Leu Ala Arg Val Gln Ser Gln				
598	603	608	613	
aat ggc ata gta ctg tca tgg agt gtc ctg gag gtg gat cga agc tgt				2167
Asn Gly Ile Val Leu Ser Trp Ser Val Leu Glu Val Asp Arg Ser Cys				
614	619	624	629	

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Ala Thr Val Asp Ser Tyr His Leu Tyr Ala Tyr His Glu Glu Pro Ser	
630 635 640 645	
gcc act gtg ccc tca caa tgg aaa aag att ggg gaa gtc aag gca ctt	2263
Ala Thr Val Pro Ser Gln Trp Lys Lys Ile Gly Glu Val Lys Ala Leu	
646 651 656 661	
ccc ttg ccc atg gca tgt act ctc acc cag ttt gta tct ggt agc aaa	2311
Pro Leu Pro Met Ala Cys Thr Leu Thr Gln Phe Val Ser Gly Ser Lys	
662 667 672 677	
tac tac ttt gca gta cga gcc aag gat att tat gga cgt ttt ggg cct	2359
Tyr Tyr Phe Ala Val Arg Ala Lys Asp Ile Tyr Gly Arg Phe Gly Pro	
678 683 688 693	
ttc tgt gat cct cag tca aca gat gtg atc tct tct acc cag agc agt	2407
Phe Cys Asp Pro Gln Ser Thr Asp Val Ile Ser Ser Thr Gln Ser Ser	
694 699 704 709	
taa acct tggagccttt atattttcct cttttaaaat ttccaccttt tgggtcttgtt	2464
* 710	
tttaatcttg tgcatagata cccatgtaaa atccaccttg tgcaagattt cttggacaga	2524
tgtgtgtata cactacattt gtttataacc agaagcaaaa taaactcagc ccacaaagct	2584
agaatctttt cctggacagt ttaggctttg gggtttgga atgtaaatgt gtaccttgct	2644
ttagttttga ggctggggaa tatgtgtggg tgtttatgtg tgtttttcct tatgtagggtg	2704
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agccttttac ccttgatttc tccttcattc ctaccaaata tagcacaact cctcaagtaa	3184
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aaccacgtgg ctagcctgcc tgaagtcttc acctctccag gaaggcgggg ggtttctaata      180
ggctgcagct gcgctggggg ctgggggctc ccgctgggac tccacttcg tggatgtcta      240
agcttcacct ttcttgcgcc cgcaggggca tgactcaggt gaaaggagc cattttctca      300
gacctctggc ctc      atg cag ccc ttc agc atc ccc gtg caa atc aca ctt      349
                        Met Gln Pro Phe Ser Ile Pro Val Gln Ile Thr Leu
                        1              5              10

cag ggc agc cgg agg cgc cag ggg agg aca gcc ttt cct gcc tca ggg      397
Gln Gly Ser Arg Arg Arg Gln Gly Arg Thr Ala Phe Pro Ala Ser Gly
 13              18              23              28

aag aag aga gag aca gac tac agt gat gga gac cca cta gat gtg cac      445
Lys Lys Arg Glu Thr Asp Tyr Ser Asp Gly Asp Pro Leu Asp Val His
 29              34              39              44

aag agg ctg cca tcc agt act gga gag gac cga gcc gtg atg ctg ggg      493
Lys Arg Leu Pro Ser Ser Thr Gly Glu Asp Arg Ala Val Met Leu Gly
 45              50              55              60

ttt gcc atg atg ggc ttc tca gtc cta atg ttc ttc ttg ctc gga aca      541
Phe Ala Met Met Gly Phe Ser Val Leu Met Phe Phe Leu Leu Gly Thr
 61              66              71              76

acc att cta aag cct ttt atg ctc agc att cag aga gaa gaa tcg acc      589
Thr Ile Leu Lys Pro Phe Met Leu Ser Ile Gln Arg Glu Glu Ser Thr
 77              82              87              92

tgc act gcc atc cac aca gat atc atg gac gac tgg ctg gac tgt gcc      637
Cys Thr Ala Ile His Thr Asp Ile Met Asp Asp Trp Leu Asp Cys Ala
 93              98              103              108

ttc acc tgt ggt gtg cac tgc cac ggt cag ggg aag tac cca tgt ctt      685
Phe Thr Cys Gly Val His Cys His Gly Gln Gly Lys Tyr Pro Cys Leu
109              114              119              124

cag gtg ttt gtg aac ctc agc cat cca ggt cag aaa gct ctc cta cat      733
Gln Val Phe Val Asn Leu Ser His Pro Gly Gln Lys Ala Leu Leu His
125              130              135              140

tat aat gaa gag gct gtc cag ata aat ccc aag tgc ttt tac aca cct      781
Tyr Asn Glu Glu Ala Val Gln Ile Asn Pro Lys Cys Phe Tyr Thr Pro
141              146              151              156
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aag tgc cac caa gat aga aat gat ttg ctc aac agt gct ctg gac ata	829
Lys Cys His Gln Asp Arg Asn Asp Leu Leu Asn Ser Ala Leu Asp Ile	
157 162 167 172	
aaa gaa ttc ttc gat cac aaa aat gga act ccc ttt tca tgc ttc tac	877
Lys Glu Phe Phe Asp His Lys Asn Gly Thr Pro Phe Ser Cys Phe Tyr	
173 178 183 188	
agt cca gcc agc caa tct gaa gat gtc att ctt ata aaa aag tat gac	925
Ser Pro Ala Ser Gln Ser Glu Asp Val Ile Leu Ile Lys Lys Tyr Asp	
189 194 199 204	
caa atg gct atc ttc cac tgt tta ttt tgg cct tca ctg act ctg cta	973
Gln Met Ala Ile Phe His Cys Leu Phe Trp Pro Ser Leu Thr Leu Leu	
205 210 215 220	
ggg ggt gcc ctg att gtt ggc atg gtg aga tta aca caa cac ctg tcc	1021
Gly Gly Ala Leu Ile Val Gly Met Val Arg Leu Thr Gln His Leu Ser	
221 226 231 236	
tta ctg tgt gaa aaa tat agc act gta gtc aga gat gag gta ggt gga	1069
Leu Leu Cys Glu Lys Tyr Ser Thr Val Val Arg Asp Glu Val Gly Gly	
237 242 247 252	
aaa gta cct tat ata gaa cag cat cag ttc aaa ctg tgc att atg agg	1117
Lys Val Pro Tyr Ile Glu Gln His Gln Phe Lys Leu Cys Ile Met Arg	
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atg gcc tgc ctg agc	113
Met Ala Cys Leu Ser	
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ccc tcg cag ctc cag aag ttc caa cag gat gga ttc ctg gtg ctg gaa	161
Pro Ser Gln Leu Gln Lys Phe Gln Gln Asp Gly Phe Leu Val Leu Glu	
6 11 16 21	
gga ttc ttg tct gcg gaa gag tgt gtg gcc atg caa caa agg att ggc	209

Gly	Phe	Leu	Ser	Ala	Glu	Glu	Cys	Val	Ala	Met	Gln	Gln	Arg	Ile	Gly		
22					27					32					37		
gag	ata	gtg	gct	gaa	atg	gat	gtt	cct	ctc	cac	tgc	cgc	aca	gaa	ttc	257	
Glu	Ile	Val	Ala	Glu	Met	Asp	Val	Pro	Leu	His	Cys	Arg	Thr	Glu	Phe		
38					43					48					53		
tcc	acc	cag	gaa	gag	gag	cag	ctt	cga	gcc	cag	ggc	agc	aca	gac	tat	305	
Ser	Thr	Gln	Glu	Glu	Glu	Gln	Leu	Arg	Ala	Gln	Gly	Ser	Thr	Asp	Tyr		
54					59					64					69		
ttc	ttg	agc	agt	ggg	gac	aag	att	cga	ttc	ttc	ttt	gag	aaa	ggc	gtt	353	
Phe	Leu	Ser	Ser	Gly	Asp	Lys	Ile	Arg	Phe	Phe	Phe	Glu	Lys	Gly	Val		
70					75					80					85		
ttt	gat	gag	aaa	gga	aat	ttc	ctg	gtc	cct	ccg	gag	aaa	tcc	atc	aac	401	
Phe	Asp	Glu	Lys	Gly	Asn	Phe	Leu	Val	Pro	Pro	Glu	Lys	Ser	Ile	Asn		
86					91					96					101		
aaa	att	ggc	cac	gct	ctg	cac	gcc	cac	gac	ccc	gtc	ttc	aag	agc	atc	449	
Lys	Ile	Gly	His	Ala	Leu	His	Ala	His	Asp	Pro	Val	Phe	Lys	Ser	Ile		
102					107					112					117		
aca	cac	tcc	ttc	aag	gtg	cag	acc	ttg	gcc	aga	agt	ctg	ggc	ctc	cag	497	
Thr	His	Ser	Phe	Lys	Val	Gln	Thr	Leu	Ala	Arg	Ser	Leu	Gly	Leu	Gln		
118					123					128					133		
atg	ccc	gtg	gtg	gtg	cag	agc	atg	tac	atc	ttt	aag	caa	cct	cac	ttt	545	
Met	Pro	Val	Val	Val	Gln	Ser	Met	Tyr	Ile	Phe	Lys	Gln	Pro	His	Phe		
134					139					144					149		
ggc	ggg	gaa	gtc	tcc	cct	cat	cag	gac	gcc	tcc	ttc	ctg	tac	acg	gag	593	
Gly	Gly	Glu	Val	Ser	Pro	His	Gln	Asp	Ala	Ser	Phe	Leu	Tyr	Thr	Glu		
150					155					160					165		
ccc	ctg	ggc	cgg	gtg	ctg	ggc	gtg	tgg	atc	gca	gtg	gag	gat	gcc	acg	641	
Pro	Leu	Gly	Arg	Val	Leu	Gly	Val	Trp	Ile	Ala	Val	Glu	Asp	Ala	Thr		
166					171					176					181		
ctg	gag	aac	ggc	tgt	ctc	tgg	ttc	atc	cct	ggc	tcc	cac	acc	agt	ggg	689	
Leu	Glu	Asn	Gly	Cys	Leu	Trp	Phe	Ile	Pro	Gly	Ser	His	Thr	Ser	Gly		
182					187					192					197		
gtg	tca	aga	agg	atg	gtc	cgg	gcc	cct	gtt	ggc	tca	gcg	cct	ggg	acc	737	
Val	Ser	Arg	Arg	Met	Val	Arg	Ala	Pro	Val	Gly	Ser	Ala	Pro	Gly	Thr		
198					203					208					213		
agc	ttc	ctt	ggg	tca	gag	cca	gcc	cgg	gat	aac	agc	ctc	ttt	gtg	ccc	785	
Ser	Phe	Leu	Gly	Ser	Glu	Pro	Ala	Arg	Asp	Asn	Ser	Leu	Phe	Val	Pro		
214					219					224					229		
acc	cca	gtg	cag	aga	ggg	gcc	ctg	gtc	ctc	atc	cat	gga	gaa	gtg	gta	833	
Thr	Pro	Val	Gln	Arg	Gly	Ala	Leu	Val	Leu	Ile	His	Gly	Glu	Val	Val		
230					235					240					245		
cac	aag	agc	aag	cag	aac	ctc	tct	gac	cgc	tcg	cgc	cag	gcc	tac	act	881	
His	Lys	Ser	Lys	Gln	Asn	Leu	Ser	Asp	Arg	Ser	Arg	Gln	Ala	Tyr	Thr		

246	251	256	261	
ttc cac ctc atg gag gcc tct ggc acc acc tgg agc ccg gag aac tgg				929
Phe His Leu Met Glu Ala Ser Gly Thr Thr Trp Ser Pro Glu Asn Trp				
262	267	272	277	
ctc cag cca aca gct gaa ctg ccc ttt ccc caa ctg tac acc taa agg				977
Leu Gln Pro Thr Ala Glu Leu Pro Phe Pro Gln Leu Tyr Thr *				
278	283	288		
ctctcgcagg gcaggagccc tcgcccctcc cgggtgaagc tgtgggctgt aaacaccagt				1037
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ctgccctgtg ggcagcagcc taggctgggt caggggcttc cctaagatct tcacctctct				1157
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aagacaggtc tcttgccaag gcacccaaga tgaaatcttg aaa atg aga aac aca	175
Met Arg Asn Thr	
1	

ttt gct gaa ctg aag aat tca tta gag gct ctc agc agt aga atg gac	223
Phe Ala Glu Leu Lys Asn Ser Leu Glu Ala Leu Ser Ser Arg Met Asp	
5 10 15 20	

cag gca gag gaa aga att ggg acc cag gct gga gtg cag tgg cgt gat	271
Gln Ala Glu Glu Arg Ile Gly Thr Gln Ala Gly Val Gln Trp Arg Asp	
21 26 31 36	

cat ggc tca ctg cag cct caa cct cct gaa ttc aag caa tgc ttc cac	319
His Gly Ser Leu Gln Pro Gln Pro Pro Glu Phe Lys Gln Cys Phe His	
37 42 47 52	

ctc agt ctc cca agt agc tgg gac tac agg gcg tgc ctt tct tag agc	367
Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ala Cys Leu Ser *	

53

58

63

aatcctggtg ccactaaaag ctgcattttc aatatgagat aaaaatgtat ttacaaaaa 427
 gtgcaaggtc ttcattgtctg ctggcattgc tgcaacagtg gcttgtgtga gagatcactt 487
 ttacggcaa tacccaattt attggagaga caaactgctc aagcaaggat gattagcatt 547
 ctatggcatt ttaaaaggat acttgcaatg cttgacctta ccacaatagc aacaggaggt 607
 agctacaaaa ttattacaat agtagagtat ggtaccacag ttaattttat gtagctataa 667
 ttttaactcg catctttaat gttgttcaca tttctctgga 707

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<211> 929

<212> DNA

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<220>

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<222> (78)..(779)

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<223> n = a,t,c or g

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cagccatgga ctggctc atg ggg aag tcc aaa gcc aag ccc aat ggc aag 110
 Met Gly Lys Ser Lys Ala Lys Pro Asn Gly Lys
 1 5

aag ccc gct gcg gag gag agg aag gcc tac ctg gag cct gag cac acc 158
 Lys Pro Ala Ala Glu Arg Lys Ala Tyr Leu Glu Pro Glu His Thr
 12 17 22 27

aag gcc agg atc acc gac ttc cag ttc aag gag ctg gtg gtg ctg ccc 206
 Lys Ala Arg Ile Thr Asp Phe Gln Phe Lys Glu Leu Val Val Leu Pro
 28 33 38 43

cgc gag att gac ctt aac gag tgg ctg gcc agc aac acc acg acg ttt 254
 Arg Glu Ile Asp Leu Asn Glu Trp Leu Ala Ser Asn Thr Thr Thr Phe
 44 49 54 59

ttc cac cac atc aac ctg cag tat agc acc atc tcg gag ttc tgc aca 302
 Phe His His Ile Asn Leu Gln Tyr Ser Thr Ile Ser Glu Phe Cys Thr
 60 65 70 75

gga gag acg tgt cag acg atg gcc gtg tgc aac aca cag tac tac tgg 350
 Gly Glu Thr Cys Gln Thr Met Ala Val Cys Asn Thr Gln Tyr Tyr Trp
 76 81 86 91

tat gac gag cgg ggg aag aag gtc aag tgc acg gcc cca cag tac gtt	398
Tyr Asp Glu Arg Gly Lys Lys Val Lys Cys Thr Ala Pro Gln Tyr Val	
92 97 102 107	
gac ttc gtc atg agc tcc gtg cag aag ctg gtg acg gat gag gac gtg	446
Asp Phe Val Met Ser Ser Val Gln Lys Leu Val Thr Asp Glu Asp Val	
108 113 118 123	
ttc ccc aca aaa tac ggc aga gaa ttc ccc agc tcc ttt gag tcc ctg	494
Phe Pro Thr Lys Tyr Gly Arg Glu Phe Pro Ser Ser Phe Glu Ser Leu	
124 129 134 139	
gtg agg aag atc tgc aga cac ctg ttc cac gtg ctg gca cac atc tac	542
Val Arg Lys Ile Cys Arg His Leu Phe His Val Leu Ala His Ile Tyr	
140 145 150 155	
tgg gcc cac ttc aag gag acg ctg gcc ctg gag ctg cac gga cac ttg	590
Trp Ala His Phe Lys Glu Thr Leu Ala Leu Glu Leu His Gly His Leu	
156 161 166 171	
aac acg ctc tac gtc cac ttc atc ctc ttt gct cgg gag ttc aac ctg	638
Asn Thr Leu Tyr Val His Phe Ile Leu Phe Ala Arg Glu Phe Asn Leu	
172 177 182 187	
ctg gac ccc aaa gag acc gcc atc atg gac gac ctc acc gag gtg cta	686
Leu Asp Pro Lys Glu Thr Ala Ile Met Asp Asp Leu Thr Glu Val Leu	
188 193 198 203	
tgc agc ggg gcc ggc ggg gtc cac agt ggg ggc agt ggg gat ggg gcc	734
Cys Ser Gly Ala Gly Gly Val His Ser Gly Gly Ser Gly Asp Gly Ala	
204 209 214 219	
ggc agc ggg ggc ccg gga gca cag aac cac gtg aag gag aga tga gcc	782
Gly Ser Gly Gly Pro Gly Ala Gln Asn His Val Lys Glu Arg *	
220 225 230	
ccccgggccg gacaggggca cacgtgtgca aagagacggt ggtgtgtgtt ctctcctgca	842
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catcttcccc gggggctccg gggagctaga actggcgcta gaggaggagc tggcgctgct	240
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cag gtc cac gcc ctc aga gaa gac ttt cgg gag aaa aac tca tca acc	944
Gln Val His Ala Leu Arg Glu Asp Phe Arg Glu Lys Asn Ser Ser Thr	
2 7 12 17	
aac cag cac att atc cgg ctg gag agc ctt cag gcc gag atc aag atg	992
Asn Gln His Ile Ile Arg Leu Glu Ser Leu Gln Ala Glu Ile Lys Met	
18 23 28 33	
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Leu Ser Asp Arg Lys Arg Glu Leu Glu His Arg Leu Ser Ala Thr Leu	
34 39 44 49	
gag gaa aat gac ctg ctc caa ggg acc gtg gag gag cta cag gac cgg	1088
Glu Glu Asn Asp Leu Leu Gln Gly Thr Val Glu Glu Leu Gln Asp Arg	
50 55 60 65	
gtg cta atc ctg gag agg cag ggc cat gac aag gac cta cag ctg cac	1136
Val Leu Ile Leu Glu Arg Gln Gly His Asp Lys Asp Leu Gln Leu His	
66 71 76 81	
caa agc cag ctg gag ctt cag gag gtg cgt ctc tcc tgc cga cag ctg	1184
Gln Ser Gln Leu Glu Leu Gln Glu Val Arg Leu Ser Cys Arg Gln Leu	
82 87 92 97	
cag gtg aag gtg gaa gaa ctc act gag gag agg agt ctg cag agc tct	1232
Gln Val Lys Val Glu Glu Leu Thr Glu Glu Arg Ser Leu Gln Ser Ser	

98	103	108	113	
gcc gcc acc agc aca tcc ctc ctg tca gag atc gag cag agc atg gag				1280
Ala Ala Thr Ser Thr Ser Leu Leu Ser Glu Ile Glu Gln Ser Met Glu				
114	119	124	129	
gct gag gag ctg gag cag gag cga gag cag gtg aca ctg ctg agt gtg				1328
Ala Glu Glu Leu Glu Gln Glu Arg Glu Gln Val Thr Leu Leu Ser Val				
130	135	140	145	
gag atg act gcc cta aaa gag gag aga gac cga ctc aga gtc act tct				1376
Glu Met Thr Ala Leu Lys Glu Glu Arg Asp Arg Leu Arg Val Thr Ser				
146	151	156	161	
gag gac aag gag cca aag gag cag ctt cag aag gcc atc agg gac cgc				1424
Glu Asp Lys Glu Pro Lys Glu Gln Leu Gln Lys Ala Ile Arg Asp Arg				
162	167	172	177	
gac gag gcc att gca aag aag aat gct gtg gag ctg gaa ctt gcc aag				1472
Asp Glu Ala Ile Ala Lys Lys Asn Ala Val Glu Leu Glu Leu Ala Lys				
178	183	188	193	
tgc agg atg gat atg atg tct ctg aac agc cag ttg ctg gat gcc att				1520
Cys Arg Met Asp Met Met Ser Leu Asn Ser Gln Leu Leu Asp Ala Ile				
194	199	204	209	
cag cag aaa ctg aac ctc tcg cag cag ctg gaa gct tgg cag gat gac				1568
Gln Gln Lys Leu Asn Leu Ser Gln Gln Leu Glu Ala Trp Gln Asp Asp				
210	215	220	225	
atg cac agg gtc att gac cgg cag ctg atg gac acg cac ctg aaa gaa				1616
Met His Arg Val Ile Asp Arg Gln Leu Met Asp Thr His Leu Lys Glu				
226	231	236	241	
cgg agc cag ccg gct gct gcc ctc tgc agg ggc cac agc gct ggg cgg				1664
Arg Ser Gln Pro Ala Ala Ala Leu Cys Arg Gly His Ser Ala Gly Arg				
242	247	252	257	
ggg gat gag ccc agc atc gct gaa ggc aaa cga ctc ttc tca ttc ttc				1712
Gly Asp Glu Pro Ser Ile Ala Glu Gly Lys Arg Leu Phe Ser Phe Phe				
258	263	268	273	
agg aaa att taa gtt gggaggagtc aggccaccaa agatgggtgg actggaggca				1767
Arg Lys Ile *				
274				
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 Val Gly Gly Ser Arg Pro Gly Gln Thr Leu Arg Gly Ser Val Gln Asn
 17 22 27 32
 aaa ctc aat ccc cga cct gga aag gta gtg ata tat agt gaa ccc gac 144
 Lys Leu Asn Pro Arg Pro Gly Lys Val Val Ile Tyr Ser Glu Pro Asp
 33 38 43 48
 gtc tct gag aag tgc att gaa gtt ttc agt gac att cag gat tgc agt 192
 Val Ser Glu Lys Cys Ile Glu Val Phe Ser Asp Ile Gln Asp Cys Ser
 49 54 59 64
 tct tgg agc ctc tct cca gtg ata ctc ata aaa gtt gtt aga gga tgt 240
 Ser Trp Ser Leu Ser Pro Val Ile Leu Ile Lys Val Val Arg Gly Cys
 65 70 75 80
 tgg att ttg tat gag caa cca aat ttt gaa ggg cac tcc atc ccc tta 288
 Trp Ile Leu Tyr Glu Gln Pro Asn Phe Glu Gly His Ser Ile Pro Leu
 81 86 91 96
 gaa gaa gga gaa ttg gaa ctc tct ggt ctc tgg ggt ata gaa gac att 336

Glu	Glu	Gly	Glu	Leu	Glu	Leu	Ser	Gly	Leu	Trp	Gly	Ile	Glu	Asp	Ile		
97					102					107					112		
gtg	gaa	agg	cac	gaa	gaa	gca	gag	tct	gat	aag	cca	gtg	gtg	att	ggc	384	
Val	Glu	Arg	His	Glu	Glu	Ala	Glu	Ser	Asp	Lys	Pro	Val	Val	Ile	Gly		
113					118					123					128		
tcc	atc	aga	cat	gtg	gtt	cag	gat	tac	aga	gtt	agt	cac	att	gac	tta	432	
Ser	Ile	Arg	His	Val	Val	Gln	Asp	Tyr	Arg	Val	Ser	His	Ile	Asp	Leu		
129					134					139					144		
ttt	act	gaa	cca	gaa	ggg	tta	gga	atc	cta	agt	tcc	tac	ttt	gat	gat	480	
Phe	Thr	Glu	Pro	Glu	Gly	Leu	Gly	Ile	Leu	Ser	Ser	Tyr	Phe	Asp	Asp		
145					150					155					160		
act	gaa	gaa	atg	cag	gga	ttt	ggc	gta	atg	cag	aag	act	tgt	tcc	atg	528	
Thr	Glu	Glu	Met	Gln	Gly	Phe	Gly	Val	Met	Gln	Lys	Thr	Cys	Ser	Met		
161					166					171					176		
aaa	gta	cat	tgg	ggc	acg	tgg	ctg	att	tat	gaa	gaa	cct	gga	ttt	cag	576	
Lys	Val	His	Trp	Gly	Thr	Trp	Leu	Ile	Tyr	Glu	Glu	Pro	Gly	Phe	Gln		
177					182					187					192		
ggc	gtt	cct	ttc	atc	ctg	gaa	cct	ggc	gaa	tac	cct	gac	ttg	tcc	ttc	624	
Gly	Val	Pro	Phe	Ile	Leu	Glu	Pro	Gly	Glu	Tyr	Pro	Asp	Leu	Ser	Phe		
193					198					203					208		
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Trp	Asp	Thr	Glu	Ala	Ala	Tyr	Ile	Gly	Ser	Met	Arg	Pro	Leu	Lys	Met		
209					214					219					224		
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Gly	Gly	Arg	Lys	Val	Glu	Phe	Pro	Thr	Asp	Pro	Lys	Ser	Arg	Ala	Gln		
225					230					235					240		
cct	cca	gaa	gac	aac	aga	agg	aag	cca	gtt	ttg	ggg	aaa	ctt	ggc	act	768	
Pro	Pro	Glu	Asp	Asn	Arg	Arg	Lys	Pro	Val	Leu	Gly	Lys	Leu	Gly	Thr		
241					246					251					256		
cta	ttc	act	gca	gga	agg	aga	aga	aac	agt	aga	aac	ggg	tta	gag	agt	816	
Leu	Phe	Thr	Ala	Gly	Arg	Arg	Arg	Asn	Ser	Arg	Asn	Gly	Leu	Glu	Ser		
257					262					267					272		
ccc	acc	aga	tca	aat	gcc	aaa	cca	ctc	tct	ccc	aaa	gat	gtg	gta	gcc	864	
Pro	Thr	Arg	Ser	Asn	Ala	Lys	Pro	Leu	Ser	Pro	Lys	Asp	Val	Val	Ala		
273					278					283					288		
tct	cct	aag	ctc	cca	gag	aga	gag	agt	gag	agg	agc	aga	tct	cag	agc	912	
Ser	Pro	Lys	Leu	Pro	Glu	Arg	Glu	Ser	Glu	Arg	Ser	Arg	Ser	Gln	Ser		
289					294					299					304		
agc	caa	ctg	aag	caa	acg	gac	aca	agc	gag	gag	ggc	tcc	cgg	cgg	gag	960	
Ser	Gln	Leu	Lys	Gln	Thr	Asp	Thr	Ser	Glu	Glu	Gly	Ser	Pro	Arg	Glu		
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aat	ccc	cga	gag	gca	gag	ggc	gag	ctc	ccc	gag	agc	ggc	ggc	ccc	gca	1008	
Asn	Pro	Arg	Glu	Ala	Glu	Gly	Glu	Leu	Pro	Glu	Ser	Gly	Gly	Pro	Ala		

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gcc ccc cct gac gcc gag ctg tca cct cgc tgg agc agc agt gca gcg				1056
Ala Pro Pro Asp Ala Glu Leu Ser Pro Arg Trp Ser Ser Ser Ala Ala				
337	342	347	352	
gct gtg gct gtg cag cag tgc cat gaa aat gat tca ccc caa tta gaa				1104
Ala Val Ala Val Gln Gln Cys His Glu Asn Asp Ser Pro Gln Leu Glu				
353	358	363	368	
cct ctg gag gca gag gga gag cct ttc cca gat gcc acc acc act gcc				1152
Pro Leu Glu Ala Glu Gly Glu Pro Phe Pro Asp Ala Thr Thr Thr Ala				
369	374	379	384	
aag cag ctg cat tcc tcg ccg gga aat tcc tcc agg caa gag aac gca				1200
Lys Gln Leu His Ser Ser Pro Gly Asn Ser Ser Arg Gln Glu Asn Ala				
385	390	395	400	
gag acg ccc gcc cgc agt ccg ggg gag gac gct tca cca ggt gct ggc				1248
Glu Thr Pro Ala Arg Ser Pro Gly Glu Asp Ala Ser Pro Gly Ala Gly				
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cac gaa cag gag gct ttc ctg ggt gtg agg ggt gcg cca ggg tcg ccc				1296
His Glu Gln Glu Ala Phe Leu Gly Val Arg Gly Ala Pro Gly Ser Pro				
417	422	427	432	
acc cag gag cgg ccc gcg gga gga cta ggc gag gcc cct aac gca gcc				1344
Thr Gln Glu Arg Pro Ala Gly Gly Leu Gly Glu Ala Pro Asn Ala Ala				
433	438	443	448	
ccc agt gtg tgt gcc gaa gaa ggc tcc ctg ggg ccc cgc aac gcc cgc				1392
Pro Ser Val Cys Ala Glu Glu Gly Ser Leu Gly Pro Arg Asn Ala Arg				
449	454	459	464	
agc cag ccc ccc aag ggc gcg tct gat ttg cca ggt gag cct ccg gcc				1440
Ser Gln Pro Pro Lys Gly Ala Ser Asp Leu Pro Gly Glu Pro Pro Ala				
465	470	475	480	
gag ggc gca gcg cac acg gcc agc tcc gcg cag gca gac tgc aca gcc				1488
Glu Gly Ala Ala His Thr Ala Ser Ser Ala Gln Ala Asp Cys Thr Ala				
481	486	491	496	
cgc ccc aag ggt cac gcc cac cct gct aag gtg cta act ttg gac atc				1536
Arg Pro Lys Gly His Ala His Pro Ala Lys Val Leu Thr Leu Asp Ile				
497	502	507	512	
tac ttg agt aag act gag ggg gca caa gtg gac gag ccg gtc gtg att				1584
Tyr Leu Ser Lys Thr Glu Gly Ala Gln Val Asp Glu Pro Val Val Ile				
513	518	523	528	
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Thr Pro Arg Ala Glu Asp Cys Gly Asp Trp Asp Asp Met Glu Lys Arg				
529	534	539	544	
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Ser Ser Gly Arg Arg Ser Gly Arg Arg Arg Gly Ser Gln Lys Ser Thr				
545	550	555	560	

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Asp Ser Pro Gly Ala Asp Ala Glu Leu Pro Glu Ser Ala Ala Arg Asp	
561 566 571 576	
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Asp Ala Val Phe Asp Asp Glu Val Ala Pro Asn Ala Ala Ser Asp Asn	
577 582 587 592	
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Ala Ser Ala Glu Lys Lys Val Lys Ser Pro Arg Ala Ala Leu Asp Gly	
593 598 603 608	
ggc gtt gcc tcc gct gcg agc cca gag tcc aag ccc agc ccc ggt acc	1872
Gly Val Ala Ser Ala Ala Ser Pro Glu Ser Lys Pro Ser Pro Gly Thr	
609 614 619 624	
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Lys Gly Gln Leu Arg Gly Glu Ser Asp Arg Ser Lys Gln Pro Pro Pro	
625 630 635 640	
gct tcg tcc ccc acg aag agg aag ggc agg agc cgt gcc ctc gag gcc	1968
Ala Ser Ser Pro Thr Lys Arg Lys Gly Arg Ser Arg Ala Leu Glu Ala	
641 646 651 656	
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Val Pro Ala Pro Pro Ala Ser Gly Pro Arg Ala Pro Ala Lys Glu Ser	
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cca ccc aag agg gtg ccc gat ccc agc cca gtc acc aag ggc act gcg	2064
Pro Pro Lys Arg Val Pro Asp Pro Ser Pro Val Thr Lys Gly Thr Ala	
673 678 683 688	
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Ala Glu Ser Gly Glu Glu Ala Ala Arg Ala Ile Pro Arg Glu Leu Pro	
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Val Lys Ser Ser Ser Leu Leu Pro Glu Ile Lys Pro Glu His Lys Arg	
705 710 715 720	
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Gly Pro Leu Pro Asn His Phe Asn Gly Arg Ala Glu Gly Gly Arg Ser	
721 726 731 736	
aga gag ctg ggc aga gcg gcc gga gcg cct gga gct tct gac gcc gac	2256
Arg Glu Leu Gly Arg Ala Ala Gly Ala Pro Gly Ala Ser Asp Ala Asp	
737 742 747 752	
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Gly Leu Lys Pro Arg Asn His Phe Gly Val Gly Arg Ser Thr Val Thr	
753 758 763 768	
act aaa gtg acc ctc cct gcc aag ccc aaa cat gtg gaa cta aat ctt	2352
Thr Lys Val Thr Leu Pro Ala Lys Pro Lys His Val Glu Leu Asn Leu	
769 774 779 784	

aaa acc cct aag aat ctt gac agt ttg gga aat gag cac aat cca ttt	2400
Lys Thr Pro Lys Asn Leu Asp Ser Leu Gly Asn Glu His Asn Pro Phe	
785 790 795 800	
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Glu Asn Lys Arg Thr Asn Ser Ser Pro Arg His Thr Asp Ile Arg Gly	
817 822 827 832	
caa agg aat act cct gcc tct agt aaa acg ttt gtt ggg agg gca aag	2544
Gln Arg Asn Thr Pro Ala Ser Ser Lys Thr Phe Val Gly Arg Ala Lys	
833 838 843 848	
ctg aat tta gcc aaa aaa gcc aaa gaa atg gag caa cct gaa aag aaa	2592
Leu Asn Leu Ala Lys Lys Ala Lys Glu Met Glu Gln Pro Glu Lys Lys	
849 854 859 864	
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Val Met Pro Asn Ser Pro Gln Asn Gly Val Leu Val Lys Glu Thr Ala	
865 870 875 880	
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Ile Glu Thr Lys Val Thr Val Ser Glu Glu Glu Ile Leu Pro Ala Thr	
881 886 891 896	
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Arg Gly Met Asn Gly Asp Ser Ser Glu Asn Gln Ala Leu Gly Pro Gln	
897 902 907 912	
cct aac caa gat gat aaa gca gat gta caa aca gat gct ggc tgc ctt	2784
Pro Asn Gln Asp Asp Lys Ala Asp Val Gln Thr Asp Ala Gly Cys Leu	
913 918 923 928	
tca gaa cca gtg gct tct gct ctg att cct gtc aag gat cat aag ctc	2832
Ser Glu Pro Val Ala Ser Ala Leu Ile Pro Val Lys Asp His Lys Leu	
929 934 939 944	
tta gag aag gag gac tca gag gct gca gac agc aaa agc ctt gta ctt	2880
Leu Glu Lys Glu Asp Ser Glu Ala Ala Asp Ser Lys Ser Leu Val Leu	
945 950 955 960	
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Glu Asn Val Thr Asp Thr Ala Gln Asp Ile Pro Thr Thr Val Asp Thr	
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aaa gat tta cct cca acg gcc atg cca aag cca cag cat aca ttt tct	2976
Lys Asp Leu Pro Pro Thr Ala Met Pro Lys Pro Gln His Thr Phe Ser	
977 982 987 992	
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Asp Ser Gln Ser Pro Ala Glu Ser Ser Pro Gly Pro Ser Leu Ser Leu	
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1233	1238	1243	1248	
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Ser Ala Val Cys Met Pro Met Lys Arg Lys Lys Ala Arg Met Pro Asn				
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tct cct gct cct cac ttt gcc atg cct cct att cac gaa gac cat tta				3840
Ser Pro Ala Pro His Phe Ala Met Pro Pro Ile His Glu Asp His Leu				
1265	1270	1275	1280	
gaa aag gtg ttt gat ccc aaa gtg ttt acc ttt ggt ttg ggg aag aag				3888
Glu Lys Val Phe Asp Pro Lys Val Phe Thr Phe Gly Leu Gly Lys Lys				
1281	1286	1291	1296	
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Lys Glu Ser Gln Pro Glu Met Ser Pro Ala Leu His Leu Met Gln Asn				
1297	1302	1307	1312	
ctt gac aca aaa tcc aaa ctg aga ccc aaa cgt gca tct gct gaa cag				3984
Leu Asp Thr Lys Ser Lys Leu Arg Pro Lys Arg Ala Ser Ala Glu Gln				
1313	1318	1323	1328	
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Ser Val Leu Phe Lys Ser Leu His Thr Asn Thr Asn Gly Asn Ser Glu				
1329	1334	1339	1344	
cct ctg gtg atg ccg gaa atc aat gac aaa gag aac agg gac gtc aca				4080
Pro Leu Val Met Pro Glu Ile Asn Asp Lys Glu Asn Arg Asp Val Thr				
1345	1350	1355	1360	
aat ggt ggc att aag aga tcg aga cta gaa aaa agt gca ctt ttc tca				4128
Asn Gly Gly Ile Lys Arg Ser Arg Leu Glu Lys Ser Ala Leu Phe Ser				
1361	1366	1371	1376	
agc ttg tta tct tct tta cca caa gac aaa atc ttt tct cct tct gtg				4176
Ser Leu Leu Ser Ser Leu Pro Gln Asp Lys Ile Phe Ser Pro Ser Val				
1377	1382	1387	1392	
aca tca gtc aac act atg acc acg gct ttc agt act tct cag aac ggt				4224
Thr Ser Val Asn Thr Met Thr Thr Ala Phe Ser Thr Ser Gln Asn Gly				
1393	1398	1403	1408	
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Ser Leu Ser Gln Ser Ser Val Ser Gln Pro Thr Thr Glu Gly Ala Pro				
1409	1414	1419	1424	
ccc tgt ggt ttg aac aaa gaa cag tca aat ctt ctg ccc gac aac tcc				4320
Pro Cys Gly Leu Asn Lys Glu Gln Ser Asn Leu Leu Pro Asp Asn Ser				
1425	1430	1435	1440	
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Leu Lys Val Phe Asn Phe Asn Ser Ser Ser Thr Ser His Ser Ser Leu				
1441	1446	1451	1456	
aaa agt cca agc cac atg gaa aaa tac ccg caa aaa gag aaa acc aaa				4416
Lys Ser Pro Ser His Met Glu Lys Tyr Pro Gln Lys Glu Lys Thr Lys				
1457	1462	1467	1472	

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Cys Ser Met Lys Val His Trp Gly Thr Trp Leu Ile Tyr Glu Glu Pro	
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Gly Phe Gln Gly Val Pro Phe Ile Leu Glu Pro Gly Glu Tyr Pro Asp	
1713 1718 1723 1728	
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Leu Ser Phe Trp Asp Thr Glu Ala Ala Tyr Ile Gly Ser Met Arg Pro	
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Gln Tyr Leu Leu Glu Glu Gly Glu Tyr Arg Asp Trp Lys Ala Trp Gly	
1825 1830 1835 1840	
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Gly Tyr Asn Gly Glu Leu Gln Ser Leu Arg Pro Ile Leu Gly Asp Phe	
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Ser Asn Ala His Met Ile Met Tyr Ser Glu Lys Asn Phe Gly Ser Lys	
1857 1862 1867 1872	
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Gly Ser Ser Ile Asp Val Leu Gly Ile Val Ala Asn Leu Lys Glu Thr	
1873 1878 1883 1888	
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Gly Tyr Gly Val Lys Thr Gln Ser Ile Asn Val Leu Ser Gly Val Trp	
1889 1894 1899 1904	
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Val Ala Tyr Glu Asn Pro Asp Phe Thr Gly Glu Gln Tyr Ile Leu Asp	
1905 1910 1915 1920	
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Lys Gly Phe Tyr Thr Ser Phe Glu Asp Trp Gly Gly Lys Asn Tyr Lys	
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Ile Ser Ser Val Gln Pro Ile Cys Leu Asp Ser Phe Thr Gly Pro Arg	
1937 1942 1947 1952	
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Arg Arg Asn Gln Ile His Leu Phe Ser Glu Pro Gln Phe Gln Gly His	
1953 1958 1963 1968	
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Ser Gln Ser Phe Glu Glu Thr Thr Ser Gln Ile Asp Asp Ser Phe Ser	
1969 1974 1979 1984	
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1985 1990 1995 2000	
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2001 2006 2011 2016	
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Cys Leu Ser Ala Met Gly Cys Pro Pro Gly Ala Thr Phe Lys Ser Leu	
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Arg Phe Ile Asp Val Glu Phe Ser Glu Pro Thr Ile Ile Leu Phe Glu	
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Arg Glu Asp Phe Lys Gly Lys Lys Ile Glu Leu Asn Ala Glu Thr Val	
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Asn Leu Arg Ser Leu Gly Phe Asn Thr Gln Ile Arg Ser Val Gln Val	
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Ile Gly Gly Ile Trp Val Thr Tyr Glu Tyr Gly Ser Tyr Arg Gly Arg	
2081 2086 2091 2096	
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Gln Phe Leu Leu Ser Pro Ala Glu Val Pro Asn Trp Tyr Glu Phe Ser	
2097 2102 2107 2112	
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Gly Cys Arg Gln Ile Gly Ser Leu Arg Pro Phe Val Gln Lys Arg Ile	
2113 2118 2123 2128	
tat ttc aga ctt cga aac aaa gca aca ggg tta ttc atg tca acc aat	6432
Tyr Phe Arg Leu Arg Asn Lys Ala Thr Gly Leu Phe Met Ser Thr Asn	
2129 2134 2139 2144	
gga aac tta gag gat ctg aag ctt ctg agg ata cag gtc atg gag gat	6480
Gly Asn Leu Glu Asp Leu Lys Leu Leu Arg Ile Gln Val Met Glu Asp	

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Val Gly Ala Asp Asp Gln Ile Trp Ile Tyr Gln Glu Gly Cys Ile Lys				
2161	2166	2171	2176	
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Cys Arg Ile Ala Glu Asp Cys Cys Leu Thr Ile Val Gly Ser Leu Val				
2177	2182	2187	2192	
aca tct ggc tcc aag cta ggc ctg gcc ctg gac cag aat gct gac agc				6624
Thr Ser Gly Ser Lys Leu Gly Leu Ala Leu Asp Gln Asn Ala Asp Ser				
2193	2198	2203	2208	
cag ttc tgg agc ttg aag tcc gat ggc agg att tac agc aag ttg aag				6672
Gln Phe Trp Ser Leu Lys Ser Asp Gly Arg Ile Tyr Ser Lys Leu Lys				
2209	2214	2219	2224	
cca aat tta gtt tta gac att aaa ggg ggc aca cag tat gat caa aat				6720
Pro Asn Leu Val Leu Asp Ile Lys Gly Gly Thr Gln Tyr Asp Gln Asn				
2225	2230	2235	2240	
cac att atc ctc aac act gtc agc aaa gag aag ttt aca caa gtg tgg				6768
His Ile Ile Leu Asn Thr Val Ser Lys Glu Lys Phe Thr Gln Val Trp				
2241	2246	2251	2256	
gaa gcc atg gtc cta tat acc tga				6792
Glu Ala Met Val Leu Tyr Thr *				
2257	2262			

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 <211> 2101
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 <213> Homo sapiens

<220>
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aggggtaggg agtgctcccg gcggcgacgg gcccgagttc accagccgcc ggggcagtag	120
tcgaaggccc ggcgcggcat gtcttgggtg ccgcggtgcg ggcagtgaac gcgcgccggg	180
cggg atg ggc cgg cgc cgg gcg cca gag ctg tac cgg gct ccg ttc ccg	229
Met Gly Arg Arg Arg Ala Pro Glu Leu Tyr Arg Ala Pro Phe Pro	
1 5 10	
ttg tac gcg ctt cag gtc gac ccc agc act ggg ctg ctc atc gct gcg	277
Leu Tyr Ala Leu Gln Val Asp Pro Ser Thr Gly Leu Leu Ile Ala Ala	
16 21 26 31	

ggc gga gga ggc gcc gcc aag aca ggc ata aag aat ggc gtg cac ttt Gly Gly Gly Gly Ala Ala Lys Thr Gly Ile Lys Asn Gly Val His Phe 32 37 42 47	325
ctg cag cta gag ctg att aat ggg cgc ttg agt gcc tcc ttg ctg cac Leu Gln Leu Glu Leu Ile Asn Gly Arg Leu Ser Ala Ser Leu Leu His 48 53 58 63	373
tcc cat gac aca gag aca cgg gcc acc atg aac ttg gca ctg gct ggt Ser His Asp Thr Glu Thr Arg Ala Thr Met Asn Leu Ala Leu Ala Gly 64 69 74 79	421
gac atc ctt gct gca ggg cag gat gcc cac tgt cag ctc ctg cgc ttc Asp Ile Leu Ala Ala Gly Gln Asp Ala His Cys Gln Leu Leu Arg Phe 80 85 90 95	469
cag gca cat caa cag cag ggc aac aag gca gag aag gcc ggt tcc aag Gln Ala His Gln Gln Gln Gly Asn Lys Ala Glu Lys Ala Gly Ser Lys 96 101 106 111	517
gag cag ggg cct cga caa agg aag gga gca gcc cca gca gag aag aaa Glu Gln Gly Pro Arg Gln Arg Lys Gly Ala Ala Pro Ala Glu Lys Lys 112 117 122 127	565
tgt gga gcg gaa acc cag cac gag ggg cta gaa ctc agg gta gag aat Cys Gly Ala Glu Thr Gln His Glu Gly Leu Glu Leu Arg Val Glu Asn 128 133 138 143	613
ttg cag gcg gtg cag aca gac ttt agc tcc gat cca ctg cag aaa gtt Leu Gln Ala Val Gln Thr Asp Phe Ser Ser Asp Pro Leu Gln Lys Val 144 149 154 159	661
gtg tgc ttc aac cac gat aat acc ctg ctt gcc act gga gga aca gat Val Cys Phe Asn His Asp Asn Thr Leu Leu Ala Thr Gly Gly Thr Asp 160 165 170 175	709
ggc tac gtc cgt gtc tgg aag gtg ccc agc ctg gag aag gtt ctg gag Gly Tyr Val Arg Val Trp Lys Val Pro Ser Leu Glu Lys Val Leu Glu 176 181 186 191	757
ttc aaa gcc cac gaa ggg gag att gaa gac ctg gct tta ggg cct gat Phe Lys Ala His Glu Gly Glu Ile Glu Asp Leu Ala Leu Gly Pro Asp 192 197 202 207	805
ggc aag ttg gta acc gtg ggc cgg gac ctt aag gcc tct gtg tgg cag Gly Lys Leu Val Thr Val Gly Arg Asp Leu Lys Ala Ser Val Trp Gln 208 213 218 223	853
aag gat cag ctg gtg aca cag ctg cac tgg caa gaa aat gga ccc acc Lys Asp Gln Leu Val Thr Gln Leu His Trp Gln Glu Asn Gly Pro Thr 224 229 234 239	901
ttt tcc agc aca cct tac cgc tac cag gcc tgc agg ttt ggg cag gtt Phe Ser Ser Thr Pro Tyr Arg Tyr Gln Ala Cys Arg Phe Gly Gln Val 240 245 250 255	949

cca gac cag cct gct ggc ctg cga ctc ttc aca gtg caa att ccc cac	997
Pro Asp Gln Pro Ala Gly Leu Arg Leu Phe Thr Val Gln Ile Pro His	
256 261 266 271	
aag cgc ctg cgc cag ccc cct ccc tgc tac ctc aca gcc tgg gat ggc	1045
Lys Arg Leu Arg Gln Pro Pro Pro Cys Tyr Leu Thr Ala Trp Asp Gly	
272 277 282 287	
tcc aac ttc ttg ccc ctt cgg acc aag tcc tgt ggc cat gaa gtc gtc	1093
Ser Asn Phe Leu Pro Leu Arg Thr Lys Ser Cys Gly His Glu Val Val	
288 293 298 303	
tcc tgc ctc gat gtc agt gaa tcc ggc acc ttc cta ggc ctg ggc aca	1141
Ser Cys Leu Asp Val Ser Glu Ser Gly Thr Phe Leu Gly Leu Gly Thr	
304 309 314 319	
gtc act ggc tct gtt gcc atc tac ata gct ttc tct ctc cag tgc ctc	1189
Val Thr Gly Ser Val Ala Ile Tyr Ile Ala Phe Ser Leu Gln Cys Leu	
320 325 330 335	
tac tac gtg agg gag gcc cat ggc att gtg gtg acg gat gtg gcc ttt	1237
Tyr Tyr Val Arg Glu Ala His Gly Ile Val Val Thr Asp Val Ala Phe	
336 341 346 351	
cta cct gag aag ggt cgt ggt cca gag ctc ctt ggg tcc cat gaa act	1285
Leu Pro Glu Lys Gly Arg Gly Pro Glu Leu Leu Gly Ser His Glu Thr	
352 357 362 367	
gcc ctg ttc tct gtg gct gtg gac agt cgt tgc cag ctg cat ctg ttg	1333
Ala Leu Phe Ser Val Ala Val Asp Ser Arg Cys Gln Leu His Leu Leu	
368 373 378 383	
ccc tca cgg cgg agt gtt cct gtg tgg ctc ctg ctc ctg ctg tgt gtc	1381
Pro Ser Arg Arg Ser Val Pro Val Trp Leu Leu Leu Leu Cys Val	
384 389 394 399	
ggg ctt att att gtg acc atc ctg ctg ctc cag agt gcc ttt cca ggt	1429
Gly Leu Ile Ile Val Thr Ile Leu Leu Leu Gln Ser Ala Phe Pro Gly	
400 405 410 415	
ttc ctt tag cttccct gcttcctggg aatcaggagc ctggacactg ccatctctag	1485
Phe Leu *	
416	
agcagagtgg aggcctggac tccctttgct cactccattc ggggtccacag ctgaggttgc	1545
ctctgacaag atgaatgggc actgctgcc cttctagtga aaaggcttgg ctatggccct	1605
gtgtgactcc aggtcccagg aaccttgcct tcgtcatctg tggatccatc cagaacagcg	1665
gtatctgaag cccaggccat actccctgcc tcctttcttc tgcctaccag aggetccaga	1725
gttgagcttg tcctttatct agaaacatgt gaagatgccc aagagcctgg aggcactgct	1785
gtccttcctg cagaaacagt ttctctcct cccctcagcc ttgtggccag ttcctcttga	1845
catgaagccc ctggcatttg ctggggaagg gactggcctg gtacttgctg ttagggcagg	1905

aaggggcaaa aggaagactt gggtagtaat ctgggggttc agatgggtag cactaagcca 1965
gctggcctaa agatgcaata agttcctagg tagtctaccc ttaccttgag gaatgggaaa 2025
atgaacctca gccattagg caggaaaagt tgatatttaa taaacaagga aagagtgaac 2085
tgagaaaaaa aaaaaa 2101

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<211> 1851
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<213> Homo sapiens

<220>
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<222> (1063)..(1815)

<400> 333
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atcagcagca agagccacta gagcaggttg ggcggcagca ggtggacaca cagcagctgg 120
ggcggtagca ggtggctctg cagcaggttg tctggccaca gctggggcgg cagcaggtgg 180
gctggcagta cacagactgg cagcactggg gtctgaagca gctggacaca cagcagctgg 240
gacggcagca ggtggctctg cagcaagtgg tctggcagca gctggggctg cagcaggtgg 300
gctggcagca cacagactgg cagcactgcg gtctgcagca gctggacaca cagcagctgg 360
ggcggcagca ggtggctctg cagcaggttg tctggcagca gctgggacgg cagcagttct 420
tttcatatca tgggatggtg actggctcat ggttgatagt ccaatatgag gttcaacaag 480
aggatccaca gcagctgggg cggcagcaag ttgcacggca gcaggtggtc tgacagcaga 540
gtggacggca gcagctggac acaccacagc tggggcggca ggtggctctga caacagagtg 600
gacggcagca gctggacata ccacagctgg ggtggcaggt ggtctgacag cagagtgggc 660
ggcagcagct ggacacacca cagctggggc ggcaggtggt ctgacaacag actgggtggc 720
agcagctggg gcgacagcaa gtggtctggc agcaggtagt ctgagagcag gatgggcggc 780
agcagctgga tacaacacag ctggggcagc aacaggtggt ctggcagcag ctggggcggc 840
agcaggtctc ttggcagagg ccttgatcac agccctggtc agagcagaca gagccacaac 900
aagagttaac catggtgtca gaggggtggag gttagaagct gcggcagcag caagcgggtct 960
tgcagcaggt ggtctggcag cagctgggat ggcagcagat ctcttggcag aggtcttaac 1020
cacacctctc tgaacaggag cccacccttc acccctgaca cc atg acc cac tgc 1074

Met Thr His Cys

1

tgt tcc cct tgc tgt cag cct aca tgc tgc agg acc acc tgc tgc agg	1122
Cys Ser Pro Cys Cys Gln Pro Thr Cys Cys Arg Thr Thr Cys Cys Arg	
5 10 15 20	
aca acc tgc tgg aag ccc acc act gtg acc acc tgc agc agc aca ccc	1170
Thr Thr Cys Trp Lys Pro Thr Thr Val Thr Thr Cys Ser Ser Thr Pro	
21 26 31 36	
tgt tgc cag ccc tcc tgc tgt gtg ccc agc tgc tgc cag cct tgc tgc	1218
Cys Cys Gln Pro Ser Cys Cys Val Pro Ser Cys Cys Gln Pro Cys Cys	
37 42 47 52	
cac cca act tgc tgt caa aac acc tgc tgc agg acc acc tgc tgc cag	1266
His Pro Thr Cys Cys Gln Asn Thr Cys Cys Arg Thr Thr Cys Cys Gln	
53 58 63 68	
ccc act tgt gtg gcc agc tgc tgc cag cct tcc tgc tgc agc aca ccc	1314
Pro Thr Cys Val Ala Ser Cys Cys Gln Pro Ser Cys Cys Ser Thr Pro	
69 74 79 84	
tgc tgc cag ccc acc tgc tgt ggg tcc agc tgc tgt ggc caa acc agc	1362
Cys Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gly Gln Thr Ser	
85 90 95 100	
tgt ggg tcc agc tgc tgt cag cct att tgt ggg tcc agt tgc tgt cag	1410
Cys Gly Ser Ser Cys Cys Gln Pro Ile Cys Gly Ser Ser Cys Cys Gln	
101 106 111 116	
cct tgc tgt cac ccg act tgc tat caa act atc tgc ttc agg acc acc	1458
Pro Cys Cys His Pro Thr Cys Tyr Gln Thr Ile Cys Phe Arg Thr Thr	
117 122 127 132	
tgc tgc cag cct acc tgc tgc cag ccc acc tgc tgc agg aac acc tct	1506
Cys Cys Gln Pro Thr Cys Cys Gln Pro Thr Cys Cys Arg Asn Thr Ser	
133 138 143 148	
tgc cag ccc acc tgc tgt ggg tcc agc tgc tgc cag cct tgc tgc cac	1554
Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gln Pro Cys Cys His	
149 154 159 164	
cca aca tgc tgt caa acc att tgt aga tcc acc tgc tgc caa cca tcc	1602
Pro Thr Cys Cys Gln Thr Ile Cys Arg Ser Thr Cys Cys Gln Pro Ser	
165 170 175 180	
tgt gtg acc aga tgc tgc agc aca ccc tgt tgc cag cca acc tgt ggt	1650
Cys Val Thr Arg Cys Cys Ser Thr Pro Cys Cys Gln Pro Thr Cys Gly	
181 186 191 196	
ggg tcc agc tgc tgt agc caa acc tgc aat gag tcc agc tat tgt ctg	1698
Gly Ser Ser Cys Cys Ser Gln Thr Cys Asn Glu Ser Ser Tyr Cys Leu	
197 202 207 212	
cct tgc tgc cgt ccc acc tgc tgc cag acc acc tgc tac agg acc acc	1746
Pro Cys Cys Arg Pro Thr Cys Cys Gln Thr Thr Cys Tyr Arg Thr Thr	

213	218	223	228	
tgt tgc cgc ccc agc	tgt tgc tgc agt cct	tgc tgt gtc tcc agc	tgc	1794
Cys Cys Arg Pro Ser	Cys Cys Cys Ser Pro	Cys Cys Val Ser Ser	Cys	
229	234	239	244	
tgc cag cct tcc tgc	tgc taa tc cacttgctgc	agacccacca	cccaccagag	1847
Cys Gln Pro Ser Cys	Cys *			
245	250			
acat				1851

<210> 334
 <211> 3306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1050)..(3260)

<400> 334
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 ttttttccat gttgggcagg gtggttttga actccccacc ccagggtgatc cccccgcccc 120
 agcctcccaa aaaggtggga ttacagggtt tagcccccg cccgggcctg caaaaccctt 180
 ttttactttt ggggccc aaa aagatcccc atttccccgt ccttttccgg tagactattc 240
 gctactgaaa cgattttttt ttttttttga gacgaggtgg aggggcgggg gttctcgcta 300
 tcttgctcaa gctgatctcg aactcctggg ttgatcaat actcagacaa tcttggcagg 360
 cgcaggagga ccaaattcta gtgaatgaga tcgagtctct cggctctttc ccttccatgt 420
 tttctttttg attggccctc gacgatcctc agtgacgcct ccgcaccgc ctcaccagag 480
 agtcagccgc cctcgctttt ccgtgcgcac gcgcagtatc ccgattggct ctgcctagc 540
 ggattgacgg gcaggttagc caatggtctc gtaatatagg tggagcgagc cctcgaggat 600
 gtccacgacc cggcctctcg ctgaatattc atgagggagg cgggtcgacc ccgctgcaca 660
 gtccggccgg cgccatgaag tgagaagggg gctgggggtc gcgctcgcta gcgggcgcgg 720
 ggggtcttga agatgggggtc atcgggtgggc gcgcctgggt ccccaagggg gcgaggggag 780
 ggtgaagggg tgggacgggg gcagccgcag ggagcagcag tgatagcgag gagacactga 840
 gggggccccc aggctcctga ggacctgagg gttaccgggg gcgccggggc cgtcaccctt 900
 ctctgggctc gacgaccggg cactgtggag gcgggagagg ggctgagggg acgggaactg 960

acccagcagc ccctgccgcc aggtcaacg tggacgggct cctggtctac ttcccgtacg 1020
 actacatcta ccccgagcag ttctcctac atg cgg gag ctc aaa cgc acg ctg 1073
 Met Arg Glu Leu Lys Arg Thr Leu
 1 5
 gac gcc aag ggt cat gga gtc ctg gag atg ccc tca ggc acc ggg aag 1121
 Asp Ala Lys Gly His Gly Val Leu Glu Met Pro Ser Gly Thr Gly Lys
 9 14 19 24
 aca gta tcc ctg ttg gcc ctg atc atg gca tac cag aga gca tat ccg 1169
 Thr Val Ser Leu Leu Ala Leu Ile Met Ala Tyr Gln Arg Ala Tyr Pro
 25 30 35 40
 ctg gag gtg acc aaa ctc atc tac tgc tca aga act gtg cca gag att 1217
 Leu Glu Val Thr Lys Leu Ile Tyr Cys Ser Arg Thr Val Pro Glu Ile
 41 46 51 56
 gag aag gtg att gaa gag ctt cga aag ttg ctc aac ttc tat gag aag 1265
 Glu Lys Val Ile Glu Glu Leu Arg Lys Leu Leu Asn Phe Tyr Glu Lys
 57 62 67 72
 cag gag ggc gag aag ctg ccg ttt ctg gga ctg gct ctg agc tcc cgc 1313
 Gln Glu Gly Glu Lys Leu Pro Phe Leu Gly Leu Ala Leu Ser Ser Arg
 73 78 83 88
 aaa aac ttg tgt att cac cct gag gtg aca ccc ctg cgc ttt ggg aag 1361
 Lys Asn Leu Cys Ile His Pro Glu Val Thr Pro Leu Arg Phe Gly Lys
 89 94 99 104
 gac gtc gat ggg aaa tgc cac agc ctc aca gcc tcc tat gtg cgg gcg 1409
 Asp Val Asp Gly Lys Cys His Ser Leu Thr Ala Ser Tyr Val Arg Ala
 105 110 115 120
 cag tac cag cat gac acc agc ctg ccc cac tgc cga ttc tat gag gaa 1457
 Gln Tyr Gln His Asp Thr Ser Leu Pro His Cys Arg Phe Tyr Glu Glu
 121 126 131 136
 ttt gat gcc cat ggg cgt gag gtg ccc ctc ccc gct ggc atc tac aac 1505
 Phe Asp Ala His Gly Arg Glu Val Pro Leu Pro Ala Gly Ile Tyr Asn
 137 142 147 152
 ctg gat gac ctg aag gcc ctg ggg cgg cgc cag ggc tgg tgc cca tac 1553
 Leu Asp Asp Leu Lys Ala Leu Gly Arg Arg Gln Gly Trp Cys Pro Tyr
 153 158 163 168
 ttc ctt gct cga tac tca atc ctg cat gcc aat gtg gtg gtt tat agc 1601
 Phe Leu Ala Arg Tyr Ser Ile Leu His Ala Asn Val Val Val Tyr Ser
 169 174 179 184
 tac cac tac ctc ctg gac ccc aag att gca gac ctg gtg tcc aag gaa 1649
 Tyr His Tyr Leu Leu Asp Pro Lys Ile Ala Asp Leu Val Ser Lys Glu
 185 190 195 200
 ctg gcc cgc aag gcc gtc gtg gtc ttc gac gag gcc cac aac att gac 1697
 Leu Ala Arg Lys Ala Val Val Val Phe Asp Glu Ala His Asn Ile Asp
 201 206 211 216

aac gtc tgc atc gac tcc atg agc gtc aac ctc acc cgc cgg acc ctt	1745
Asn Val Cys Ile Asp Ser Met Ser Val Asn Leu Thr Arg Arg Thr Leu	
217 222 227 232	
gac cgg tgc cag ggc aac ctg gag acc ctg cag aag acg gtg ctc agg	1793
Asp Arg Cys Gln Gly Asn Leu Glu Thr Leu Gln Lys Thr Val Leu Arg	
233 238 243 248	
atc aaa gag aca gac gag cag cgc ctg cgg gac gag tac cgg cgt ctg	1841
Ile Lys Glu Thr Asp Glu Gln Arg Leu Arg Asp Glu Tyr Arg Arg Leu	
249 254 259 264	
gtg gag ggg ctg cgg gag gcc agc gcc gcc cgg gag acg gac gcc cac	1889
Val Glu Gly Leu Arg Glu Ala Ser Ala Ala Arg Glu Thr Asp Ala His	
265 270 275 280	
ctg gcc aac ccc gtg ctg ccc gac gaa gtg ctg cag gag gca gtg cct	1937
Leu Ala Asn Pro Val Leu Pro Asp Glu Val Leu Gln Glu Ala Val Pro	
281 286 291 296	
ggc tcc atc cgc acg gcc gag cat ttc ctg ggc ttc ctg agg cgg ctg	1985
Gly Ser Ile Arg Thr Ala Glu His Phe Leu Gly Phe Leu Arg Arg Leu	
297 302 307 312	
ctg gag tac gtg aag tgg cgg ctg cgt gtg cag cat gtg gtg cag gag	2033
Leu Glu Tyr Val Lys Trp Arg Leu Arg Val Gln His Val Val Gln Glu	
313 318 323 328	
agc ccg ccc gcc ttc ctg agc ggc ctg gcc cag cgc gtg tgc atc cag	2081
Ser Pro Pro Ala Phe Leu Ser Gly Leu Ala Gln Arg Val Cys Ile Gln	
329 334 339 344	
cgc aag ccc ctc aga ttc tgt gct gaa cgc ctc cgg tcc ctg ctg cat	2129
Arg Lys Pro Leu Arg Phe Cys Ala Glu Arg Leu Arg Ser Leu Leu His	
345 350 355 360	
act ctg gag atc acc gac ctt gct gac ttc tcc ccg ctc acc ctc ctt	2177
Thr Leu Glu Ile Thr Asp Leu Ala Asp Phe Ser Pro Leu Thr Leu Leu	
361 366 371 376	
gct aac ttt gcc acc ctt gtc agc acc tac gcc aaa ggc ttc acc atc	2225
Ala Asn Phe Ala Thr Leu Val Ser Thr Tyr Ala Lys Gly Phe Thr Ile	
377 382 387 392	
atc atc gag ccc ttt gac gac aga acc ccg acc att gcc aac ccc atc	2273
Ile Ile Glu Pro Phe Asp Asp Arg Thr Pro Thr Ile Ala Asn Pro Ile	
393 398 403 408	
ctg cac ttc agc tgc atg gac gcc tcg ctg gcc atc aaa ccc gta ttt	2321
Leu His Phe Ser Cys Met Asp Ala Ser Leu Ala Ile Lys Pro Val Phe	
409 414 419 424	
gag cgt ttc cag tct gtc atc atc aca tct ggg aca ctg tcc ccg ctg	2369
Glu Arg Phe Gln Ser Val Ile Ile Thr Ser Gly Thr Leu Ser Pro Leu	
425 430 435 440	

gac atc tac ccc aag atc ctg gac ttc cac ccc gtc acc atg gca acc	2417
Asp Ile Tyr Pro Lys Ile Leu Asp Phe His Pro Val Thr Met Ala Thr	
441 446 451 456	
ttc acc atg acg ctg gca cgg gtc tgc ctc tgc cct atg atc atc ggc	2465
Phe Thr Met Thr Leu Ala Arg Val Cys Leu Cys Pro Met Ile Ile Gly	
457 462 467 472	
cgt ggc aat gac cag gtg gcc atc agc tcc aaa ttt gag acc cgg gag	2513
Arg Gly Asn Asp Gln Val Ala Ile Ser Ser Lys Phe Glu Thr Arg Glu	
473 478 483 488	
gat att gct gtg atc cgg aac tat ggg aac ctc ctg ctg gag atg tcc	2561
Asp Ile Ala Val Ile Arg Asn Tyr Gly Asn Leu Leu Leu Glu Met Ser	
489 494 499 504	
gct gtg gtc cct gat ggc atc gtg gcc ttc ttc acc agc tac cag tac	2609
Ala Val Val Pro Asp Gly Ile Val Ala Phe Phe Thr Ser Tyr Gln Tyr	
505 510 515 520	
atg gag agc acc gtg gcc tcc tgg tat gag cag ggg atc ctt gag aac	2657
Met Glu Ser Thr Val Ala Ser Trp Tyr Glu Gln Gly Ile Leu Glu Asn	
521 526 531 536	
atc cag agg aac aag ctg ctc ttt att gag acc cag gat ggt gcc gaa	2705
Ile Gln Arg Asn Lys Leu Leu Phe Ile Glu Thr Gln Asp Gly Ala Glu	
537 542 547 552	
acc agt gtc gcc ctg gag aag tac cag gag gcc tgc gag aat ggc cgc	2753
Thr Ser Val Ala Leu Glu Lys Tyr Gln Glu Ala Cys Glu Asn Gly Arg	
553 558 563 568	
ggg gcc atc ctg ctg tca gtg gcc cgg ggc aaa gtg tcc gag gga atc	2801
Gly Ala Ile Leu Leu Ser Val Ala Arg Gly Lys Val Ser Glu Gly Ile	
569 574 579 584	
gac ttt gtg cac cac tac ggg cgg gcc gtc atc atg ttt ggc gtc ccc	2849
Asp Phe Val His His Tyr Gly Arg Ala Val Ile Met Phe Gly Val Pro	
585 590 595 600	
tac gtc tac aca cag agc cgc att ctc aag gcg cgg ctg gaa tac ctg	2897
Tyr Val Tyr Thr Gln Ser Arg Ile Leu Lys Ala Arg Leu Glu Tyr Leu	
601 606 611 616	
cgg gac cag ttc cag att cgt gag aat gac ttt ctt acc ttc gat gcc	2945
Arg Asp Gln Phe Gln Ile Arg Glu Asn Asp Phe Leu Thr Phe Asp Ala	
617 622 627 632	
atg cgc cac gcg gcc cag tgt gtg ggt cgg gcc atc agg ggc aag acg	2993
Met Arg His Ala Ala Gln Cys Val Gly Arg Ala Ile Arg Gly Lys Thr	
633 638 643 648	
gac tac ggc ctc atg gtc ttt gcc gac aag cgg ttt gcc cgt ggg gac	3041
Asp Tyr Gly Leu Met Val Phe Ala Asp Lys Arg Phe Ala Arg Gly Asp	
649 654 659 664	
aag cgg ggg aag ctg ccc cgc tgg atc cag gag cac ctc aca gat gcc	3089

Glu Gln Val Pro Pro Ser Asp Phe Cys Gly Val Arg Arg Cys Arg Ala
 100 105 110 115

ggg ttc caa tgc caa tga tgcgcc ttgacctatg tgggccagat ctgtcagaac 445
 Gly Phe Gln Cys Gln *
 116 121

ctcgggatgt gtacagtgat tggatagact cctgccatgc ggccaatcag taacgacaca 505

gagga 510

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<220>
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<400> 337
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cagccacgaa gatcctacca aa atg aag cgc ttc ctc ttc ctc cta ctc acc 112
 Met Lys Arg Phe Leu Phe Leu Leu Leu Thr
 1 5

atc agc ctc ctg gtt atg gta cag ata caa act gga ctc tca gga caa 160
 Ile Ser Leu Leu Val Met Val Gln Ile Gln Thr Gly Leu Ser Gly Gln
 11 16 21 26

aac gac acc agc caa acc agc agc ccc tca gca tcc agc agc atg agc 208
 Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Ser Met Ser
 27 32 37 42

gga ggc att ttc ctt ttc ttc gtg gcc aat gcc ata atc cac ctc ttc 256
 Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu Phe
 43 48 53 58

tgc ttc agt tga ggg gacacgtctc agccttagcc ctgtgcccc tgaaacagct 311
 Cys Phe Ser *
 59

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gaagatggcg ctggccgg  atg gaa atc cta atg aca gtc tcc aaa ttc gcc      171
                    Met Glu Ile Leu Met Thr Val Ser Lys Phe Ala
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tcc atc tgt acc atg ggc gcc aat gct tgc gca tta gag aaa gag att      219
Ser Ile Cys Thr Met Gly Ala Asn Ala Ser Ala Leu Glu Lys Glu Ile
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ggt cca gaa cag ttt ccg gtc aat gag cac tat ttt gga tta gtc aat      267
Gly Pro Glu Gln Phe Pro Val Asn Glu His Tyr Phe Gly Leu Val Asn
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ttt ggg aat acc tgc tac tgc aat tca gtt ctt caa gca ctt tat ttt      315
Phe Gly Asn Thr Cys Tyr Cys Asn Ser Val Leu Gln Ala Leu Tyr Phe
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tgt cgt cca ttt cgg gaa aaa gtt ctt gcg tat aag agt caa cct agg      363
Cys Arg Pro Phe Arg Glu Lys Val Leu Ala Tyr Lys Ser Gln Pro Arg
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aaa aag gag agc ctt ctt aca tgc tta gca gat ctc ttc cat agc ata      411
Lys Lys Glu Ser Leu Leu Thr Cys Leu Ala Asp Leu Phe His Ser Ile
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gcc act cag aag aaa aag gtt gga gta ata ccc cct aag aag ttc atc      459
Ala Thr Gln Lys Lys Lys Val Gly Val Ile Pro Pro Lys Lys Phe Ile
  92                      97                      102                      107

aca aga tta cgg aaa gaa aat gag ctt ttt gac aac tac atg caa caa      507
Thr Arg Leu Arg Lys Glu Asn Glu Leu Phe Asp Asn Tyr Met Gln Gln
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gat gcc cat gaa ttc tta aat tac cta cta aat aca att gct gat att      555
Asp Ala His Glu Phe Leu Asn Tyr Leu Leu Asn Thr Ile Ala Asp Ile
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tta caa gaa gag aga aag cag gaa aaa caa aat ggt cgt tta cct aat      603
Leu Gln Glu Glu Arg Lys Gln Glu Lys Gln Asn Gly Arg Leu Pro Asn
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gtt cat gag att ttt cag gga aca tta act aat gaa acc aga tgt ctt      699
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Met Lys Pro Asp Glu Thr Pro Met Phe Asp Pro
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aat cta ctc aaa gaa gtg gac tgg agt cag aat aca gct aca ttt tct	158
Asn Leu Leu Lys Glu Val Asp Trp Ser Gln Asn Thr Ala Thr Phe Ser	
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cca gcc att tcc cca aca cat cct gga gaa ggc ttg gtt ttg agg cct	206
Pro Ala Ile Ser Pro Thr His Pro Gly Glu Gly Leu Val Leu Arg Pro	
28 33 38 43	
ctt tgt act gct gac tta aat aga ggt ttt ttt aag gta ttg ggt cag	254
Leu Cys Thr Ala Asp Leu Asn Arg Gly Phe Phe Lys Val Leu Gly Gln	
44 49 54 59	
cta aca gag act gga gtt gtc agc cct gaa caa ttt atg aaa tct ttt	302
Leu Thr Glu Thr Gly Val Val Ser Pro Glu Gln Phe Met Lys Ser Phe	
60 65 70 75	
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Glu His Met Lys Lys Ser Gly Asp Tyr Tyr Val Thr Val Val Glu Asp	
76 81 86 91	
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Val Thr Leu Gly Gln Ile Val Ala Thr Ala Thr Leu Ile Ile Glu His	
92 97 102 107	
aaa ttc atc cat tcc tgt gct aag aga gga aga gta gaa gat gtt gtt	446
Lys Phe Ile His Ser Cys Ala Lys Arg Gly Arg Val Glu Asp Val Val	
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Ala Ser Asp Glu Cys Arg Gly Lys Gln Leu Gly Asn Leu Leu Leu Ser	
124 129 134 139	
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Thr Leu Thr Leu Leu Ser Lys Lys Leu Asn Cys Tyr Lys Ile Thr Leu	
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Glu Cys Leu Pro Gln Asn Val Gly Phe Tyr Lys Lys Phe Gly Tyr Thr	
156 161 166 171	
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tcgcccttcc gcagccttca ctccagccct ctgctccgcg acgcc      atg aag tcg      174
                                   Met Lys Ser
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ccg ttc tac cgc tgc cag aac acc acc tct gtg gaa aaa ggc aac tcg      222
Pro Phe Tyr Arg Cys Gln Asn Thr Thr Ser Val Glu Lys Gly Asn Ser
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gcg gtg atg ggc ggg gtg ctc ttc agc acc ggc ctc ctg ggc aac ctg      270
Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu Gly Asn Leu
  20                      25                      30                      35

ctg gcc ctg ggg ctg ctg gcg cgc tcg ggg ctg ggg tgg tgc tcg cgg      318
Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp Cys Ser Arg
  36                      41                      46                      51

cgt cca ctg cgc ccg ctg ccc tcg gtc ttc tac atg ctg gtg tgt ggc      366
Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu Val Cys Gly
  52                      57                      62                      67

ctg acg gtc acc gac ttg ctg ggc aag tgc ctc cta agc ccg gtg gtg      414
Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser Pro Val Val
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ctg gct gcc tac gct cag aac cgg agt ctg cgg gtg ctt gcg ccc gca      462
Leu Ala Ala Tyr Ala Gln Asn Arg Ser Leu Arg Val Leu Ala Pro Ala
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ttg gac aac tcg ttg tgc caa gcc ttc gcc ttc ttc atg tcc ttc ttt      510
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ggg ctc tcc tcg aca ctg caa ctc ctg gcc atg gca ctg gag tgc tgg      558
Gly Leu Ser Ser Thr Leu Gln Leu Leu Ala Met Ala Leu Glu Cys Trp
  116                      121                      126                      131

ctc tcc cta ggg cac cct ttc ttc tac cga cgg cac atc acc ctg cgc      606
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Val Leu Gly Tyr Ser Val Leu Tyr Ser Ser Leu Met Ala Leu Leu Val	
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Leu Ala Thr Val Leu Cys Asn Leu Gly Ala Met Arg Asn Leu Tyr Ala	
212 217 222 227	
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Met His Arg Arg Leu Gln Arg His Pro Arg Ser Cys Thr Arg Asp Cys	
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Glu Leu Asp His Leu Leu Leu Leu Ala Leu Met Thr Val Leu Phe Thr	
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Met Cys Ser Leu Pro Val Ile Tyr Arg Ala Tyr Tyr Gly Ala Phe Lys	
276 281 286 291	
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Asp Val Lys Glu Lys Asn Arg Thr Ser Glu Glu Ala Glu Asp Leu Arg	
292 297 302 307	
gcc ttg cga ttt cta tct gtg att tca att gtg gac cct tgg att ttt	1134
Ala Leu Arg Phe Leu Ser Val Ile Ser Ile Val Asp Pro Trp Ile Phe	
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Ile Ile Phe Arg Ser Pro Val Phe Arg Ile Phe Phe His Lys Ile Phe	
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Ile Arg Pro Leu Arg Tyr Arg Ser Arg Cys Ser Asn Ser Thr Asn Met	
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gaa tcc agt ctg tga cagtgttttt cactctgtgg taagctgagg aatatgtcac	1285
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 Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys
 17 22 27 32
 ctt ggt tct aca gcc att ggg atc cag aca tca gag ggt gtg tgc cta 264
 Leu Gly Ser Thr Ala Ile Gly Ile Gln Thr Ser Glu Gly Val Cys Leu
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 gct gtg gag aag aga att act tcc cca ctg atg gag ccc agc agc att 312
 Ala Val Glu Lys Arg Ile Thr Ser Pro Leu Met Glu Pro Ser Ser Ile
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 gag aaa att gta gag att gat gct cac ata ggt tgt gcc atg agt ggg 360
 Glu Lys Ile Val Glu Ile Asp Ala His Ile Gly Cys Ala Met Ser Gly
 65 70 75 80
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 Leu Ile Ala Asp Ala Lys Thr Leu Ile Asp Lys Ala Arg Val Glu Thr
 81 86 91 96
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 Gln Asn His Trp Phe Thr Tyr Asn Glu Thr Met Thr Val Glu Ser Val
 97 102 107 112
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 Thr Gln Ala Val Ser Asn Leu Ala Leu Gln Phe Gly Glu Glu Asp Ala
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 Asp Pro Gly Ala Met Ser Arg Pro Phe Gly Val Ala Leu Leu Phe Gly
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 Gly Val Asp Glu Lys Gly Pro Gln Leu Phe His Met Asp Pro Ser Gly
 145 150 155 160

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Thr Phe Val Gln Cys Asp Ala Arg Ala Ile Gly Ser Ala Ser Glu Gly	
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Ala Gln Ser Ser Leu Gln Glu Val Tyr His Lys Ser Met Thr Leu Lys	
177 182 187 192	
gaa gcc atc aag tct tca ctc atc atc ctc aaa caa gta atg gag gag	744
Glu Ala Ile Lys Ser Ser Leu Ile Ile Leu Lys Gln Val Met Glu Glu	
193 198 203 208	
aag ctg aat gca aca aac att gag cta gcc aca gtg cag cct ggc cag	792
Lys Leu Asn Ala Thr Asn Ile Glu Leu Ala Thr Val Gln Pro Gly Gln	
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Met Leu Gly Arg Ser Gly Tyr Arg Ala Leu Pro Leu Gly Asp Phe Asp	
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Arg Phe Gln Gln Ser Ser Phe Gly Phe Leu Gly Ser Gln Lys Gly Cys	
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Ile Val Pro Thr Tyr Glu Arg Met Ile Val Phe Arg Leu Gly Arg Ile	
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Arg Thr Pro Gln Gly Pro Gly Met Val Leu Leu Leu Pro Phe Ile Asp	
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Ser Phe Gln Arg Val Asp Leu Arg Thr Arg Ala Phe Asn Val Pro Pro	
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Cys Lys Leu Ala Ser Lys Asp Gly Ala Val Leu Ser Val Gly Ala Asp	
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Asp Leu Asn Thr Ala Thr Arg Met Thr Ala Gln Asn Ala Met Thr Lys	
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Pro Pro Gln Asp Ser Pro Ala Gly Pro Asn Leu Asp Ser Thr Leu Gln	
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Gln Leu Ala Leu His Phe Leu Gly Gly Ser Met Asn Ser Met Ala Gly	
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Gly Ala Pro Ser Pro Gly Pro Ala Asp Thr Val Glu Met Val Ser Glu	
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Val Glu Pro Pro Ala Pro Gln Val Gly Ala Arg Ser Ser Pro Lys Gln	
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Pro Leu Gly Ala Tyr Met Ser Gly Arg Leu Lys Val Lys Gly Asp Leu	
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tggtgaaata gat atg gcg acc gag ggg gat gtg gag ctg gag ttg gag 169
Met Ala Thr Glu Gly Asp Val Glu Leu Glu Leu Glu
1 5 10
act gag acc agt gga cca gag cgg cct ccg gag aag cca cgg aaa cat 217
Thr Glu Thr Ser Gly Pro Glu Arg Pro Pro Glu Lys Pro Arg Lys His
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gac agc ggt gcg gcg gac ttg gag cgg gtc acc gac tat gca gag gag 265
Asp Ser Gly Ala Ala Asp Leu Glu Arg Val Thr Asp Tyr Ala Glu Glu
29 34 39 44
aag gag atc cag agt tcc aat ctg gag acg gcc atg tct gtg att gga 313
Lys Glu Ile Gln Ser Ser Asn Leu Glu Thr Ala Met Ser Val Ile Gly
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Asp Arg Arg Ser Arg Glu Gln Lys Ala Lys Gln Glu Arg Glu Lys Glu
61 66 71 76
ctg gca aaa gtc act atc aag aag gaa gat ctg gag cta ata atg act 409
Leu Ala Lys Val Thr Ile Lys Lys Glu Asp Leu Glu Leu Ile Met Thr
77 82 87 92
gag atg gag ata tct cga gca gca gca gaa cgc agt ttg cgg gaa cac 457
Glu Met Glu Ile Ser Arg Ala Ala Ala Glu Arg Ser Leu Arg Glu His
93 98 103 108
atg ggc aac gtg gta gag gcg ctt att gcc cta acc aac tga tgcgtgc 506
Met Gly Asn Val Val Glu Ala Leu Ile Ala Leu Thr Asn *
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gaa ttg att ggc cat acc att gtc act gta tta ctg ctc atg tca ttg      249
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cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc act tgg aat ata      297
His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp Asn Ile
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tat cga tac att atg gtg ccg agt ggt aac atg gga gtg ttt gat cca      345
Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe Asp Pro
   83                          88               93           98

aca gaa ata cac aat cga ggg cag ctg aag tca cac atg aaa gaa gcc      393
Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys Glu Ala
   99                          104              109           114

atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc atg tat ctt tat      441
Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr Leu Tyr
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agt atg atc tta gct ttg ata aat gac tga a gccgtggttg aagtcagcct      492
Ser Met Ile Leu Ala Leu Ile Asn Asp  *
  131                          136

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ccgcggcagg gggcgggagc gcgcctctc ctcggctctg gttccagccg agcctctcgg 480
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Met Glu Ile Pro Lys Leu Leu Pro Ala Arg Gly Thr Leu Gln
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Gly Gly Gly Gly Gly Gly Ile Pro Ala Gly Gly Gly Arg Val His Arg
15 20 25 30
ggc cct gac tcg ccg gct ggc cag gtc ccc acg cgc cgc ctc ctg ctg 626
Gly Pro Asp Ser Pro Ala Gly Gln Val Pro Thr Arg Arg Leu Leu Leu
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ctc cgg ggc ccc caa gat ggc ggg ccc ggg cgg cgc gag gag gcc 674
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agc acg gca tca cgg ggc cct ggc cca agc ctg ttg gcg ccg agg acc 722
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Asp Gln Pro Ser Gly Gly Gly Gly Gly Gly Gly Asp Asp Phe Phe Leu
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Val Leu Leu Asp Pro Val Gly Gly Asp Val Glu Thr Ala Gly Ser Gly

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Gly Cys Pro Ala Glu Gly Cys Gly Lys Ser Phe Thr Thr Val Tyr Asn	
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Leu Lys Ala His Met Lys Gly His Glu Gln Glu Asn Ser Phe Lys Cys	
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Gln Arg Ser His Phe Glu Pro Glu Arg Pro Tyr Gln Cys Ala Phe Ser	
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Ser His Thr Gly Glu Arg Pro Phe Leu Cys Asp Phe Asp Gly Cys Gly	
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Trp Asn Phe Thr Ser Met Ser Lys Leu Leu Arg His Lys Arg Lys His	
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Phe Thr Arg Ala Glu His Leu Lys Gly His Ser Ile Thr His Leu Gly	
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Thr Lys Pro Phe Val Cys Pro Val Ala Gly Cys Cys Ala Arg Phe Ser	
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Asp Thr Trp Lys Ser Arg Cys Pro Ile Ser Ser Cys Asn Lys Leu Phe	
543 548 553 558	

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Ile Val Ser Leu Phe Ser Asp Val Pro Asp Ser Thr Ser Ala Ala Leu	
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Ser Val Gly Gln Ala Val Asp Pro Pro Ser Leu Met Ala Thr Ser Asp	
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Gly Phe Gln Gln Ser Ser Leu Asn Met Asp Glu Val Ser Ser Val Ser	
687 692 697 702	
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Val Gly Pro Leu Gly Ser Leu Asp Ser Leu Ala Met Lys Asn Ser Ser	
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Cys Tyr Tyr Gly Thr Leu Lys Leu Ala Gly Pro Glu Ser Leu Arg Trp	
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Glu Gly Ala Met Ser Glu Gly Gly Gly Lys Asn Ser His Cys Leu Leu	
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Asp Pro Gly Pro Ala Arg Val Ala Ser Arg Arg Leu Gly Ala Ala Val	
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Gly Leu Leu Ser Ala Asp Thr Leu Trp Pro Leu Asn Gly Leu Ala Arg	
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Leu Ala Lys Gln His Asn Ser Leu Glu Arg Ala Phe His Ser Ala Pro	
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Lys Ala Val His Cys Thr Ser Ser Val Glu Gln Met Cys Leu Val Ala	
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Pro Phe Asn Pro Met Leu Gly Glu Thr Phe Glu Leu Asp Arg Leu Asp	
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Asp Met Gly Leu Arg Ser Leu Cys Glu Gln Val Ser His His Pro Pro	
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ccg	cta	ggt	gcc	atc	cac	tta	gaa	ttc	cag	gcc	agt	ggg	aat	cac	tac	2016
Pro	Leu	Gly	Ala	Ile	His	Leu	Glu	Phe	Gln	Ala	Ser	Gly	Asn	His	Tyr	
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gtg	tgg	agg	aag	agc	acc	tca	act	gtt	cac	aac	atc	atc	gtg	ggc	aag	2064
Val	Trp	Arg	Lys	Ser	Thr	Ser	Thr	Val	His	Asn	Ile	Ile	Val	Gly	Lys	
673					678					683					688	
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Leu	Trp	Ile	Asp	Gln	Ser	Gly	Asp	Ile	Glu	Ile	Val	Asn	His	Lys	Thr	
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Asn	Asp	Arg	Cys	Gln	Leu	Lys	Phe	Leu	Pro	Tyr	Ser	Tyr	Phe	Ser	Lys	
705					710					715					720	
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Glu	Ala	Ala	Arg	Lys	Val	Thr	Gly	Val	Val	Ser	Asp	Ser	Gln	Gly	Lys	
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gcc	cat	tac	gtg	ctg	tcc	ggc	tcg	tgg	gat	gaa	caa	atg	gag	tgc	tcc	2256
Ala	His	Tyr	Val	Leu	Ser	Gly	Ser	Trp	Asp	Glu	Gln	Met	Glu	Cys	Ser	
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Lys	Val	Met	His	Ser	Ser	Pro	Ser	Ser	Pro	Ser	Ser	Asp	Gly	Lys	Gln	
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Pro	Leu	Pro	Glu	Asn	Ala	Glu	Asn	Met	Tyr	Tyr	Phe	Ser	Glu	Leu	Ala	
785					790					795					800	
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Leu	Thr	Leu	Asn	Glu	His	Glu	Glu	Gly	Val	Ala	Pro	Thr	Asp	Ser	Arg	
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ctg	cgg	ccc	gac	cag	cgg	ctg	atg	gag	aag	ggc	cgt	tgg	gac	gag	gcc	2496
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Asn	Thr	Glu	Lys	Gln	Arg	Leu	Glu	Glu	Lys	Gln	Arg	Leu	Ser	Arg	Arg	
833					838					843					848	
cgg	cgg	ctg	gag	gcc	tgc	ggg	ccg	ggc	agc	agc	tgc	agc	tcg	gag	gaa	2592
Arg	Arg	Leu	Glu	Ala	Cys	Gly	Pro	Gly	Ser	Ser	Cys	Ser	Ser	Glu	Glu	

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Glu Gly Val Lys Ala Phe Asp Lys Ile Gln Pro Val Ser Arg Gly His				
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Ser Pro Arg Phe Ile Leu Cys Asp Cys Cys Pro Leu Ala Pro Asn Ser				
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ggc agg act ggc aac tac cgg aag ctc gcg agg ctt cca aag cgc atg				2736
Gly Arg Thr Gly Asn Tyr Arg Lys Leu Ala Arg Leu Pro Lys Arg Met				
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cgc agg tca cgg tac ggg cac gtg cgg cgc gcc agc aaa acc acg cag				2784
Arg Arg Ser Arg Tyr Gly His Val Arg Arg Ala Ser Lys Thr Thr Gln				
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Ala Ser Cys Arg Phe Arg Leu Glu Arg Val Ala Gly Leu Arg Lys Pro				
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Met Gly Ile	
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Phe Val Lys Thr Ile Phe Pro Asn Gly Ser Ala Ala Glu Asp Gly Arg	
4 9 14 19	
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Leu Lys Glu Gly Asp Glu Ile Leu Asp Val Asn Gly Ile Pro Ile Lys	
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Ser His Arg Ala Ser Gly Leu Phe His Lys	Gln Val Thr Val Ala Arg			
276	281	286	291	
caa gcc agt ctc ccc gga agc cca cag gcc ctc	cga aac cct ctc ctc	1089		
Gln Ala Ser Leu Pro Gly Ser Pro Gln Ala	Leu Arg Asn Pro Leu Leu			
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cgc cag agg aag gta ggc tgc tac gat gcc aac	gat gcc agt gat gag	1137		
Arg Gln Arg Lys Val Gly Cys Tyr Asp Ala	Asn Asp Ala Ser Asp Glu			
308	313	318	323	
gaa gag ttt gac aga gaa ggg gac tgc att tca	ctc cca ggg gcc ctc	1185		
Glu Glu Phe Asp Arg Glu Gly Asp Cys Ile	Ser Leu Pro Gly Ala Leu			
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ccg ggt ccc atc agg cct ctg tca gag gat gac	ccg agg cgt gtc tca	1233		
Pro Gly Pro Ile Arg Pro Leu Ser Glu Asp	Asp Pro Arg Arg Val Ser			
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att tcc tct tcc aag ggc atg gac gtc cac aac	caa gag gaa cga ccc	1281		
Ile Ser Ser Ser Lys Gly Met Asp Val His	Asn Gln Glu Glu Arg Pro			
356	361	366	371	
cgg aaa aca ctg gtg agc aag gcc atc tgc gca	cct ctt ctt ggt agc	1329		
Arg Lys Thr Leu Val Ser Lys Ala Ile Ser	Ala Pro Leu Leu Gly Ser			
372	377	382	387	
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Ser Val Asp Leu Glu Glu Ser Ile Pro Glu	Gly Met Val Asp Ala Ala			
388	393	398	403	
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Ser Tyr Ala Ala Asn Leu Thr Asp Ser Ala	Glu Ala Pro Lys Gly Ser			
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aaa ttg gaa tac aca gtc cgt aca gac acc	cag agt ccg acg aac act	1521		
Lys Leu Glu Tyr Thr Val Arg Thr Asp Thr	Gln Ser Pro Thr Asn Thr			
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452	457	462	467	
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His Arg Pro Val Ala Arg Val Ser Pro His	Cys Lys Arg Ser Glu Ala			
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gag gcc aag ccc agt ggc tca cag aca gtg	aac ctg act ggc aga gcc	1665		
Glu Ala Lys Pro Ser Gly Ser Gln Thr Val	Asn Leu Thr Gly Arg Ala			
484	489	494	499	

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Asn Asp Pro Cys Asp Leu Asp Ser Arg Val Gln Ala Thr Ser Val Lys	
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Val Thr Val Ala Gly Phe Gln Pro Gly Gly Ala Val Glu Lys Glu Ser	
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Asp Ser Ser Ser Asp Leu Ile Ser Ser Pro Gly Lys Lys Gly Ala Ala	
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His Pro Asp Pro Ser Lys Thr Ser Val Asp Thr Gly Lys Val Ser Arg	
596 601 606 611	
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Pro Glu Asn Pro Ser Gln Pro Ala Ser Pro Arg Val Ala Lys Cys Lys	
612 617 622 627	
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Glu Thr Ser Thr Pro His Asn Thr Arg Arg Val Ala Ala Leu Arg Gly	
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Gly Asp Pro Leu Thr Ser Gln Glu Gln Arg Gln Gly Ala Pro Gly Asn	
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Lys Arg Leu Ser Leu Lys Gly Lys Ala Lys Val Asn Ser Glu Ala Pro				
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Ile Ser Pro Gln Thr Ser His Lys Thr Leu Ser Lys Ala Val Ser Gln				
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Arg Leu His Val Ala Asp His Glu Asp Pro Asp Arg Asn Thr Thr Ala				
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Ala Pro Arg Ser Pro Gln Cys Val Leu Glu Ser Lys Pro Pro Leu Ala				
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Thr Ser Gly Pro Leu Lys Pro Ser Val Ser Asp Thr Ser Ile Arg Thr				
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Phe Val Ser Pro Leu Thr Ser Pro Lys Pro Val Pro Glu Gln Gly Met				
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Trp Ser Arg Phe His Met Ala Val Leu Ser Glu Pro Asp Arg Gly Cys				
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cca acc acc cct aaa tct cct aag tgt aga gca gag ggc agg gcg ccc				4305
Pro Thr Thr Pro Lys Ser Pro Lys Cys Arg Ala Glu Gly Arg Ala Pro				
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cgt gct gac tcc ggg ccg gtg agt ccg gca gcg tct agg aac ggc atg				4353
Arg Ala Asp Ser Gly Pro Val Ser Pro Ala Ala Ser Arg Asn Gly Met				
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Ser Val Ala Gly Asn Arg Gln Ser Glu Pro Arg Leu Ala Ser His Val				
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Ile Met Ala Ser Asp Arg Leu Glu Arg Thr Asn Gln Leu Lys Ile Val	
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Ser Leu Ala Asn Gly Gln Gly Ile Tyr Ser Val Lys Pro Leu Leu Asp	
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Phe	Ile	Val	Leu	Asn	Arg	Lys	Glu	Gly	Ser	Gly	Leu	Gly	Phe	Ser	Val	
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Ala	Gly	Gly	Thr	Asp	Val	Glu	Pro	Lys	Ser	Ile	Thr	Val	His	Arg	Val	
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Phe	Ser	Gln	Gly	Ala	Ala	Ser	Gln	Glu	Gly	Thr	Met	Asn	Arg	Gly	Asp	
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ggg gga aaa tca tcg gtg acg gga gat ggg ccc ttg gtc att aaa aga Gly Gly Lys Ser Ser Val Thr Gly Asp Gly Pro Leu Val Ile Lys Arg 2116 2121 2126 2131			6561
gtg tac aaa ggt ggt gtg gct gaa caa gct gga ata ata gaa gct gga Val Tyr Lys Gly Gly Val Ala Glu Gln Ala Gly Ile Ile Glu Ala Gly 2132 2137 2142 2147			6609
gat gaa att ctt gct att aat ggg aaa cct ctg gtt ggg ctc atg cac Asp Glu Ile Leu Ala Ile Asn Gly Lys Pro Leu Val Gly Leu Met His 2148 2153 2158 2163			6657
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 Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
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 Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp

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Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser Lys Leu Met Asp	
75 80 85 90	
cag tta gaa gct cta aag aag cag ttg ggt gat aat gaa gct att act	579
Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn Glu Ala Ile Thr	
91 96 101 106	
caa gaa ata gtg ggc tgt gcc cat ttg gag aat tat gct ttg aaa atg	627
Gln Glu Ile Val Gly Cys Ala His Leu Glu Asn Tyr Ala Leu Lys Met	
107 112 117 122	
ttt ttg tat gca gac aat gaa gat cgt gct gga cga ttt cac aaa aac	675
Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg Phe His Lys Asn	
123 128 133 138	
atg atc aag tcc ttc tat act gca agt ctt ttg ata gat gtc ata aca	723
Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile Asp Val Ile Thr	
139 144 149 154	
gta ttt gga gaa ctc act gat gaa aat gtg aaa cac agg aag tat gcc	771
Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His Arg Lys Tyr Ala	
155 160 165 170	
aga tgg aag gca aca tac atc cat aat tgt tta aag aat ggg gag act	819
Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys Asn Gly Glu Thr	
171 176 181 186	

cct caa gca ggc cct gtt gga att gaa gaa gat aat gat att gaa gaa	867
Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn Asp Ile Glu Glu	
187 192 197 202	
aat gaa gat gct gga gca gcc tct ctg ccc act cag cca act cag cca	915
Asn Glu Asp Ala Gly Ala Ala Ser Leu Pro Thr Gln Pro Thr Gln Pro	
203 208 213 218	
tca tca tct tca act tat gac cca agc aac atg cca tca ggc aac tat	963
Ser Ser Ser Ser Thr Tyr Asp Pro Ser Asn Met Pro Ser Gly Asn Tyr	
219 224 229 234	
act gga ata cag att cct ccg ggt gca cac gct cca gct aat aca cca	1011
Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala Asn Thr Pro	
235 240 245 250	
gca gaa gtg cct cac agc aca ggt gta gca agt aat act atc caa cct	1059
Ala Glu Val Pro His Ser Thr Gly Val Ala Ser Asn Thr Ile Gln Pro	
251 256 261 266	
act cca cag act ata cct gcc att gat ccc gca ctt ttc aat aca att	1107
Thr Pro Gln Thr Ile Pro Ala Ile Asp Pro Ala Leu Phe Asn Thr Ile	
267 272 277 282	
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Ser Gln Gly Asp Val Arg Leu Thr Pro Glu Asp Phe Ala Arg Ala Gln	
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Lys Tyr Cys Lys Tyr Ala Gly Ser Ala Leu Gln Tyr Glu Asp Val Ser	
299 304 309 314	
act gct gtc cag aat cta caa aag gct ctc aag tta ctg acg aca ggc	1251
Thr Ala Val Gln Asn Leu Gln Lys Ala Leu Lys Leu Leu Thr Thr Gly	
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331	
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Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe	
107 112 117 122	
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Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro	
123 128 133 138	
tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat gat cat gag	484
Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu	
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Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg	
155 160 165 170	
aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc aag agg cat	580
Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His	
171 176 181 186	
ttg acg ata atg atg gat att gat ggc aag cat gag tgg agg gac tgc	628
Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys	
187 192 197 202	
att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac ttc ggc acc	676
Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr	
203 208 213 218	
tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc att tcc ttg	724
Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu	
219 224 229 234	
aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag gaa aag ctc	772
Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	
235 240 245 250	
cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag ctg cct gag	820
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu	
251 256 261 266	
atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc ttc ctc atc	868
Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile	
267 272 277 282	
gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc att ggt atc	916
Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile	
283 288 293 298	
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Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr *	
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 Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp
 1 5 10 15
 gag gat cta cag cag gac ttc cag aac atc cag gag acc cat cgg ctc 152
 Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu
 17 22 27 32
 tac cgc ctg aag ctg gag gag ctg acc aaa ctt cag aac aat tgc acc 200
 Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr
 33 38 43 48
 agc tcc atc acg cgg cag aag aag cgg ctc cag gag ctg gcc ctc gcc 248
 Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala
 49 54 59 64
 ctg aag aaa tgc aaa ccc tcc ctc cca gca gag gcc gag ggg gcc gca 296
 Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala
 65 70 75 80
 cag gag ctg gag aac cag atg aaa gag cgc caa ggc ctc ttc ttt gac 344
 Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp
 81 86 91 96
 atg gag gcc tat ttg cct aag aag aat gga ttg tac ctg agc ctg gtt 392
 Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val
 97 102 107 112
 ctg ggg aac gtc aac gtc acg ctc ctg agc aag cag gct aag ttt gcc 440
 Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala
 113 118 123 128
 tac aag gac gag tat gag aag ttc aag ctc tac ctc acc atc atc ctc 488
 Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu
 129 134 139 144

atc ctc atc tcc ttc act tgc cgc ttc ctg ctc aac tcc agg gtg aca	536
Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr	
145 150 155 160	
gat gct gcc ttc aac ttc ctg ctg gtc tgg tac tac tgc acc ctg acc	584
Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr	
161 166 171 176	
atc cgg gag agc atc ctc atc aac aac ggc tcc cgg atc aaa ggc tgg	632
Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp	
177 182 187 192	
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Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu	
193 198 203 208	
acg tgg ccc gac ggt ctc atg tac cag aaa ttc cgg aac caa ttc ctc	728
Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu	
209 214 219 224	
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Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr	
225 230 235 240	
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Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr	
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Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu	
257 262 267 272	
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Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe	
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289 294 299 304	
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Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly	
305 310 315 320	
aat ttc ttc acc acc ctg agg gtt gtg cac cag ctc cat cac gcg gca	1064
Asn Phe Phe Thr Thr Leu Arg Val Val His Gln Leu His His Ala Ala	
321 326 331 336	
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337 342 347 352	
ctc cct ccc agc aga ggc cga ggg ggc cgc aca gga gct gga gaa cca	1160
Leu Pro Pro Ser Arg Gly Arg Gly Gly Arg Thr Gly Ala Gly Glu Pro	
353 358 363 368	

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Asp Glu Arg Ala Pro Arg Pro Leu Leu *	
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gagtgtgcgt gtatcagggg gtctcttcta ttctcccttg ggttttatgg gcgctgtggg	2171
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cattatgcct tacaaactta cacagtgcct tgggaattcc aaagtactca gtggagagag 180

gtgttttcagg agccgtagag ccagatcgtc atc atg tct gca ttg tgg ctg ctg 234
Met Ser Ala Leu Trp Leu Leu
1 5

ctg ggc ctc ctt gcc ctg atg gac ttg tct gaa agc agc aac tgg gga 282
Leu Gly Leu Leu Ala Leu Met Asp Leu Ser Glu Ser Ser Asn Trp Gly
8 13 18 23

tgc tat gga aac atc caa agc ctg gac acc cct gga gca tct tgt ggg 330
Cys Tyr Gly Asn Ile Gln Ser Leu Asp Thr Pro Gly Ala Ser Cys Gly
24 29 34 39

att gga aga cgt cac ggc ctg aac tac tgt gga gtt cgt gct tct gaa 378
Ile Gly Arg Arg His Gly Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu
40 45 50 55

agg ctg gct gaa ata gac atg cca tac ctc ctg aaa tat caa ccc atg 426
Arg Leu Ala Glu Ile Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met
56 61 66 71

atg caa acc att ggc caa aag tac tgc atg gat cct gcc gtg atc gct 474
Met Gln Thr Ile Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala
72 77 82 87

ggg gtc ttg tcc agg aag tct ccc ggt gac aaa att ctg gtc aac atg 522
Gly Val Leu Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met
88 93 98 103

ggc gat agg act agc atg gtg cag gac cct ggc tct caa gct ccc aca 570
Gly Asp Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr
104 109 114 119

tcc tgg att agt gag tct cag gtt tcc cag aca act gaa gtt ctg act 618
Ser Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
120 125 130 135

act aga atc aaa gaa atc cag agg agg ttt cca acc tgg acc cct gac 666
Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro Asp
136 141 146 151

cag tac ctg aga ggt gga ctc tgt gcc tac agt ggg ggt gct ggc tat 714
Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala Gly Tyr
152 157 162 167

gtc cga agc agc cag gac ctg agc tgt gac ttc tgc aat gat gtc ctt 762
Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn Asp Val Leu
168 173 178 183

gca cga gcc aag tac ctc aag aga cat ggc ttc taa catc tcagatgaaa 812
Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe *
184 189 194

cccaagacca tgatcacata tgcagcctca aatgttacac agataaaact agccaagggc 872

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963

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Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Phe His Met Glu Ala Ser
9 14 19 24

gtt gaa aac tgc att att gtg agc atg aac acc gct gac cct ggc agc 147
Val Glu Asn Cys Ile Ile Val Ser Met Asn Thr Ala Asp Pro Gly Ser
25 30 35 40

cag ggc atc aca cac agc ctc ttg cta cag gtc att gat gac aag ggc 195
Gln Gly Ile Thr His Ser Leu Leu Leu Gln Val Ile Asp Asp Lys Gly
41 46 51 56

agc atc ctg cca cct aac aca gaa gga aac att ggc atc aga atc aaa 243
Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile Gly Ile Arg Ile Lys
57 62 67 72

cct gtc agg cct gtg agc ctc ttc atg tgc tat gag ggt gac cca gag 291
Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr Glu Gly Asp Pro Glu
73 78 83 88

aag aca gct aaa gtg gaa tgt ggg gac ttc tac aac act ggg gac aga 339
Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr Asn Thr Gly Asp Arg
89 94 99 104

gga aag atg gat gaa gag ggc tac att tgt ttc ctg ggg agg agt gat 387
Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe Leu Gly Arg Ser Asp
105 110 115 120

gac atc att aat gcc tct ggg tat cgc atc ggg cct gca gag gtt gaa 435
Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly Pro Ala Glu Val Glu
121 126 131 136

agc gct ttg gtg gag cac cca gcg gtg gcg gag tca gcc gtg gtg ggc 483
Ser Ala Leu Val Glu His Pro Ala Val Ala Glu Ser Ala Val Val Gly
137 142 147 152

agc cca gac ccg att cga ggg gag gtg gtg aag gcc ttt att gtc ctg 531

Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe Ile Val Leu	
153 158 163 168	
acc cca cag ttc ctg tcc cat gac aag gat cag ctg acc aag gaa ctg	579
Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln Leu Thr Lys Glu Leu	
169 174 179 184	
cag cag cat gtc aag tca gtg aca gcc cca tac aag tac cca agg aag	627
Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys	
185 190 195 200	
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Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile Thr Gly Lys Ile Glu	
201 206 211 216	
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Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln Met *	
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Met Lys Ile Lys	
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ccg ggt ttc atg ggg aag gcc act cca ccc tat gac gtc cag gtc att	283
Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val Ile	
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gat gac aag ggc agc atc ctg cca cct aac aca gaa gga aac att ggc	331

Asp	Asp	Lys	Gly	Ser	Ile	Leu	Pro	Pro	Asn	Thr	Glu	Gly	Asn	Ile	Gly		
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Ile	Arg	Ile	Lys	Pro	Val	Arg	Pro	Val	Ser	Leu	Phe	Met	Cys	Tyr	Glu		
37					42					47					52		
ggc	gac	cca	gag	aag	aca	gct	aaa	gtg	gaa	tgt	ggg	gac	ttc	tac	aac	427	
Gly	Asp	Pro	Glu	Lys	Thr	Ala	Lys	Val	Glu	Cys	Gly	Asp	Phe	Tyr	Asn		
53					58					63					68		
act	ggg	gac	aga	gga	aag	atg	gat	gaa	gag	ggc	tac	att	tgt	ttc	ctg	475	
Thr	Gly	Asp	Arg	Gly	Lys	Met	Asp	Glu	Glu	Gly	Tyr	Ile	Cys	Phe	Leu		
69					74					79					84		
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Gly	Arg	Ser	Asp	Asp	Ile	Ile	Asn	Ala	Ser	Gly	Tyr	Arg	Ile	Gly	Pro		
85					90					95					100		
gca	gag	gtt	gaa	agc	gct	ttg	gtg	gag	cac	cca	gcg	gtg	gcg	gag	tca	571	
Ala	Glu	Val	Glu	Ser	Ala	Leu	Val	Glu	His	Pro	Ala	Val	Ala	Glu	Ser		
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gcc	gtg	gtg	ggc	agc	cca	gac	ccg	att	cga	ggg	gag	gtg	gtg	aag	gcc	619	
Ala	Val	Val	Gly	Ser	Pro	Asp	Pro	Ile	Arg	Gly	Glu	Val	Val	Lys	Ala		
117					122					127					132		
ttt	att	gtc	ctg	acc	cca	cag	ttc	ctg	tcc	cat	gac	aag	gat	cag	ctg	667	
Phe	Ile	Val	Leu	Thr	Pro	Gln	Phe	Leu	Ser	His	Asp	Lys	Asp	Gln	Leu		
133					138					143					148		
acc	aag	gaa	ctg	cag	cag	cat	gtc	aag	tca	gtg	aca	gcc	cca	tac	aag	715	
Thr	Lys	Glu	Leu	Gln	Gln	His	Val	Lys	Ser	Val	Thr	Ala	Pro	Tyr	Lys		
149					154					159					164		
tac	cca	agg	aag	gtg	gag	ttt	gtc	tca	gag	ctg	cca	aaa	acc	atc	act	763	
Tyr	Pro	Arg	Lys	Val	Glu	Phe	Val	Ser	Glu	Leu	Pro	Lys	Thr	Ile	Thr		
165					170					175					180		
ggc	aag	att	gaa	cgg	aag	gaa	ctt	cgg	aaa	aag	gag	act	ggc	cag	atg	811	
Gly	Lys	Ile	Glu	Arg	Lys	Glu	Leu	Arg	Lys	Lys	Glu	Thr	Gly	Gln	Met		
181					186					191					196		
taa	tcgg	cagtgaactc	agaacgcact	gcacacctga	ggcaaataccc	tgccacttt	868										
*																	
197																	
agtctcccca	ctatggtgag	gacgagggtg	gggcattgag	agtgttgatt	tgggaaagta	928											
tcaggagtgc	catgattcca	atgttttcct	tcttttaaat	taaattcagt	tgctctgctt	988											
cctccaagtc	ctctgtatct	ttagaatttc	ccagggtgagc	actcataacg	caagtaataa	1048											
aatactgata	tcaacaaaaa	aaaaaaaa				1075											

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<220>
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<400> 356

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gcctcggggc tcatgtgcgg agcccacttt tactgatacg gga  atg gtg gct cac      115
                                     Met Val Ala His
                                     1

ata aac aac agc cgg ctc aag gcc aag ggc gtg ggc cag cac gac aac      163
Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly Gln His Asp Asn
  5                               10                               15                               20

gcc cag aac ttt ggt aac cag agc ttt gag gag ctg cga gca gcc tgt      211
Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu Arg Ala Ala Cys
  21                               26                               31                               36

cta aga aag ggg gag ctc ttc gag gac ccc tta ttc cct gct gaa ccc      259
Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe Pro Ala Glu Pro
  37                               42                               47                               52

agc tca ctg ggc ttc aag gac ctg ggc ccc aac tcc aaa aat gtg cag      307
Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser Lys Asn Val Gln
  53                               58                               63                               68

aac atc tcc tgg cag cgg ccc aag gat atc ata aac aac cct cta ttc      355
Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn Asn Pro Leu Phe
  69                               74                               79                               84

atc atg gat ggg att tct cca aca gac atc tgc cag ggg atc ctc ggg      403
Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln Gly Ile Leu Gly
  85                               90                               95                               100

gac tgc tgg ctg ctg gct gcc atc ggc tcc ctt acc acc tgc ccc aaa      451
Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr Thr Cys Pro Lys
  101                               106                               111                               116

ctg cta tac cgc gtg gtg ccc aga gga cag agc ttc aag aaa aac tat      499
Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe Lys Lys Asn Tyr
  117                               122                               127                               132

gct ggc atc ttc cat ttt cag att tgg cag ttt gga cag tgg gtg aac      547
Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly Gln Trp Val Asn
  133                               138                               143                               148

gtg gtg gta gat gac cgg ctg ccc aca aag aat gac aag ctg gtg ttt      595
Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp Lys Leu Val Phe
  149                               154                               159                               164
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gtg cac tca acc gaa cgc agt gag ttc tgg agt gcc ctg ctg gag aag	643
Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala Leu Leu Glu Lys	
165 170 175 180	
gcg tat gcc aag ctg agt ggg tcc tat gaa gca ttg tca ggg ggc agt	691
Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu Ser Gly Gly Ser	
181 186 191 196	
acc atg gag ggc ctt gag gac ttc aca gga ggc gtg gcc cag agc ttc	739
Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val Ala Gln Ser Phe	
197 202 207 212	
caa ctc cag agg ccc cct cag aac ctg ctc agg ctc ctt agg aag gcc	787
Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu Leu Arg Lys Ala	
213 218 223 228	
gtg gag cga tcc tcc ctc atg ggt tgc tcc att gaa gtc acc agt gat	835
Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu Val Thr Ser Asp	
229 234 239 244	
agt gaa ctg gaa tcc atg act gac aag atg ctg gtg aga ggg cac gct	883
Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val Arg Gly His Ala	
245 250 255 260	
tac tct gtg act ggc ctt cag gat gtc cac tac aga ggc aaa atg gaa	931
Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg Gly Lys Met Glu	
261 266 271 276	
aca ctg att cgg gtc cgg aat ccc tgg ggc cgg att gag tgg aat gga	979
Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile Glu Trp Asn Gly	
277 282 287 292	
gct tgg agt gac agt gcc agg gag tgg gaa gag gtg gcc tca gac atc	1027
Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val Ala Ser Asp Ile	
293 298 303 308	
cag atg cag ctg ctg cac aag acg gag gac ggg gag ttc tgg atg tcc	1075
Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu Phe Trp Met Ser	
309 314 319 324	
tac caa gat ttc ctg aac aac ttc acg ctc ctg gag atc tgc aac ctc	1123
Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu Ile Cys Asn Leu	
325 330 335 340	
acg cct gat aca ctc tct ggg gac tac aag agc tac tgg cac acc acc	1171
Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr Trp His Thr Thr	
341 346 351 356	
ttc tac gag ggc agc tgg cgc aga ggc agc tcc gca ggg ggc tgc agg	1219
Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala Gly Gly Cys Arg	
357 362 367 372	
aac cac cct ggc acg ttc tgg acc aac ccc cag ttt aag atc tct ctt	1267
Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe Lys Ile Ser Leu	
373 378 383 388	
cct gag ggg gat gac cca gag gat gac gca gag ggc aat gtt gtg gtc	1315

Pro Glu Gly Asp Asp	Pro Glu Asp Asp Ala	Glu Gly Asn Val Val Val	
389	394	399	404
tgc acc tgc ctg gtg gcc cta atg cag aag	aac tgg cgg cat gca cgg	1363	
Cys Thr Cys Leu Val Ala Leu Met Gln Lys	Asn Trp Arg His Ala Arg		
405	410	415	420
cag cag gga gcc cag ctg cag acc att ggc	ttt gtc ctc tac gcg gtc	1411	
Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly	Phe Val Leu Tyr Ala Val		
421	426	431	436
cca aaa gag ttt cag aac att cag gat gtc	cac ttg aag aag gaa ttc	1459	
Pro Lys Glu Phe Gln Asn Ile Gln Asp Val	His Leu Lys Lys Glu Phe		
437	442	447	452
ttc acg aag tat cag gac cac ggc ttc tca	gag atc ttc acc aac tca	1507	
Phe Thr Lys Tyr Gln Asp His Gly Phe Ser	Glu Ile Phe Thr Asn Ser		
453	458	463	468
cgg gag gtg agc agc caa ctc cgg ctg cct	ccg ggg gaa tat atc att	1555	
Arg Glu Val Ser Ser Gln Leu Arg Leu Pro	Pro Gly Glu Tyr Ile Ile		
469	474	479	484
att ccc tcc acc ttt gag cca cac aga gat	gct gac ttc ctg ctt cgg	1603	
Ile Pro Ser Thr Phe Glu Pro His Arg Asp	Ala Asp Phe Leu Leu Arg		
485	490	495	500
gtc ttc acc gag aag cac agc gag tca tgg	gaa ttg gat gaa gtc aac	1651	
Val Phe Thr Glu Lys His Ser Glu Ser Trp	Glu Leu Asp Glu Val Asn		
501	506	511	516
tat gct gag caa ctc caa gag gaa aag gtc	tct gag gat gac atg gac	1699	
Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val	Ser Glu Asp Asp Met Asp		
517	522	527	532
cag gac ttc cta cat ttg ttt aag ata gtg	gca gga gag ggc aag gag	1747	
Gln Asp Phe Leu His Leu Phe Lys Ile Val	Ala Gly Glu Gly Lys Glu		
533	538	543	548
ata ggg gtg tat gag ctc cag agg ctg ctc	aac agg atg gcc atc aaa	1795	
Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu	Asn Arg Met Ala Ile Lys		
549	554	559	564
ttc aaa agc ttc aag acc aag ggc ttt ggc	ctg gat gct tgc cgc tgc	1843	
Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly	Leu Asp Ala Cys Arg Cys		
565	570	575	580
atg atc aac ctc atg gat aaa gat ggc tct	ggc aag ctg ggg ctt cta	1891	
Met Ile Asn Leu Met Asp Lys Asp Gly Ser	Gly Lys Leu Gly Leu Leu		
581	586	591	596
gag ttc aag atc ctg tgg aaa aaa ctc aag	aaa tgg atg gac atc ttc	1939	
Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys	Lys Trp Met Asp Ile Phe		
597	602	607	612
aga gag tgt gac cag gac cat tca ggc acc	ttg aac tcc tat gag atg	1987	
Arg Glu Cys Asp Gln Asp His Ser Gly Thr	Leu Asn Ser Tyr Glu Met		

613	618	623	628	
cgc ctg gtt att gag aaa gca ggc atc aag	ctg aac aac aag gta atg	2035		
Arg Leu Val Ile Glu Lys Ala Gly Ile Lys	Leu Asn Asn Lys Val Met			
629	634	639	644	
cag gtc ctg gtg gcc agg tat gca gat gat	gac ctg atc ata gac ttt	2083		
Gln Val Leu Val Ala Arg Tyr Ala Asp Asp	Asp Leu Ile Ile Asp Phe			
645	650	655	660	
gac agc ttc atc agc tgt ttc ctg agg cta	aag acc atg ttc aca ttc	2131		
Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu	Lys Thr Met Phe Thr Phe			
661	666	671	676	
ttt cta acc atg gac ccc aag aat act ggc	cat att tgc ttg agc ctg	2179		
Phe Leu Thr Met Asp Pro Lys Asn Thr Gly	His Ile Cys Leu Ser Leu			
677	682	687	692	
gaa cag tgg ctg cag atg acc atg tgg gga	tag aggcgctg taggagcctg	2230		
Glu Gln Trp Leu Gln Met Thr Met Trp Gly	*			
693	698	703		
gtcatctcta ccagcagcag cagcagcgag gttctagccc aggaggggtgg ggtgcttctt				2290
gtagccctca gctctccagt ctctgctgat gaaatgggat ccaggtgg				2338
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<211> 1541				
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cgagaagccg tccaggaaac	atg ctc tca ggg gac ccc cat ctg cct cag	110		
	Met Leu Ser Gly Asp Pro His Leu Pro Gln			
	1 5			
cct ctt tgt cac tgc ctg gac cat tgt ccc tgc tgt ttc tca ggc acc	158			
Pro Leu Cys His Cys Leu Asp His Cys Pro Cys Cys Phe Ser Gly Thr				
11 16 21 26				
acc agg acc agc tga tcattccagc ccacagcaat ggagccacat gactcctccc	213			
Thr Arg Thr Ser *				
27				
acatggactc tgagttccga tacactctct tcccgattgt ttacagcatc atctttgtgc	273			
tcgggggtcat tgctaattggc tacgtgctgt ggggtctttgc ccgcctgtac ccttgcaaga	333			

aattcaatga gataaagatc ttcatggtga acctcaccat ggcggacatg ctcttcttga	393
tcaccctgcc actttggatt gtctactacc aaaaccaggg caactggata ctccccaat	453
tcctgtgcaa cgtggctggc tgccttttct tcatcaacac ctactgctct gtggccttcc	513
tgggggtcat cacttataac cgcttccagg cagtaactcg gcccatcaag actgctcagg	573
ccaacacccg caagcgtggc atctctttgt ccttgggtcat ctgggtggcc attgtgggag	633
ctgcatccta ctctctcatc ctggactoca ccaacacagt gcccgacagt gctggctcag	693
gcaacgtcac tcgctgcttt gagcattacg agaagggcag cgtgccagtc ctcatcatcc	753
acatcttcat cgtgttcagc ttcttctctg tcttctcat catcctcttc tgcaacctgg	813
tcatcatccg taccttgctc atgcagccgg tgcagcagca gcgcaacgct gaagtcaagc	873
gccgggcgct gtggatggtg tgcacgggtc tggcggtgtt catcatctgc ttcgtgcccc	933
accacgtggt gcagctgccc tggacccttg ctgagctggg cttccaggac agcaaattcc	993
accaggccat taatgatgca catcagggtc cctctgctt ccttagcacc aactgtgtct	1053
tagaccctgt tatctactgt ttctcacca aaaagttccg caagcacctc accgaaaagt	1113
tctacagcat gcgcagtagc cggaattgct cccggggccac cacggatacg gtcactgaag	1173
tggttgtgcc attcaaccag atccctggca attccctcaa aaattagtcc ctgcttccat	1233
gcctgaagtc ttctctcca tgaacatcat ggactgagct gggggaagaa gggatatcta	1293
ctgtgggtct gggcaccacc tctgtgggct ctggtgggcc attagatttg gaggtacct	1353
cacctgggca gggatgatgg cagagccagg ctgttggaat atccagaact caaatgagcc	1413
ccttcatccg cctgtgggag catactacag taactgtgac tgatgacttt atcctgagtc	1473
ccttaatctt atggggcccg aaggaatgtc agggccaggc gcagaccttg ggggaagact	1533
ttaaacca	1541

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 <213> Homo sapiens

<220>
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 <222> (71) .. (448)

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	Met Thr Tyr Ile Lys Ser Pro Ala Pro Cys Gln Thr Gln	
	1 5 10	
acg tgc tat gtc cag ggt gct tct cct tgc cag agc tat tat gtt caa	157	
Thr Cys Tyr Val Gln Gly Ala Ser Pro Cys Gln Ser Tyr Tyr Val Gln		
14 19 24 29		
gct cct gca agt ggc tca acc tcc cag tac tgt gtc act gac cca tgc	205	
Ala Pro Ala Ser Gly Ser Thr Ser Gln Tyr Cys Val Thr Asp Pro Cys		
30 35 40 45		
tct gct ccc tgt tcc acc agc tac tgc tgt ctg gct ccc cgg acc ttc	253	
Ser Ala Pro Cys Ser Thr Ser Tyr Cys Cys Leu Ala Pro Arg Thr Phe		
46 51 56 61		
ggg gtg agt ccc ctg aga cgc tgg att cag cgg ccc cag aac tgc aac	301	
Gly Val Ser Pro Leu Arg Arg Trp Ile Gln Arg Pro Gln Asn Cys Asn		
62 67 72 77		
aca gga tca tct ggc tgc tgt gag aat tcg gga agc tct ggg tgc tgt	349	
Thr Gly Ser Ser Gly Cys Cys Glu Asn Ser Gly Ser Ser Gly Cys Cys		
78 83 88 93		
ggg tct ggg ggc tgt ggc tgc agc tgt gga tgt ggc agc tct ggg tgc	397	
Gly Ser Gly Gly Cys Gly Cys Ser Cys Gly Cys Gly Ser Ser Gly Cys		
94 99 104 109		
tgc tgt ttg gga att atc ccc atg aag tcc cga agt cct gcg ttg ctg	445	
Cys Cys Leu Gly Ile Ile Pro Met Lys Ser Arg Ser Pro Ala Leu Leu		
110 115 120 125		
tga ccat gaggatgact gctgctgcta aacatacgac agctcaactc cagaatgcac	502	
*		
126		
tgccccgcta cccctctgga a	523	

<210> 359
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 <213> Homo sapiens

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<220>
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 <222> (1) ... (1783)
 <223> n = a,t,c or g

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aggaggcttc agtctcagtg gctcagcctt cccagctgat ctgaagctcc tgtgcagcct 120

cagccctaca cc atg acc tcc ttc tac agc acc tcc tca tgc cct ctg 168
Met Thr Ser Phe Tyr Ser Thr Ser Ser Cys Pro Leu
1 5 10

ggt tgc acc atg gct cct gga gca aga aat gtc ttt gtc tct cct atc 216
Gly Cys Thr Met Ala Pro Gly Ala Arg Asn Val Phe Val Ser Pro Ile
13 18 23 28

gat gtt ggg tgc cag cct gtg gca gag gcc aat gct gcc tcc atg tgc 264
Asp Val Gly Cys Gln Pro Val Ala Glu Ala Asn Ala Ala Ser Met Cys
29 34 39 44

ctc ttg gcc aac gtg gca cac gcc aac aga gtc cgt gtg ggg tgc act 312
Leu Leu Ala Asn Val Ala His Ala Asn Arg Val Arg Val Gly Ser Thr
45 50 55 60

ccc ctg ggc cgc ccc agc ctc tgt ctg ccc cca acc agt cac act gct 360
Pro Leu Gly Arg Pro Ser Leu Cys Leu Pro Pro Thr Ser His Thr Ala
61 66 71 76

tgt ccc ttg cca ggg acc tgt cac att ccc ggc aac atc gga atc tgt 408
Cys Pro Leu Pro Gly Thr Cys His Ile Pro Gly Asn Ile Gly Ile Cys
77 82 87 92

ggg gcc tac ggc aaa aac acc ctg aat ggc cat gag aag gag acc atg 456
Gly Ala Tyr Gly Lys Asn Thr Leu Asn Gly His Glu Lys Glu Thr Met
93 98 103 108

aag ttc ctg aat gac cgc ctg gcc aac tac ctg gag aag gtg cgc cag 504
Lys Phe Leu Asn Asp Arg Leu Ala Asn Tyr Leu Glu Lys Val Arg Gln
109 114 119 124

ctg gag cag gag aat gca gag ctg gag acc aca ctc ctc gag agg agc 552
Leu Glu Gln Glu Asn Ala Glu Leu Glu Thr Thr Leu Leu Glu Arg Ser
125 130 135 140

aag tgc cac gag tcc acc gtg tgc ccc gac tac cag tcc tac ttc cgt 600
Lys Cys His Glu Ser Thr Val Cys Pro Asp Tyr Gln Ser Tyr Phe Arg
141 146 151 156

aca atc gag gag ctc cag cag aag atc ctg tgc agc aag gct gag aat 648
Thr Ile Glu Glu Leu Gln Gln Lys Ile Leu Cys Ser Lys Ala Glu Asn
157 162 167 172

gcc agg ctg att gta caa att gac aac gcg aag ctg gct gct gat gac 696
Ala Arg Leu Ile Val Gln Ile Asp Asn Ala Lys Leu Ala Ala Asp Asp
173 178 183 188

ttt agg atc aag ctg gag agt gag cgc tcc ctt cac cag ctg gtg gag 744
Phe Arg Ile Lys Leu Glu Ser Glu Arg Ser Leu His Gln Leu Val Glu
189 194 199 204

gcg gac aag tgc ggg acg cag aag ctc ctg gat gac gcg acc ctg gcc 792
Ala Asp Lys Cys Gly Thr Gln Lys Leu Leu Asp Asp Ala Thr Leu Ala

205	210	215	220	
aag gcc gac ctg gag gcc cag cag gag tcc ctg aag gag gag cag ctc				840
Lys Ala Asp Leu Glu Ala Gln Gln Glu Ser Leu Lys Glu Glu Gln Leu				
221	226	231	236	
tcc ctc aag agc aac cac gag cag gaa gta aag att ctg agg agt cag				888
Ser Leu Lys Ser Asn His Glu Gln Glu Val Lys Ile Leu Arg Ser Gln				
237	242	247	252	
ctg ggg gag aag ttc cgg atc gag ctg gac att gag ccc acc att gac				936
Leu Gly Glu Lys Phe Arg Ile Glu Leu Asp Ile Glu Pro Thr Ile Asp				
253	258	263	268	
ctg aac agg gtg ttg ggg gag atg cgg gct cag tac gag gcc atg gtg				984
Leu Asn Arg Val Leu Gly Glu Met Arg Ala Gln Tyr Glu Ala Met Val				
269	274	279	284	
gag acc aac cac cag gat gtg gaa cag tgg ttc caa gcc cag tct gaa				1032
Glu Thr Asn His Gln Asp Val Glu Gln Trp Phe Gln Ala Gln Ser Glu				
285	290	295	300	
ggc atc agc ctg cag gcc atg tcc tgc tcc gag gag ctg cag tgc tgc				1080
Gly Ile Ser Leu Gln Ala Met Ser Cys Ser Glu Glu Leu Gln Cys Cys				
301	306	311	316	
cag tcg gag atc ctg gag ctg aga tgc acg gtg aat gcc ctg gag gtg				1128
Gln Ser Glu Ile Leu Glu Leu Arg Cys Thr Val Asn Ala Leu Glu Val				
317	322	327	332	
gag cgc caa gcc cag cac acc ttg aag gac tgt ctg cag aac tcc ctg				1176
Glu Arg Gln Ala Gln His Thr Leu Lys Asp Cys Leu Gln Asn Ser Leu				
333	338	343	348	
tgt gaa gcg gag gac cgc tac ggc aca gag ctg gcc cag atg cag agc				1224
Cys Glu Ala Glu Asp Arg Tyr Gly Thr Glu Leu Ala Gln Met Gln Ser				
349	354	359	364	
ctc att agc aac ttg gaa gag cag ttg tct gag atc cgg gcc gac ctg				1272
Leu Ile Ser Asn Leu Glu Glu Gln Leu Ser Glu Ile Arg Ala Asp Leu				
365	370	375	380	
gag cgg cag aac cag gag tac cag gtg ctg ctg gac gtg aag gcc cgg				1320
Glu Arg Gln Asn Gln Glu Tyr Gln Val Leu Leu Asp Val Lys Ala Arg				
381	386	391	396	
ttg gag aac gag att gcc aca tac cgg aac ctt act ccc ctg caa tcc				1368
Leu Glu Asn Glu Ile Ala Thr Tyr Arg Asn Leu Thr Pro Leu Gln Ser				
397	402	407	412	
ctg ttc cac gcc tgc ctc ctg tac ttc ttg tcc aag ctg tgg ccc tgt				1416
Leu Phe His Ala Cys Leu Leu Tyr Phe Leu Ser Lys Leu Trp Pro Cys				
413	418	423	428	
cac cgg tgg gtc tcc ctc tgg cca tgg agc cag cat ggg gag atg att				1464
His Arg Trp Val Ser Leu Trp Pro Trp Ser Gln His Gly Glu Met Ile				
429	434	439	444	

ctg aag gcc cga gtt agg aga ttg agg ctg gtt gca ctg ggg tca gga	1512
Leu Lys Ala Arg Val Arg Arg Leu Arg Leu Val Ala Leu Gly Ser Gly	
445 450 455 460	
gtg ccc tca cct tgc cca gtc ttc ctt caa gac tag actc actgaggcat	1562
Val Pro Ser Pro Cys Pro Val Phe Leu Gln Asp *	
461 466 471	
tttccctaaa tcaaccggta gcagatactt ccaaggagtg gtcacctgcc tatgcctcta	1622
agctgtatatt tttgttggtg ctaaaatggt gtaattatct tccatgaaag caattatttt	1682
tcctgggtgtc tcttcttggt acttttagtt ctattccagt gtttcagaat ctccaaaaat	1742
gtaactgggt tccctgcatt aaatggtcaa taaacctcct t	1783

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 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (47)..(403)

<220>
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 <222> (1)...(422)
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Met Ser Cys	
1	
cag cag agc cag cag cag tgc cag cct cct ccc aaa tgt acc cct aaa	103
Gln Gln Ser Gln Gln Gln Cys Gln Pro Pro Pro Lys Cys Thr Pro Lys	
4 9 14 19	
tgc cct ccc aag tgt act cct aag tgt cct ccc aag tgt ccc cca aaa	151
Cys Pro Pro Lys Cys Thr Pro Lys Cys Pro Pro Lys Cys Pro Pro Lys	
20 25 30 35	
tgc cct ccc cag tat tca gcc cca tgc cca cct cca gtc tct tcc tgc	199
Cys Pro Pro Gln Tyr Ser Ala Pro Cys Pro Pro Pro Val Ser Ser Cys	
36 41 46 51	
tgt ggt tcc agc tct ggg ggc tgc tgc agc tct gag ggt ggt ggc tgc	247
Cys Gly Ser Ser Ser Gly Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys	
52 57 62 67	
tgc ctg agc cac cac agg ccc cgc cag tcc ctc cga cgc cga cct cag	295
Cys Leu Ser His His Arg Pro Arg Gln Ser Leu Arg Arg Arg Pro Gln	

68	73	78	83	
agt tcc agc tgc tgt ggc agt ggc agt ggc cag cag tct ggg ggc tcc				343
Ser Ser Ser Cys Cys Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser				
84	89	94	99	
agc tgc tgc cac agc tct ggg ggc tct ggc tgc tgc cac agc tct gga				391
Ser Cys Cys His Ser Ser Gly Gly Ser Gly Cys Cys His Ser Ser Gly				
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agccaaaaat ggtggcttgc ttctgtttct ctttttttcc ccacacatag cagtaccaat	180
atg aag tgg gta cag ttt tca aac cta cac gtt gat gtt cca aag gat	228
Met Lys Trp Val Gln Phe Ser Asn Leu His Val Asp Val Pro Lys Asp	
1 5 10 15	
ttg acc aaa cct gtg gta aca atc tct gat gaa cca gac ata tta tat	276
Leu Thr Lys Pro Val Val Thr Ile Ser Asp Glu Pro Asp Ile Leu Tyr	
17 22 27 32	
aag cgc ctc tcg gtt ttg gtg aaa ggt cac gat aag gct gta ttg gac	324
Lys Arg Leu Ser Val Leu Val Lys Gly His Asp Lys Ala Val Leu Asp	
33 38 43 48	
agt tat gaa tat ttt gct gtg ctt gct gct aaa gaa ctt ggt atc tct	372
Ser Tyr Glu Tyr Phe Ala Val Leu Ala Ala Lys Glu Leu Gly Ile Ser	
49 54 59 64	
att aaa gta cat gaa cct cca agg aaa ata gag cga ttt act ctt ctc	420
Ile Lys Val His Glu Pro Pro Arg Lys Ile Glu Arg Phe Thr Leu Leu	
65 70 75 80	
caa tca gtg cat att tac aag aag cac aga gtt cag tat gaa atg aga	468
Gln Ser Val His Ile Tyr Lys Lys His Arg Val Gln Tyr Glu Met Arg	
81 86 91 96	

aca ctt tac aga tgt tta gag tta gaa cat cta act gga agc aca gca	516
Thr Leu Tyr Arg Cys Leu Glu Leu Glu His Leu Thr Gly Ser Thr Ala	
97 102 107 112	
gat gtc tac ttg gaa tat att cag cga aac tta cct gaa ggg gtt gcc	564
Asp Val Tyr Leu Glu Tyr Ile Gln Arg Asn Leu Pro Glu Gly Val Ala	
113 118 123 128	
atg gaa gta aca aag ttt tgt ttc ttt att ttt tta gac aca att aga	612
Met Glu Val Thr Lys Phe Cys Phe Phe Ile Phe Leu Asp Thr Ile Arg	
129 134 139 144	
aca gtt acc aga aca cat caa gga gcc aat ctg gga aac act atc aga	660
Thr Val Thr Arg Thr His Gln Gly Ala Asn Leu Gly Asn Thr Ile Arg	
145 150 155 160	
aga aaa aga aga aag caa gtc ata aag cct cag gga ggc cat ttt tgc	708
Arg Lys Arg Arg Lys Gln Val Ile Lys Pro Gln Gly Gly His Phe Cys	
161 166 171 176	
cta aat ttg aaa tga ggggtgggcca gatgagtatg ttttaagtga gagtgcttcc	763
Leu Asn Leu Lys *	
177	
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 Ser Cys Gln Gln Asn Gln Gln Gln Cys Gln Pro Pro Pro Lys Cys Pro
 2 7 12 17

atc ccc aag tat ccc cca aaa tgt ccc tca aag tgt gca tcc tca tgc 151
 Ile Pro Lys Tyr Pro Pro Lys Cys Pro Ser Lys Cys Ala Ser Ser Cys
 18 23 28 33

cca cct cca atc tct tcc tgc tgt ggc tcc agc tct ggg ggc tgc tgt 199
 Pro Pro Pro Ile Ser Ser Cys Cys Gly Ser Ser Ser Gly Gly Cys Cys
 34 39 44 49

agc tct ggg ggc tgt ggt tgc tgc agc tct gag gga ggt ggc tgc tgc 247
 Ser Ser Gly Gly Cys Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys Cys
 50 55 60 65

ctg agc cac cac aga cac cat agg tcc cac tgc cac aga ccc aag agc 295
 Leu Ser His His Arg His His Arg Ser His Cys His Arg Pro Lys Ser
 66 71 76 81

tcc aat tgc tat ggc agt ggc agt ggc cag cag tct ggg ggt tct ggc 343
 Ser Asn Cys Tyr Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser Gly
 82 87 92 97

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 Cys Cys Ser Gly Gly Gly Cys Cys *
 98 103

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gagggccctca gagtgaaagc gtaagggttca gtcagcctgc tgcagctttg cagacctcag 180

ctgggcatct ccagactccc ctgaaggaag agccttcctc acccaaacc acaaaag 237
atg ctg aaa aag cct ctc tca gct gtg acc tgg ctc tgc att ttc atc 285
Met Leu Lys Lys Pro Leu Ser Ala Val Thr Trp Leu Cys Ile Phe Ile
1 5 10 15

gtg gcc ttt gtc agc cac cca gcg tgg ctg cag aag ctc tct aag cac 333
Val Ala Phe Val Ser His Pro Ala Trp Leu Gln Lys Leu Ser Lys His
17 22 27 32

aag aca cca gca cag cca cag ctc aaa gcg gcc aac tgc tgt gag gag 381
Lys Thr Pro Ala Gln Pro Gln Leu Lys Ala Ala Asn Cys Cys Glu Glu
33 38 43 48

gtg aag gag ctc aag gcc caa gtt gcc aac ctt agc agc ctg ctg agt 429
Val Lys Glu Leu Lys Ala Gln Val Ala Asn Leu Ser Ser Leu Leu Ser
49 54 59 64

gaa ctg aac aag aag cag gag agg gac tgg gtc agc gtg gtc atg cag 477
Glu Leu Asn Lys Lys Gln Glu Arg Asp Trp Val Ser Val Val Met Gln
65 70 75 80

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Val Met Glu Leu Glu Ser Asn Ser Lys Arg Met Glu Ser Arg Leu Thr
81 86 91 96

gat gct gag agc aag tac tcc gag atg aac aac caa att gac atc atg 573
Asp Ala Glu Ser Lys Tyr Ser Glu Met Asn Asn Gln Ile Asp Ile Met
97 102 107 112

cag ctg cag gca gca cag acg gtc act cag acc tcc gca gat gcc atc 621
Gln Leu Gln Ala Ala Gln Thr Val Thr Gln Thr Ser Ala Asp Ala Ile
113 118 123 128

tac gac tgc tct tcc ctc tac cag aag aac tac cgc atc tct gga gtg 669
Tyr Asp Cys Ser Ser Leu Tyr Gln Lys Asn Tyr Arg Ile Ser Gly Val
129 134 139 144

tat aag ctt cct cct gat gac ttc ctg ggc agc cct gaa ctg gag gtg 717
Tyr Lys Leu Pro Pro Asp Asp Phe Leu Gly Ser Pro Glu Leu Glu Val
145 150 155 160

ttc tgt gac atg gag act tca ggc gga ggc tgg acc atc atc cag aga 765
Phe Cys Asp Met Glu Thr Ser Gly Gly Gly Trp Thr Ile Ile Gln Arg
161 166 171 176

cga aaa agt ggc ctt gtc tcc ttc tac cgg gac tgg aag cag tac aag 813
Arg Lys Ser Gly Leu Val Ser Phe Tyr Arg Asp Trp Lys Gln Tyr Lys
177 182 187 192

cag ggc ttt ggc agc atc cgt ggg gac ttc tgg ctg ggg aac gaa cac 861
Gln Gly Phe Gly Ser Ile Arg Gly Asp Phe Trp Leu Gly Asn Glu His
193 198 203 208

atc cac cgg ctc tcc aga cag cca acc cgg ctg cgt gta gag atg gag 909
Ile His Arg Leu Ser Arg Gln Pro Thr Arg Leu Arg Val Glu Met Glu

209	214	219	224	
gac tgg gag ggc aac ctg cgc tac gct gag tat agc cac ttt gtt ttg				957
Asp Trp Glu Gly Asn Leu Arg Tyr Ala Glu Tyr Ser His Phe Val Leu				
225	230	235	240	
ggc aat gaa ctc aac agc tat cgc ctc ttc ctg ggg aac tac act ggc				1005
Gly Asn Glu Leu Asn Ser Tyr Arg Leu Phe Leu Gly Asn Tyr Thr Gly				
241	246	251	256	
aat gtg ggg aac gac gcc ctc cag tat cat aac aac aca gcc ttc agc				1053
Asn Val Gly Asn Asp Ala Leu Gln Tyr His Asn Asn Thr Ala Phe Ser				
257	262	267	272	
acc aag gac aag gac aat gac aac tgc ttg gac aag tgt gca cag ctc				1101
Thr Lys Asp Lys Asp Asn Asp Asn Cys Leu Asp Lys Cys Ala Gln Leu				
273	278	283	288	
cgc aaa ggt ggc tac tgg tac aac tgc tgc aca gac tcc aac ctc aat				1149
Arg Lys Gly Gly Tyr Trp Tyr Asn Cys Cys Thr Asp Ser Asn Leu Asn				
289	294	299	304	
gga gtg tac tac cgc ctg ggt gag cac aat aag cac ctg gat ggc atc				1197
Gly Val Tyr Tyr Arg Leu Gly Glu His Asn Lys His Leu Asp Gly Ile				
305	310	315	320	
acc tgg tat ggc tgg cat gga tct acc tac tcc ctc aaa cgg gtg gag				1245
Thr Trp Tyr Gly Trp His Gly Ser Thr Tyr Ser Leu Lys Arg Val Glu				
321	326	331	336	
atg aaa atc cgc cca gaa gac ttc aag cct taa aaggaggc tgccgtggag				1296
Met Lys Ile Arg Pro Glu Asp Phe Lys Pro *				
337	342	347		
cacggataca gaaactgaga cacgtggaga ctggatgagg gcagatgagg acaggaagag				1356
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 Asn Thr Val Trp Asn Met Glu Asp Leu Asp Leu Glu Tyr Ala Lys Thr
 3 8 13 18
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 Asp Ile Asn Cys Gly Thr Asp Leu Met Phe Tyr Ile Glu Met Asp Pro
 19 24 29 34
 cca gca ctg cct cct aaa cca cca aaa cct act act gta gcc aac aac 199
 Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn
 35 40 45 50
 ggt atg aat aac aat atg tcc tta caa gat gct gaa tgg tac tgg gga 247
 Gly Met Asn Asn Asn Met Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly
 51 56 61 66
 gat atc tcg agg gaa gaa gtg aat gaa aaa ctt cga gat aca gca gac 295
 Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp
 67 72 77 82
 ggg acc ttt ttg gta cga gat gcg tct act aaa atg cat ggt gat tat 343
 Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr
 83 88 93 98
 act ctt aca cta agg aaa ggg gga aat aac aaa tta atc aaa ata ttt 391
 Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe
 99 104 109 114
 cat cga gat ggg aaa tat ggc ttc tct gac cca tta acc ttc agt tct 439
 His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
 115 120 125 130

gtg gtt gaa tta ata aac cac tac cgg aat gaa tct cta gct cag tat	487
Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr	
131 136 141 146	
aat ccc aaa ttg gat gtg aaa tta ctt tat cca gta tcc aaa tac caa	535
Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln	
147 152 157 162	
cag gat caa gtt gtc aaa gaa gat aat att gaa gct gta ggg aaa aaa	583
Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys	
163 168 173 178	
tta cat gaa tat aac act cag ttt caa gaa aaa agt cga gaa tat gat	631
Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp	
179 184 189 194	
aga tta tat gaa gaa tat acc cgc aca tcc cag gaa atc caa atg aaa	679
Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys	
195 200 205 210	
agg aca gct att gaa gca ttt aat gaa acc ata aaa ata ttt gaa gaa	727
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu	
211 216 221 226	
cag tgc cag acc caa gag cgg tac agc aaa gaa tac ata gaa aag ttt	775
Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe	
227 232 237 242	
aaa cgt gaa ggc aat gag aaa gaa ata caa agg att atg cat aat tat	823
Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr	
243 248 253 258	
gat aag ttg aag tct cga atc agt gaa att att gac agt aga aga aga	871
Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg	
259 264 269 274	
ttg gaa gaa gac ttg aag aag cag gca gct gag tat cga gaa att gac	919
Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp	
275 280 285 290	
aaa cgt atg aac agc att aaa cca gac ctt atc cag ctg aga aag acg	967
Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr	
291 296 301 306	
aga gac caa tac ttg atg tgg ttg act caa aaa ggt gtt cgg caa aag	1015
Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys	
307 312 317 322	
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Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser	
323 328 333 338	
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Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp	
339 344 349 354	

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Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile	
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Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr	
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419 424 429 434	
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Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala	
435 440 445 450	
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451	
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aag gca aac ttg gag aag gcc cag gcg gag ctg gtg ggg aca gct gac      641
Lys Ala Asn Leu Glu Lys Ala Gln Ala Glu Leu Val Gly Thr Ala Asp
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gag gcc acg cgg gca gag atc cag atc cga atc gag gcc aac gag gcc      689
Glu Ala Thr Arg Ala Glu Ile Gln Ile Arg Ile Glu Ala Asn Glu Ala
  24                29                34                39

ctg gtg aag gcc ctg gag tag gc gagccagccg ccaaggttga cctcagcttc      742
Leu Val Lys Ala Leu Glu  *
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Ile Lys His Glu Ile Pro Lys Ser Lys Lys Glu Lys Glu Asn Ala Pro	
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Lys Pro Gln Asp Ala Ala Glu Val Ser Ser Glu Gln Glu Lys Glu Gln	
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Glu Thr Leu Ile Ser Gln Lys Ser Ile Pro Glu Pro Leu Pro Ala Ala	
233 238 243 248	
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Asp Met Lys Lys Lys Ile Glu Gly Tyr Gln Glu Phe Ser Ala Lys Pro	
249 254 259 264	
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Leu Ala Ser Arg Val Asp Pro Glu Lys Asp Asn Glu Thr Asp Gln Gly	
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Ser Asn Ser Glu Lys Val Ala Glu Glu Ala Gly Glu Lys Gly Pro Thr	
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Pro Pro Leu Pro Ser Ala Pro Leu Ala Pro Glu Lys Asp Ser Ala Leu	
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gtc cct ggg gcc agc aaa cag cca ctc acc tct cct agt gcc ctg gtg	1312
Val Pro Gly Ala Ser Lys Gln Pro Leu Thr Ser Pro Ser Ala Leu Val	
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gac tca aaa caa gaa tcc aaa ctg tgc tgt ttt aca gag agc cct gaa	1360
Asp Ser Lys Gln Glu Ser Lys Leu Cys Cys Phe Thr Glu Ser Pro Glu	
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Ser Glu Pro Gln Glu Ala Ser Phe Pro Ser Phe Pro Thr Thr Gln Ala	
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Thr Ala Gly Lys Pro Glu *	
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agatggcaag ggatgcccct ctttttcata aaactctcca aggttcaatc aatgcaatgt 3621
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 ctgcaggag atg tgt aca aag aca atc cca gtc ctc tgg gga tgt ttc 168
 Met Cys Thr Lys Thr Ile Pro Val Leu Trp Gly Cys Phe
 1 5 10
 ctc ctg tgg aat ctc tat gtc tca tcc tct cag acc att tac cct gga 216
 Leu Leu Trp Asn Leu Tyr Val Ser Ser Ser Gln Thr Ile Tyr Pro Gly
 14 19 24 29
 atc aag gca agg att act cag agg gca ctt gac tat ggt gtt caa gct 264
 Ile Lys Ala Arg Ile Thr Gln Arg Ala Leu Asp Tyr Gly Val Gln Ala
 30 35 40 45
 gga atg aag atg att gag caa atg cta aaa gaa aag aaa ctc cca gat 312
 Gly Met Lys Met Ile Glu Gln Met Leu Lys Glu Lys Lys Leu Pro Asp
 46 51 56 61
 tta agc ggt tct gag tct ctt gaa ttt cta aaa gtt gat tat gta aac 360
 Leu Ser Gly Ser Glu Ser Leu Glu Phe Leu Lys Val Asp Tyr Val Asn
 62 67 72 77
 tac aat ttt tca aat ata aaa atc agt gcc ttt tca ttt cca aat acc 408
 Tyr Asn Phe Ser Asn Ile Lys Ile Ser Ala Phe Ser Phe Pro Asn Thr
 78 83 88 93
 tca ttg gct ttt gtg cct gga gtg gga atc aaa gcg cta acc aac cat 456
 Ser Leu Ala Phe Val Pro Gly Val Gly Ile Lys Ala Leu Thr Asn His
 94 99 104 109
 ggc act gcc aac atc agc aca gac tgg ggg ttc gag tct cca ctt ttt 504
 Gly Thr Ala Asn Ile Ser Thr Asp Trp Gly Phe Glu Ser Pro Leu Phe
 110 115 120 125
 gtt ctg tat aac tcc ttt gct gag ccc atg gag aaa ccc att tta aag 552
 Val Leu Tyr Asn Ser Phe Ala Glu Pro Met Glu Lys Pro Ile Leu Lys

126	131	136	141	
aac tta aat gaa atg ctc tgt ccc att att gca agt gaa gtc aaa gcg				600
Asn Leu Asn Glu Met Leu Cys Pro Ile Ile Ala Ser Glu Val Lys Ala				
142	147	152	157	
cta aat gcc aac ctc agc aca ctg gag gtt tta acc aag att gac aac				648
Leu Asn Ala Asn Leu Ser Thr Leu Glu Val Leu Thr Lys Ile Asp Asn				
158	163	168	173	
tac act ctg ctg gat tac tcc cta atc agt tct cca gaa att act gag				696
Tyr Thr Leu Leu Asp Tyr Ser Leu Ile Ser Ser Pro Glu Ile Thr Glu				
174	179	184	189	
aac tac ctt gac ctg aac ttg aag ggt gta ttc tac cca ctg gaa aac				744
Asn Tyr Leu Asp Leu Asn Leu Lys Gly Val Phe Tyr Pro Leu Glu Asn				
190	195	200	205	
ctc acc gac ccc ccc ttc tca cca gtt cct ttt gtg ctc cca gaa cgc				792
Leu Thr Asp Pro Pro Phe Ser Pro Val Pro Phe Val Leu Pro Glu Arg				
206	211	216	221	
agc aac tcc atg ctc tac att gga atc gcc gag tat ttc ttt aaa tct				840
Ser Asn Ser Met Leu Tyr Ile Gly Ile Ala Glu Tyr Phe Phe Lys Ser				
222	227	232	237	
gcg tcc ttt gct cat ttc aca gct ggg gtt ttc aat gtc act ctc tcc				888
Ala Ser Phe Ala His Phe Thr Ala Gly Val Phe Asn Val Thr Leu Ser				
238	243	248	253	
acc gaa gag att tcc aac cat ttt gtt caa aac tct caa ggc ctt ggc				936
Thr Glu Glu Ile Ser Asn His Phe Val Gln Asn Ser Gln Gly Leu Gly				
254	259	264	269	
aac gtg ctc tcc cgg att gca gag atc tac atc ttg tcc cag ccc ttc				984
Asn Val Leu Ser Arg Ile Ala Glu Ile Tyr Ile Leu Ser Gln Pro Phe				
270	275	280	285	
atg gtg agg atc atg gcc aca gag cct ccc ata atc aat cta caa cca				1032
Met Val Arg Ile Met Ala Thr Glu Pro Pro Ile Ile Asn Leu Gln Pro				
286	291	296	301	
ggc aat ttc acc ctg gac atc cct gcc tcc atc atg atg ctc acc caa				1080
Gly Asn Phe Thr Leu Asp Ile Pro Ala Ser Ile Met Met Leu Thr Gln				
302	307	312	317	
ccc aag aac tcc aca gtt gaa acc atc gtt tcc atg gac ttc gtt gct				1128
Pro Lys Asn Ser Thr Val Glu Thr Ile Val Ser Met Asp Phe Val Ala				
318	323	328	333	
agt acc agt gtt ggc ctg gtt att ttg gga caa aga ctg gtc tgc tcc				1176
Ser Thr Ser Val Gly Leu Val Ile Leu Gly Gln Arg Leu Val Cys Ser				
334	339	344	349	
ttg tct ctg aac aga ttc cgc ctt gct ttg cca gag tcc aat cgc agc				1224
Leu Ser Leu Asn Arg Phe Arg Leu Ala Leu Pro Glu Ser Asn Arg Ser				
350	355	360	365	

aac att gag gtc ttg agg ttt gaa aat att cta tcg tcc att ctt cac	1272
Asn Ile Glu Val Leu Arg Phe Glu Asn Ile Leu Ser Ser Ile Leu His	
366 371 376 381	
ttt gga gtc ctc cca ctg gcc aat gca aaa ttg cag caa gga ttt cct	1320
Phe Gly Val Leu Pro Leu Ala Asn Ala Lys Leu Gln Gln Gly Phe Pro	
382 387 392 397	
ctg ccc aat cca cac aaa ttc tta ttc gtc aat tca gat att gaa gtt	1368
Leu Pro Asn Pro His Lys Phe Leu Phe Val Asn Ser Asp Ile Glu Val	
398 403 408 413	
ctt gag ggt ttc ctt ttg att tcc acc gac ctg aag tat gaa aca tcc	1416
Leu Glu Gly Phe Leu Leu Ile Ser Thr Asp Leu Lys Tyr Glu Thr Ser	
414 419 424 429	
tca aag cag cag cca agt ttc cac gta tgg gaa ggt ctg aac ctg ata	1464
Ser Lys Gln Gln Pro Ser Phe His Val Trp Glu Gly Leu Asn Leu Ile	
430 435 440 445	
agc aga cag tgg agg ggg aag tca gcc cct tga ttgccggt ttgcaattca	1515
Ser Arg Gln Trp Arg Gly Lys Ser Ala Pro *	
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tacacactgg aattgtaaag cccttgtaga ttgcttaggc agaaagtttt ctttcttaag	1635
ccttcaggaa ccagaataa ggcagactct gttaaaggga taaatagagg tgtctgaatg	1695
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gagaccagcc tgggcaacat agcgagcacc ccattctccag aaaaaattta aaaattggct	180

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 <222> (262)..(594)

<400> 369

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gagccacaca tggacacgta agtatcttgt gtgtggacct gtataggcag gtgaatctcc      180
gaactgcaag gccggcgaag gctctcctga cattcttccct ttctaatacct tcagctctcc      240
ttcctccact aagagcggaa a  atg aac aaa tcc cag gaa caa gtg tca ttc      291
                        Met Asn Lys Ser Gln Glu Gln Val Ser Phe
                        1                      5

aag gat gta tgt gtg gac ttc act cag gaa gag tgg tat ctg ctg gac      339
Lys Asp Val Cys Val Asp Phe Thr Gln Glu Glu Trp Tyr Leu Leu Asp
 11                      16                      21                      26

cct gct cag aag att cta tac aga gat gtg atc ctg gaa aat tat agc      387
Pro Ala Gln Lys Ile Leu Tyr Arg Asp Val Ile Leu Glu Asn Tyr Ser
 27                      32                      37                      42

aat ctt gtc tca gta ggg tat tgc att act aaa cca gaa gtg atc ttt      435
Asn Leu Val Ser Val Gly Tyr Cys Ile Thr Lys Pro Glu Val Ile Phe
 43                      48                      53                      58

aag atc gag caa gga gaa gag ccc tgg ata tta gaa aaa gga ttc cca      483
Lys Ile Glu Gln Gly Glu Glu Pro Trp Ile Leu Glu Lys Gly Phe Pro
 59                      64                      69                      74

agc cag tgc caa cca gaa agg gaa tgg gaa gtt gat gac gtg tta gag      531
Ser Gln Cys Gln Pro Glu Arg Glu Trp Glu Val Asp Asp Val Leu Glu
 75                      80                      85                      90

agc agc cag gaa cat gaa gat gac cca ttt tgg gag ctt cta ttc ccc      579
Ser Ser Gln Glu His Glu Asp Asp Pro Phe Trp Glu Leu Leu Phe Pro
 91                      96                      101                      106

aac aac aaa cag taa gtgtagaaaa tggggataga ggaagcaaac tttcaatttg      634
Asn Asn Lys Gln *
107

gggcaagacc ctgttcttta agaattaccc tataaatttg tgcccatgtg aatgatttgg      694

gaattttggg gttaattttt gtaaagactt tccgaaagtc ctggtggttt atgttta      751

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 <213> Homo sapiens

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<400> 370

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gacagtggaa aaagccatgg tgtgtggttt ctgggaacca ccaacacttg caggtttagc      180
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gagtgtgcct aaattaacca tccccathtt tatcatatht ccaccatcac ttcagggttt      300
taagagtcag tgctcacctg ggcggagctg gtagtacatt ttgcttctta gaaagctaag      360
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gtaattttct ggagtttggt ttgcagggat agctgggagt atggccaccc tgctccacga      480
tgcggtaatg aatccagcag aagtggtgaa gcagcgcttg cagatgtaca actcgagca      540
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gctgccttgt gacatccggg      atg gcg cct tca tta cta tgc cct ttc act      1010
                        Met Ala Pro Ser Leu Leu Cys Pro Phe Thr
                        1                      5

gct atg cac aaa acc gtg ggg agg gcc tcc tgc gcc ccg ccg agc tgg      1058
Ala Met His Lys Thr Val Gly Arg Ala Ser Cys Ala Pro Pro Ser Trp
  11                16                21                26

cgg atg gag ctg cgc agc ggg agc gtg ggc agc cag gcg gtg gcg cgg      1106
Arg Met Glu Leu Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg
  27                32                37                42

agg atg gat ggg gac agc cga gat ggc ggc ggc ggc aag gac gcc acc      1154
Arg Met Asp Gly Asp Ser Arg Asp Gly Gly Gly Gly Lys Asp Ala Thr

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43	48	53	58	
ggg tcg gag gac tac gag aac ctg ccg act agc gcc tcc gtg tcc acc				1202
Gly Ser Glu Asp Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr				
59	64	69	74	
cac atg aca gca gga gcg atg gcc ggg atc ctg gag cac tcg gtc atg				1250
His Met Thr Ala Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met				
75	80	85	90	
tac ccg gtg gac tcg gtg aag aca cga atg cag agt ttg agt cca gat				1298
Tyr Pro Val Asp Ser Val Lys Thr Arg Met Gln Ser Leu Ser Pro Asp				
91	96	101	106	
ccc aaa gcc cag tac aca agt gtc tac gga gcc ctc aag aaa atc atg				1346
Pro Lys Ala Gln Tyr Thr Ser Val Tyr Gly Ala Leu Lys Lys Ile Met				
107	112	117	122	
cgg acc gaa ggc ttc tgg agg ccc ttg cga ggc gtc aac gtc atg atc				1394
Arg Thr Glu Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile				
123	128	133	138	
atg ggt gca ggg cca gcc cat gcc atg tat ttt gcc tgc tat gaa aac				1442
Met Gly Ala Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn				
139	144	149	154	
atg aaa agg act tta aat gac gtt ttc cac cac caa gga aac agc cac				1490
Met Lys Arg Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His				
155	160	165	170	
cta gcc aac ggg ata gct ggg agt atg gcc acc ctg ctc cac gat gcg				1538
Leu Ala Asn Gly Ile Ala Gly Ser Met Ala Thr Leu Leu His Asp Ala				
171	176	181	186	
gta atg aat cca gca gaa gtg gtg aag cag cgc ttg cag atg tac aac				1586
Val Met Asn Pro Ala Glu Val Val Lys Gln Arg Leu Gln Met Tyr Asn				
187	192	197	202	
tcg cag cac cgg tca gca atc agc tgc atc cgg acg gtg tgg agg acc				1634
Ser Gln His Arg Ser Ala Ile Ser Cys Ile Arg Thr Val Trp Arg Thr				
203	208	213	218	
gag ggg ttg ggg gcc ttc tac cgg agc tac acc acg cag ctg acc atg				1682
Glu Gly Leu Gly Ala Phe Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met				
219	224	229	234	
aac atc ccc ttc cag tcc atc cac ttc atc acc tat gag ttc ctg cag				1730
Asn Ile Pro Phe Gln Ser Ile His Phe Ile Thr Tyr Glu Phe Leu Gln				
235	240	245	250	
gag cag gtc aac ccc cac cgg acc tac aac ccg cag tcc cac atc atc				1778
Glu Gln Val Asn Pro His Arg Thr Tyr Asn Pro Gln Ser His Ile Ile				
251	256	261	266	
tca ggc ggg ctg gcc ggg gcc ctc gcc gcg gcc gcg aat tcg gat cct				1826
Ser Gly Gly Leu Ala Gly Ala Leu Ala Ala Ala Asn Ser Asp Pro				
267	272	277	282	

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Leu Pro Val Pro Tyr Lys Leu Pro Val Ser Leu Ser Val Gly Ser Cys
  4                      9                      14                      19

gtg ata atc aaa ggg aca cca atc cac tct ttt atc aat gac cca cag      153
Val Ile Ile Lys Gly Thr Pro Ile His Ser Phe Ile Asn Asp Pro Gln
  20                      25                      30                      35

ctg cag gtg gat ttc tac act gac atg gat gag gat tca gat att gcc      201
Leu Gln Val Asp Phe Tyr Thr Asp Met Asp Glu Asp Ser Asp Ile Ala
  36                      41                      46                      51

ttc cgt ttc cga gtg cac ttt ggc aat cat gtg gtc atg aac agg cgt      249
Phe Arg Phe Arg Val His Phe Gly Asn His Val Val Met Asn Arg Arg
  52                      57                      62                      67

gag ttt ggg ata tgg atg ttg gag gag aca aca gac tac gtg ccc ttt      297
Glu Phe Gly Ile Trp Met Leu Glu Glu Thr Thr Asp Tyr Val Pro Phe
  68                      73                      78                      83

gag gat ggc aaa caa ttt gag ctg tgc atc tac gta cat tac aat gag      345
Glu Asp Gly Lys Gln Phe Glu Leu Cys Ile Tyr Val His Tyr Asn Glu
  84                      89                      94                      99

tat gag ata aag gtc aat ggc ata cgc att tac ggc ttt gtc cat cga      393
Tyr Glu Ile Lys Val Asn Gly Ile Arg Ile Tyr Gly Phe Val His Arg
 100                      105                      110                      115

atc ccg cca tca ttt gtg aag atg gtg caa gtg tcg aga gat atc tcc      441
Ile Pro Pro Ser Phe Val Lys Met Val Gln Val Ser Arg Asp Ile Ser
 116                      121                      126                      131

ctg acc tca gtg tgt gtc tgc aat tga gggag atgatcacac tcctcattgt      493
Leu Thr Ser Val Cys Val Cys Asn  *
 132                      137

tgaggaatcc ctctttctac ctgaccatgg gattcccaga acctgctaac agaataatcc      553

ctgctcacat tttcccctac actttgtcat taaaacagca cgaaaactca aaaaa      608

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 <222> (40)..(1179)

<400> 373

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	Met Ser Ser Pro Ser	
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ctc agt gac ctg ggc aag aga gag ccg gcc gcc gcc gcg gac gag cgg		102
Leu Ser Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Ala Asp Glu Arg		
6 11 16 21		
ggc acg cag cag cgc cgg gcc tgc gcc aac gcc acc tgg aac agc atc		150
Gly Thr Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile		
22 27 32 37		
cac aac ggg gtg atc gcc gtc ttc cag cgc aag ggg ctg ccc gac cag		198
His Asn Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln		
38 43 48 53		
gag ctc ttc agc ctc aac gag ggc gtc cgg cag ctg ttg aag aca gag		246
Glu Leu Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu		
54 59 64 69		
ctg ggg tcc ttc ttc acg gag tac ctg cag aac cag ctg ctg aca aaa		294
Leu Gly Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys		
70 75 80 85		
ggc atg gtg atc ctt cgg gac aag att cgc ttc tat gag gga cag aag		342
Gly Met Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys		
86 91 96 101		
ctg ctg gac tca ctg gca gag acc tgg gac ttc ttc ttc agt gac gtg		390
Leu Leu Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val		
102 107 112 117		
ctg ccc atg ctg cag gcc atc ttc tac ccg gtg cag ggc aag gag cca		438
Leu Pro Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro		
118 123 128 133		
tcg gtg cgc cag ctg gcc ctg ctg cac ttc cgg aat gcc atc acc ctc		486
Ser Val Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu		
134 139 144 149		
agt gtg aag cta gag gat gcg ctg gcc cgg gcc cat gcc cgt gtg ccc		534
Ser Val Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro		
150 155 160 165		

cct gcc atc gtg cag atg ctg ctg gtg ctg cag ggg gta cat gag tcc	582
Pro Ala Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser	
166 171 176 181	
agg ggc gtg act gag gac tac ctg cgc ctg gag acg ctg gtc cag aag	630
Arg Gly Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys	
182 187 192 197	
gtg gtg tcg cca tac ctg ggc acc tac ggc ctc cac tcc agc gag ggg	678
Val Val Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly	
198 203 208 213	
ccc ttc acc cat tcc tgc atc ctg gaa aag cgc ctc ctc cgc cgc tcc	726
Pro Phe Thr His Ser Cys Ile Leu Glu Lys Arg Leu Leu Arg Arg Ser	
214 219 224 229	
cgc tcg ggg gac gtg ctg gcc aag aac cct gtg gtg cgc tcc aag agc	774
Arg Ser Gly Asp Val Leu Ala Lys Asn Pro Val Val Arg Ser Lys Ser	
230 235 240 245	
tac aac acg cct ctg ctg aac ccc gtg cag gag cac gag gcg gag ggc	822
Tyr Asn Thr Pro Leu Leu Asn Pro Val Gln Glu His Glu Ala Glu Gly	
246 251 256 261	
gcg gcg gcc ggc ggt acc agc atc cgc agg cac tct gtg tcg gag atg	870
Ala Ala Ala Gly Gly Thr Ser Ile Arg Arg His Ser Val Ser Glu Met	
262 267 272 277	
acg tcc tgc ccc gag cct cag ggc ttc tcc gac ccg ccc ggc cag ggc	918
Thr Ser Cys Pro Glu Pro Gln Gly Phe Ser Asp Pro Pro Gly Gln Gly	
278 283 288 293	
ccc acc ggg acc ttc agg tcc tcc ccg gcg ccc cac tca ggg ccc tgc	966
Pro Thr Gly Thr Phe Arg Ser Ser Pro Ala Pro His Ser Gly Pro Cys	
294 299 304 309	
ccc agc aga ctg tac ccc acg acc cag ccc cct gag cag ggc ttg gat	1014
Pro Ser Arg Leu Tyr Pro Thr Thr Gln Pro Pro Glu Gln Gly Leu Asp	
310 315 320 325	
ccc acc cgc agc tcc ctg ccc cgc tcc agc ccg gag aac ctg gtg gac	1062
Pro Thr Arg Ser Ser Leu Pro Arg Ser Ser Pro Glu Asn Leu Val Asp	
326 331 336 341	
cag atc ctg gag tcc gtg gac tcg gat tct gaa ggg att ttc att gac	1110
Gln Ile Leu Glu Ser Val Asp Ser Asp Ser Glu Gly Ile Phe Ile Asp	
342 347 352 357	
ttt ggc cgg ggc cgg ggc tct ggc atg tcc gac ttg gag ggc tct ggg	1158
Phe Gly Arg Gly Arg Gly Ser Gly Met Ser Asp Leu Glu Gly Ser Gly	
358 363 368 373	
ggc cgg cag agt gtc gtg tga gg cctcacagct ggccttgagt ttttactgac	1211
Gly Arg Gln Ser Val *	
374 379	
acgtccctgt gtgcgggggt gtccatgtgg cgtgtgtgtg agtgagactt ttttactgcg	1271

tcccgccccg ccagccctat cggcctcgtc actggccttg gtcactttgt atttctgtct 1331
 tggttgaaaa taccatcagc cttccttgct cggcccaggt ctgtttcagg catctgagtc 1391
 ggcgtttacc caggggcccgg gccagagacg ggggtcggcc gctcgcctcc acgctcctcc 1451
 tgccccagcc ctctggtgtc cacacctgcc cacagagaat gtaaaccag tgggctctgc 1511
 ccacgccggg ccccaaagt accagactcc agcacacctg tctcctctg cctgggggtg 1571
 ccatggggat ggaagggggg ggaataaac ctgtcaacct ggaaaaaaaa aaaa 1625

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 <211> 1116
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 <213> Homo sapiens

<220>
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 <222> (163)..(789)

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 ctaaaggga taagcttgcg gccgccgga gtctggtatc ctgagcttcg tgagttgagc 120
 gctgctgctc cgcggtggag tcaccgcacc gctcccgga tc atg gtg ttc tac 174
 Met Val Phe Tyr
 1
 ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga 222
 Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
 5 10 15 20
 aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc tgg cct gaa 270
 Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Trp Pro Glu
 21 26 31 36
 gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt 318
 Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
 37 42 47 52
 cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg 366
 Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
 53 58 63 68
 atg gac tgt gcc cac ctt gtg aag gcc aat agc att caa ggc tgc aag 414
 Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile Gln Gly Cys Lys
 69 74 79 84
 atg aac aac gtt aat gtg gta tat acg ccg tgg tct aac ctg aag aaa 462
 Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser Asn Leu Lys Lys
 85 90 95 100

aca gct gac atg gat gtg ggg cag ata ggc ttt cac agg cag aag gat	510
Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His Arg Gln Lys Asp	
101 106 111 116	
gta aaa att gtg aca gtg gag aag aaa gta aat gag atc ctg aac cga	558
Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu Ile Leu Asn Arg	
117 122 127 132	
tta gaa aag acc aaa gtc gag cgg ttc tca gac cta gca gca gag aaa	606
Leu Glu Lys Thr Lys Val Glu Arg Phe Ser Asp Leu Ala Ala Glu Lys	
133 138 143 148	
gaa tgc aga gat cgt gaa gag agg aat gag aaa aaa gcc caa att cag	654
Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys Ala Gln Ile Gln	
149 154 159 164	
gaa atg aaa aag aga gaa aaa gaa gaa atg aag aag aag agg gaa atg	702
Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys Lys Arg Glu Met	
165 170 175 180	
gat gaa ctt agg agc tat tca tca cta atg aaa gtt gaa aat atg tct	750
Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val Glu Asn Met Ser	
181 186 191 196	
tca aat cag gat ggc aat gat tca gat gaa ttc atg taa aaggagaaaa	799
Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met *	
197 202 207	
ggagaaaagg acctttgaaa gatgtgaatg tagagacaat tgcagacctt ttggtttcat	859
ctgtgttctg aaatataaaa tacaaccaa attctacctt catcctaccc agaaattatt	919
gattttcaag ttttaaaaaa attgtacctt ttttgctgac agaaaaggat cagatatgta	979
taaaatagtt gaacttgaca gcatataact taaagtgaaa atgtttttgc cagaacatgt	1039
cttggtacct tgtgaaagca ggctgccctt gttcttgaga tagactttaa aatgaaccag	1099
ctctgaaaaa aaaaaaa	1116

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (163)..(423)

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ctaaagggaa taagcttgcg gccgccgcga gtctggtatc ctgagcttcg tgagttgagc	120

gctgctgctc cgcggtggag tcaccgcacc gctccccgga tc atg gtg ttc tac 174
Met Val Phe Tyr
1

ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga 222
Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
5 10 15 20

aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc tgg cct gaa 270
Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Trp Pro Glu
21 26 31 36

gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt 318
Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
37 42 47 52

cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg 366
Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
53 58 63 68

atg gac tgt gcc cac ctt gtg aag gcc aat agc att caa gga gct att 414
Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile Gln Gly Ala Ile
69 74 79 84

cat cac taa tgaaagt tgaaaatatg tcttcaaatc aggatggcca tgattcatat 470
His His *
85

gaattcatgt aaaaggagaa gaggagaaaa ggacctttga 510

<210> 376
<211> 2430
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (959)..(1345)

<400> 376

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ctcacactag tacgtggccc ctcggtgggt ttgtctcgag gtcgaaggtc cagatgtcca 180

ggggctgccc tggactccag agtgggtgcgg ctgagcaggc tgtggtcttg ggtgcttggg 240

cacctccgt ctctccctgc tcagagttct tctctcctgg gcagccagaa aggatcagaa 300

ccggtcacat gcagagcggc ctcccgatc ccacagcagc tccgttctct aatctgggtc 360

ttcagatgcg gctgtgtctc ccggcacctt gctggaatgt ggtgcatccc tcggagtcca 420

gcagccctta ggcagagctg ggtgccgagc ttgagtccag gagggcctca gacacctgcg 480

atcttgacgc ctgttgccct ggacagtggg tgtgctgtgg gtggaggatg gcgccctgcc 540

tccacggaag catccccagc ttgccctca gtcacacgaa gcgtctgtcc ccagcctggg 600

gcatttctga gtggcctcca cttggcctct tcctttttct ggagcaagta tttgaactcc 660

tgcaggcgcc agagatctcc ttacctgttt cccgctaccc ttctccagcc aggtttctgc 720

cctcagccag attgtcctgc agtgacttgc ttttggccat ggagtagtgg ctgctcagtg 780

cctgagattg ttttagcagc agaagggacc ggggtccccct gctgctggca acacagacgc 840

ttgcttacag ttctctggtc ctggacacct gaggtctcgg cctccccagg acggcccttc 900

cagattctca ggaccacctt gccctccctg ccctgtctcc taggtgaccc tggcaaag 958

atg aga gtg cac att tgc tcc tgc ctg aag gtc cag gag cag atg gcc 1006

Met Arg Val His Ile Ser Ser Cys Leu Lys Val Gln Glu Gln Met Ala

1 5 10 15

aac tgc ccc aag ttc gtc ccc gtg gtg ccc aca tca cag cct atc ccc 1054

Asn Cys Pro Lys Phe Val Pro Val Val Pro Thr Ser Gln Pro Ile Pro

17 22 27 32

agc aac atc ccc aac agg tcc acc ttc gcc tgc ccg tac tgt ggt gcc 1102

Ser Asn Ile Pro Asn Arg Ser Thr Phe Ala Cys Pro Tyr Cys Gly Ala

33 38 43 48

cgc aac ctg gac cag cag gag ctg gtg aag cac tgt gtg gaa agc cac 1150

Arg Asn Leu Asp Gln Gln Glu Leu Val Lys His Cys Val Glu Ser His

49 54 59 64

cgc agc gac ccc aac cgc gtg gtg tgc ccc atc tgc tgc gca atg ccc 1198

Arg Ser Asp Pro Asn Arg Val Val Cys Pro Ile Cys Ser Ala Met Pro

65 70 75 80

tgg ggg gac ccc agc tac aag agc gcc aac ttc ctg cag cac ctg ctt 1246

Trp Gly Asp Pro Ser Tyr Lys Ser Ala Asn Phe Leu Gln His Leu Leu

81 86 91 96

cac cga cac aag ttc tcc tac gac acc ttt gtg gac tac agt att gac 1294

His Arg His Lys Phe Ser Tyr Asp Thr Phe Val Asp Tyr Ser Ile Asp

97 102 107 112

gag gag gcc gcc ttc cag gct gct ctg gcc ctg tct ctc tct gag aac 1342

Glu Glu Ala Ala Phe Gln Ala Ala Leu Ala Leu Ser Leu Ser Glu Asn

113 118 123 128

tga aggg aagcgcagcc acccgctgc gtctggggtc agggatgtcc ccgctcctgt 1399

*

129

gtcgcacctg gcacctgtc gggagcgcac ctcaccggac tgagctcaca ggaggagcct 1459

gcacccgcgc agaaggggag ccggggccga gcctccgggc ctgaatacgg gccagccgcc 1519

gagggccgcca gagcagggcc gacctggtccc accggcgctcg ctgggttctt cgggtgcttct 1579
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gcttccacct tgccgatttg gtactggctt ttgtgatact taggaaccct ggcatctttt 1819
ctatatatc cagtgtgata atcttttcac gttttataga gcaaagacag agcagttact 1879
cttcataattg caatatctgt gtttgactag gaataatagt atttttatgg aacatttaca 1939
aaattatatt ttttaagaaa acaatcaaaa caagcattgg gggattgggg caaggatgga 1999
aggagcagtg gggcagctgc cagagctcag gcgagccatg gggctctgctg tggggtctgc 2059
cctggccacc cactgtgtgt ctgggtcctt gaggtttgta cgtttctctt tgatgaccag 2119
gaagaaatcc cagcacccca gccacaggct gtggctgctc ccagcagagg cggggccggc 2179
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caggggcccc cttggcgggc cgggcaacac gtcaacattc ttttctgttc ttggcattaa 2359
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aaaaaaaaa a 2430

<210> 377
<211> 5371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (108)..(1856)

<400> 377
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tgccccggcc gcggctgagg aggaggagga ggaggaggag gaggagg atg atc tcc 116
Met Ile Ser
1
aga tac act cgg aag gcg gtg cca cag agc ttg gag ctg aaa gga ata 164
Arg Tyr Thr Arg Lys Ala Val Pro Gln Ser Leu Glu Leu Lys Gly Ile
4 9 14 19
aca aaa cat gct ctt aac cat cat ccc cct cca gag aag ctg gag gaa 212

Thr	Lys	His	Ala	Leu	Asn	His	His	Pro	Pro	Pro	Glu	Lys	Leu	Glu	Glu		
20					25					30					35		
att	tcc	ccc	acc	agt	gac	agt	cat	gag	aaa	gac	aca	agt	tcc	caa	agc		260
Ile	Ser	Pro	Thr	Ser	Asp	Ser	His	Glu	Lys	Asp	Thr	Ser	Ser	Gln	Ser		
36					41					46					51		
aag	tct	gac	atc	aca	aga	gaa	tca	tct	ttt	aca	tca	gcc	gac	act	ggg		308
Lys	Ser	Asp	Ile	Thr	Arg	Glu	Ser	Ser	Phe	Thr	Ser	Ala	Asp	Thr	Gly		
52					57					62					67		
aat	tca	ctg	tct	gct	ttt	cca	agt	tat	aca	ggc	gca	ggg	ata	tct	act		356
Asn	Ser	Leu	Ser	Ala	Phe	Pro	Ser	Tyr	Thr	Gly	Ala	Gly	Ile	Ser	Thr		
68					73					78					83		
gaa	gga	agc	tcg	gac	ttc	tcc	tgg	gga	tat	ggg	gaa	ctc	gat	caa	aat		404
Glu	Gly	Ser	Ser	Asp	Phe	Ser	Trp	Gly	Tyr	Gly	Glu	Leu	Asp	Gln	Asn		
84					89					94					99		
gcc	act	gaa	aaa	gtc	cag	aca	atg	ttc	aca	gcc	att	gat	gaa	ctc	ttg		452
Ala	Thr	Glu	Lys	Val	Gln	Thr	Met	Phe	Thr	Ala	Ile	Asp	Glu	Leu	Leu		
100					105					110					115		
tat	gag	cag	aag	ttg	agt	gtg	cat	acc	aag	agt	cta	caa	gaa	gag	tgc		500
Tyr	Glu	Gln	Lys	Leu	Ser	Val	His	Thr	Lys	Ser	Leu	Gln	Glu	Glu	Cys		
116					121					126					131		
caa	cag	tgg	aca	gct	agc	ttt	cct	cac	ctc	agg	att	cta	ggg	agg	cag		548
Gln	Gln	Trp	Thr	Ala	Ser	Phe	Pro	His	Leu	Arg	Ile	Leu	Gly	Arg	Gln		
132					137					142					147		
ata	atc	act	cca	agt	gaa	ggg	tat	aga	ttg	tat	cct	aga	tcc	cct	tct		596
Ile	Ile	Thr	Pro	Ser	Glu	Gly	Tyr	Arg	Leu	Tyr	Pro	Arg	Ser	Pro	Ser		
148					153					158					163		
gct	gtt	tcc	gct	tca	tat	gaa	aca	acc	ttg	tct	caa	gaa	aga	gat	tct		644
Ala	Val	Ser	Ala	Ser	Tyr	Glu	Thr	Thr	Leu	Ser	Gln	Glu	Arg	Asp	Ser		
164					169					174					179		
act	ata	ttt	ggg	ata	agg	gga	aag	aag	tta	cat	ttt	tca	tct	tct	tat		692
Thr	Ile	Phe	Gly	Ile	Arg	Gly	Lys	Lys	Leu	His	Phe	Ser	Ser	Ser	Tyr		
180					185					190					195		
gct	cat	aaa	gca	tct	tcc	att	gcc	aaa	tcc	tcc	agc	ttt	tgt	tct	atg		740
Ala	His	Lys	Ala	Ser	Ser	Ile	Ala	Lys	Ser	Ser	Ser	Phe	Cys	Ser	Met		
196					201					206					211		
gaa	aga	gat	gag	gaa	gac	tct	ata	atc	gtc	tca	gaa	gga	ata	att	gag		788
Glu	Arg	Asp	Glu	Glu	Asp	Ser	Ile	Ile	Val	Ser	Glu	Gly	Ile	Ile	Glu		
212					217					222					227		
gaa	tac	cta	gca	ttc	gat	cac	ata	gat	ata	gaa	gag	gga	ttt	cat	ggg		836
Glu	Tyr	Leu	Ala	Phe	Asp	His	Ile	Asp	Ile	Glu	Glu	Gly	Phe	His	Gly		
228					233					238					243		
aag	aaa	tca	gaa	gca	gct	aca	gag	aaa	cag	aaa	tta	ggg	tat	cct	ccc		884
Lys	Lys	Ser	Glu	Ala	Ala	Thr	Glu	Lys	Gln	Lys	Leu	Gly	Tyr	Pro	Pro		

244	249	254	259	
att gct cca ttt tac tgc atg aaa gaa gat gtc ctt gct tat gtg ttt				932
Ile Ala Pro Phe Tyr Cys Met Lys Glu Asp Val Leu Ala Tyr Val Phe				
260	265	270	275	
gac agt gta tgg tgc aag gtt gtg agc tgt atg gag cag ttg aca cgt				980
Asp Ser Val Trp Cys Lys Val Val Ser Cys Met Glu Gln Leu Thr Arg				
276	281	286	291	
agt cac tgg gaa gga ttt gcc tct gat gat gag agt aat gtt gca gtt				1028
Ser His Trp Glu Gly Phe Ala Ser Asp Asp Glu Ser Asn Val Ala Val				
292	297	302	307	
acc aga ccc gat tca gaa agt tcc tgt gtg ctg agt gaa cta cat cct				1076
Thr Arg Pro Asp Ser Glu Ser Ser Cys Val Leu Ser Glu Leu His Pro				
308	313	318	323	
ttg gtg tta ccg cga gtg cca cag tct aag gtg ctg tac att acc tca				1124
Leu Val Leu Pro Arg Val Pro Gln Ser Lys Val Leu Tyr Ile Thr Ser				
324	329	334	339	
aat ccg atg agt ctc tgt caa gca agc aga cat cag cca aat gtg aat				1172
Asn Pro Met Ser Leu Cys Gln Ala Ser Arg His Gln Pro Asn Val Asn				
340	345	350	355	
gat ctc ttg gtt cat gga atg cct cta cag cca aga aat ctc tcc cta				1220
Asp Leu Leu Val His Gly Met Pro Leu Gln Pro Arg Asn Leu Ser Leu				
356	361	366	371	
atg gac aag ctc cta gat ctt gat gac aag cta ctt atg agg cct ggg				1268
Met Asp Lys Leu Leu Asp Leu Asp Asp Lys Leu Leu Met Arg Pro Gly				
372	377	382	387	
tcc agt acc atc ctt tca act cga aat tgg cca aat cga gct gtg gag				1316
Ser Ser Thr Ile Leu Ser Thr Arg Asn Trp Pro Asn Arg Ala Val Glu				
388	393	398	403	
ttt agt aca tca tct ctg tca tac aca gtg cag tcc acc agg aga cgc				1364
Phe Ser Thr Ser Ser Leu Ser Tyr Thr Val Gln Ser Thr Arg Arg Arg				
404	409	414	419	
aat cca cca cca cga act ctt cat ccg atc agc acg agc cat tca tgt				1412
Asn Pro Pro Pro Arg Thr Leu His Pro Ile Ser Thr Ser His Ser Cys				
420	425	430	435	
gct gaa aca cca aga tct gtg gaa gaa atc ctc aga gga gcc cga gtc				1460
Ala Glu Thr Pro Arg Ser Val Glu Glu Ile Leu Arg Gly Ala Arg Val				
436	441	446	451	
cca gtg gca ccc gac tgc ctc tcc tct ccc tca ccg acg ccc ctg agt				1508
Pro Val Ala Pro Asp Ser Leu Ser Ser Pro Ser Pro Thr Pro Leu Ser				
452	457	462	467	
cga aat aat ctg cta cca cct att ggc aca gct gaa gtg gaa cat gtg				1556
Arg Asn Asn Leu Leu Pro Pro Ile Gly Thr Ala Glu Val Glu His Val				
468	473	478	483	

agc act gtg ggg cca caa aga cag atg aaa ccc cat ggc gac tct agt	1604
Ser Thr Val Gly Pro Gln Arg Gln Met Lys Pro His Gly Asp Ser Ser	
484 489 494 499	
cga gct caa agt gcg gtg gtg gat gaa cct aac tat cag cag cca caa	1652
Arg Ala Gln Ser Ala Val Val Asp Glu Pro Asn Tyr Gln Gln Pro Gln	
500 505 510 515	
gaa agg ctc ctt ttg ccc gac ttt ttc ccc agg ccc aac aca act caa	1700
Glu Arg Leu Leu Leu Pro Asp Phe Phe Pro Arg Pro Asn Thr Thr Gln	
516 521 526 531	
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Ser Phe Leu Leu Asp Thr Gln Tyr Arg Arg Ser Cys Ala Val Glu Tyr	
532 537 542 547	
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Pro His Gln Ala Arg Pro Gly Arg Gly Ser Ala Gly Pro Gln Leu His	
548 553 558 563	
ggg tct aca aaa tct caa agc gga ggc aga cca gtc tct cga acc agg	1844
Gly Ser Thr Lys Ser Gln Ser Gly Gly Arg Pro Val Ser Arg Thr Arg	
564 569 574 579	
cag gga cca taa ggc aaatgagaag aatctatcag gctgcaggaa acacgagatt	1899
Gln Gly Pro *	
580	
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ggtagtaagt actctggcac tcataaatca catgatgata aaaaggaaca tgaggccggg	5079
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gtgggaagat ggcttcagtc tgagagttca ggctgcaata agctgtgatc atgcctctgc	5319
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	Met Arg
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Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro Ile Leu	
3 8 13 18	
gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt gag ggc ccg	153
Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu Gly Pro	
19 24 29 34	
agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg ctt gta cag	201

Arg	Met	Leu	Ser	Trp	Cys	Pro	Phe	Tyr	Lys	Val	Leu	Leu	Leu	Val	Gln	
35					40					45					50	
aca	gcc	atc	tac	tct	gtc	gtg	ggc	tat	gcc	tcc	tac	ctg	gtg	tgg	aag	249
Thr	Ala	Ile	Tyr	Ser	Val	Val	Gly	Tyr	Ala	Ser	Tyr	Leu	Val	Trp	Lys	
51					56					61					66	
gac	ctg	gga	ggg	ggc	ttg	ggg	tgg	ccc	ctg	gcc	ctg	cct	ctt	ggc	ctc	297
Asp	Leu	Gly	Gly	Gly	Leu	Gly	Trp	Pro	Leu	Ala	Leu	Pro	Leu	Gly	Leu	
67					72					77					82	
tat	gct	gtt	cag	ctc	acc	atc	agc	tgg	act	gtc	ctg	gtt	ctc	ttt	ttc	345
Tyr	Ala	Val	Gln	Leu	Thr	Ile	Ser	Trp	Thr	Val	Leu	Val	Leu	Phe	Phe	
83					88					93					98	
aca	gtc	cac	aac	cct	ggt	ctg	gcc	ctg	ctg	cac	ctg	ctg	ctg	ctg	tat	393
Thr	Val	His	Asn	Pro	Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	Leu	Leu	Tyr	
99					104					109					114	
ggg	ctg	gtg	gtg	agc	aca	gca	ctg	atc	tgg	cat	ccc	atc	aac	aaa	ctg	441
Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile	Asn	Lys	Leu	
115					120					125					130	
gct	gcc	ctg	tta	ctg	ctg	ccc	tac	cta	gcc	tgg	ctc	acc	gtg	act	tca	489
Ala	Ala	Leu	Leu	Leu	Leu	Pro	Tyr	Leu	Ala	Trp	Leu	Thr	Val	Thr	Ser	
131					136					141					146	
gcc	ctc	acc	tac	cac	ctg	tgg	agg	gac	agc	ctt	tgt	cca	gtg	cac	cag	537
Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro	Val	His	Gln	
147					152					157					162	
cct	cag	ccc	acg	gag	aag	agt	gac	tga	ggccc	tagggcatgg	gagaggaggg					589
Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp	*								
163					168											
acgcccaggg	tggggaggaa	gagtctgcaa	gcagggtgt	ggagttagg	ttcaccccaa											649
tgggaccacc	ctcctgggtc	ccctggagcc	gtttttcctt	agaaatcaga	gaaatgggaa											709
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aaaaa																774

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 gccgccagag aagcctttcc cagctgggtca tcccgcagcc cccaggagcg ctcacgggtc 180
 ctgaaccagg tggcggattt gctggagcag tccctggagg agtttgccca ggccgagtct 240
 aaagaccaag ggaaaacctt agcactggca agaacc atg gac att ccc cgg tct 294
 Met Asp Ile Pro Arg Ser
 1
 gtg cag aac ttc agg ttc ttc gct tcc tcc agc ctg cac cac acg tca 342
 Val Gln Asn Phe Arg Phe Phe Ala Ser Ser Ser Leu His His Thr Ser
 7 12 17 22
 gag tgc acg cag atg gac cac ctg ggc tgc atg cac tac acg gtg cgg 390
 Glu Cys Thr Gln Met Asp His Leu Gly Cys Met His Tyr Thr Val Arg
 23 28 33 38
 gcc ccg ggg gga gtc gct ggt ctg atc agc ccc tgg aat ttg cca ctc 438
 Ala Pro Gly Gly Val Ala Gly Leu Ile Ser Pro Trp Asn Leu Pro Leu
 39 44 49 54
 tac ttg ctg acc tgg aag ata gct cca gcg atg gct gca ggg aac act 486
 Tyr Leu Leu Thr Trp Lys Ile Ala Pro Ala Met Ala Ala Gly Asn Thr
 55 60 65 70
 gtg ata gcc aag ccc agt gag ctg act tca gtg act gcg tgg atg ttg 534
 Val Ile Ala Lys Pro Ser Glu Leu Thr Ser Val Thr Ala Trp Met Leu
 71 76 81 86
 tgc aaa ctc ctg gat aaa gca ggt gtt cca cca ggt gtg gtc aat att 582
 Cys Lys Leu Leu Asp Lys Ala Gly Val Pro Pro Gly Val Val Asn Ile
 87 92 97 102
 gtg ttt gga acc ggg ccc agg gtg ggt gag gcc ctg gtg tcc cac cca 630
 Val Phe Gly Thr Gly Pro Arg Val Gly Glu Ala Leu Val Ser His Pro
 103 108 113 118
 gag gtg ccc ctg atc tcc ttc acc ggg agc cag ccc acc gct gag cgg 678
 Glu Val Pro Leu Ile Ser Phe Thr Gly Ser Gln Pro Thr Ala Glu Arg
 119 124 129 134
 atc acc cag ctg agc gct ccc cac tgc aaa aag ctc tcc ctg gag ctg 726
 Ile Thr Gln Leu Ser Ala Pro His Cys Lys Lys Leu Ser Leu Glu Leu
 135 140 145 150
 ggg ggc aag aat cct gcc atc atc ttt gag gac gcc aac ctg gat gag 774
 Gly Gly Lys Asn Pro Ala Ile Ile Phe Glu Asp Ala Asn Leu Asp Glu
 151 156 161 166
 tgc att ccg gca acc gtc agg tcc agc ttt gcc aac cag ggt gaa atc 822
 Cys Ile Pro Ala Thr Val Arg Ser Ser Phe Ala Asn Gln Gly Glu Ile
 167 172 177 182
 tgt ctc tgt acc agc agg atc ttt gtc cag aag agc atc tat agt gaa 870
 Cys Leu Cys Thr Ser Arg Ile Phe Val Gln Lys Ser Ile Tyr Ser Glu

183	188	193	198	
ttt tta aag aga ttt gta gaa gct acc aga aag tgg aaa gtc ggc att				918
Phe Leu Lys Arg Phe Val Glu Ala Thr Arg Lys Trp Lys Val Gly Ile				
199	204	209	214	
ccc tct gat cca ctg gtg agc ata ggt gct ctg ata agt aaa gca cat				966
Pro Ser Asp Pro Leu Val Ser Ile Gly Ala Leu Ile Ser Lys Ala His				
215	220	225	230	
ttg gag aaa gtc aga agt tac gtc aag aga gct ctt gct gaa ggt gcc				1014
Leu Glu Lys Val Arg Ser Tyr Val Lys Arg Ala Leu Ala Glu Gly Ala				
231	236	241	246	
caa att tgg tgc ggt gag gga gtg gat aag ttg agc ctc cct gcc agg				1062
Gln Ile Trp Cys Gly Glu Gly Val Asp Lys Leu Ser Leu Pro Ala Arg				
247	252	257	262	
aac cag gca ggc tac ttt atg ctt ccc acg gtg ata aca gac att aag				1110
Asn Gln Ala Gly Tyr Phe Met Leu Pro Thr Val Ile Thr Asp Ile Lys				
263	268	273	278	
gat gaa tcc tgc tgc atg acg gaa gag ata ttt ggt cca gtg acg tgt				1158
Asp Glu Ser Cys Cys Met Thr Glu Glu Ile Phe Gly Pro Val Thr Cys				
279	284	289	294	
gtc gtc ccc ttt gat agt gaa gag gag gtg att gaa aga gcc aac aac				1206
Val Val Pro Phe Asp Ser Glu Glu Glu Val Ile Glu Arg Ala Asn Asn				
295	300	305	310	
gtt aag tat ggg ctg gcg gct acc gtg tgg tcc agc aat gtg ggg cgc				1254
Val Lys Tyr Gly Leu Ala Ala Thr Val Trp Ser Ser Asn Val Gly Arg				
311	316	321	326	
gtc cac cgg gtg gct aag aag ctg cag tct ggc ttg gtc tgg acc aac				1302
Val His Arg Val Ala Lys Lys Leu Gln Ser Gly Leu Val Trp Thr Asn				
327	332	337	342	
tgc tgg ctc atc agg gag ctg aac ctt cct ttc ggg ggg atg aag agt				1350
Cys Trp Leu Ile Arg Glu Leu Asn Leu Pro Phe Gly Gly Met Lys Ser				
343	348	353	358	
tct gga ata ggt aga gag gga gcc aag gac tct tac gac ttc ttc act				1398
Ser Gly Ile Gly Arg Glu Gly Ala Lys Asp Ser Tyr Asp Phe Phe Thr				
359	364	369	374	
gag atc aaa acc atc acc gtt aaa cac tga t ctttgctaatt ggtggagcca				1449
Glu Ile Lys Thr Ile Thr Val Lys His *				
375	380			
ctatggccaa tgcctggctg caggcatcag ttgttcaatg tggtagatga aaatcatggc				1509
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<220>
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 <222> (1)..(1698)

<400> 380

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1 5 10	
gcc tca tct aca cca aag gat cac agc gcc tcg cca gca acg gaa caa	96
Ala Ser Ser Thr Pro Lys Asp His Ser Ala Ser Pro Ala Thr Glu Gln	
17 22 27 32	
agc tgg atg ggg aat gac ttt gat gag ttg aca gaa tta ggc ttc aga	144
Ser Trp Met Gly Asn Asp Phe Asp Glu Leu Thr Glu Leu Gly Phe Arg	
33 38 43 48	
aaa tcg gta atg aca aac ttc tcc cag cta aag gag gat gtt cga acc	192
Lys Ser Val Met Thr Asn Phe Ser Gln Leu Lys Glu Asp Val Arg Thr	
49 54 59 64	
cat cac aaa gaa gct aaa aac cta gaa aaa aga tta gac aaa tgg cta	240
His His Lys Glu Ala Lys Asn Leu Glu Lys Arg Leu Asp Lys Trp Leu	
65 70 75 80	
act aga ata aac agc ata gag gag acc tta aat gac ctg atg gag ctg	288
Thr Arg Ile Asn Ser Ile Glu Glu Thr Leu Asn Asp Leu Met Glu Leu	
81 86 91 96	
aaa acc atg gca cga gaa cta cgt gac aca tgc aca agc ttc agt agc	336
Lys Thr Met Ala Arg Glu Leu Arg Asp Thr Cys Thr Ser Phe Ser Ser	
97 102 107 112	
cga ttc gat caa gtg gaa gaa ggg gaa ata caa act acc atc aga gaa	384
Arg Phe Asp Gln Val Glu Glu Gly Glu Ile Gln Thr Thr Ile Arg Glu	
113 118 123 128	
tat tat gaa cac ctc tac gca aat aaa cta gaa aat cta gaa gaa atg	432
Tyr Tyr Glu His Leu Tyr Ala Asn Lys Leu Glu Asn Leu Glu Glu Met	
129 134 139 144	
gat aaa ttc ctg gac aca tac act ctc cca aga cta aac cag gaa gaa	480
Asp Lys Phe Leu Asp Thr Tyr Thr Leu Pro Arg Leu Asn Gln Glu Glu	
145 150 155 160	
gtt gaa tcc ctg aat aga cca ata aca ggt tct gaa att gag gca ata	528
Val Glu Ser Leu Asn Arg Pro Ile Thr Gly Ser Glu Ile Glu Ala Ile	
161 166 171 176	
att aat agc cta cca acc aaa aaa att cca ggg cca gac aga ttc aca	576

Ile	Asn	Ser	Leu	Pro	Thr	Lys	Lys	Ile	Pro	Gly	Pro	Asp	Arg	Phe	Thr		
177					182					187					192		
gcc	aaa	ttc	tac	cag	agg	tac	aaa	gag	gag	ctg	agt	aac	ctg	atc	cac	624	
Ala	Lys	Phe	Tyr	Gln	Arg	Tyr	Lys	Glu	Glu	Leu	Ser	Asn	Leu	Ile	His		
193					198					203					208		
tac	ctg	gga	ctg	agc	cat	cac	ctg	ctg	gca	ctg	aat	ttt	atc	att	gtt	672	
Tyr	Leu	Gly	Leu	Ser	His	His	Leu	Leu	Ala	Leu	Asn	Phe	Ile	Ile	Val		
209					214					219					224		
tct	ttt	ggc	aaa	aaa	agc	gcg	tgg	tct	tct	gcc	caa	gtg	aag	gtg	acc	720	
Ser	Phe	Gly	Lys	Lys	Ser	Ala	Trp	Ser	Ser	Ala	Gln	Val	Lys	Val	Thr		
225					230					235					240		
gac	aca	gac	ttt	gat	ggg	gtg	gaa	gtc	aga	gtg	ttt	gaa	ggc	cct	ccg	768	
Asp	Thr	Asp	Phe	Asp	Gly	Val	Glu	Val	Arg	Val	Phe	Glu	Gly	Pro	Pro		
241					246					251					256		
aag	ccc	gaa	gag	cca	ctg	aaa	cgc	agc	gtc	gtt	tat	atc	cac	gga	gga	816	
Lys	Pro	Glu	Glu	Pro	Leu	Lys	Arg	Ser	Val	Val	Tyr	Ile	His	Gly	Gly		
257					262					267					272		
ggc	tgg	gcc	ttg	gca	agt	gca	aaa	atc	agg	tat	tat	gat	gag	ctg	tgt	864	
Gly	Trp	Ala	Leu	Ala	Ser	Ala	Lys	Ile	Arg	Tyr	Tyr	Asp	Glu	Leu	Cys		
273					278					283					288		
aca	gca	atg	gct	gag	gaa	ttg	aat	gct	gtc	att	gtt	tcc	att	gaa	tac	912	
Thr	Ala	Met	Ala	Glu	Glu	Leu	Asn	Ala	Val	Ile	Val	Ser	Ile	Glu	Tyr		
289					294					299					304		
agg	cta	gtt	cca	aag	gtt	tat	ttt	cct	gag	caa	att	cat	gat	gtt	gta	960	
Arg	Leu	Val	Pro	Lys	Val	Tyr	Phe	Pro	Glu	Gln	Ile	His	Asp	Val	Val		
305					310					315					320		
cgg	gcc	aca	aag	tat	ttc	ctg	aag	cca	gaa	gtc	tta	cag	aag	tat	atg	1008	
Arg	Ala	Thr	Lys	Tyr	Phe	Leu	Lys	Pro	Glu	Val	Leu	Gln	Lys	Tyr	Met		
321					326					331					336		
gtt	gat	cca	ggc	aga	att	tgc	att	tct	ggg	gac	agt	gct	ggg	gga	aat	1056	
Val	Asp	Pro	Gly	Arg	Ile	Cys	Ile	Ser	Gly	Asp	Ser	Ala	Gly	Gly	Asn		
337					342					347					352		
ctg	gct	gct	gcc	ctt	gga	caa	cag	ttt	act	caa	gat	gcc	agc	cta	aaa	1104	
Leu	Ala	Ala	Ala	Leu	Gly	Gln	Gln	Phe	Thr	Gln	Asp	Ala	Ser	Leu	Lys		
353					358					363					368		
aat	aag	ctc	aaa	cta	caa	gct	tta	att	tat	cca	gtt	ctt	caa	gct	tta	1152	
Asn	Lys	Leu	Lys	Leu	Gln	Ala	Leu	Ile	Tyr	Pro	Val	Leu	Gln	Ala	Leu		
369					374					379					384		
gat	ttt	aac	aca	cca	tct	tat	cag	caa	aat	gtg	aac	acc	cca	atc	ctg	1200	
Asp	Phe	Asn	Thr	Pro	Ser	Tyr	Gln	Gln	Asn	Val	Asn	Thr	Pro	Ile	Leu		
385					390					395					400		
ccc	cgc	tat	gtc	atg	gtg	aag	tat	tgg	gtg	gac	tac	ttc	aaa	ggc	aac	1248	
Pro	Arg	Tyr	Val	Met	Val	Lys	Tyr	Trp	Val	Asp	Tyr	Phe	Lys	Gly	Asn		

401	406	411	416	
tat gac ttt gtg cag gca atg atc gtt aac aat cac act tca ctt gat				1296
Tyr Asp Phe Val Gln Ala Met Ile Val Asn Asn His Thr Ser Leu Asp				
417	422	427	432	
gtg gaa gag gct gct gct gtc agg gcc cgt cta aac tgg aca tcc ctc				1344
Val Glu Glu Ala Ala Val Arg Ala Arg Leu Asn Trp Thr Ser Leu				
433	438	443	448	
ttg cct gca tcc ttc aca aag aac tac aag cct gtt gta cag acc aca				1392
Leu Pro Ala Ser Phe Thr Lys Asn Tyr Lys Pro Val Val Gln Thr Thr				
449	454	459	464	
ggc aat gcc agg att gtc cag gag ctt cct cag ttg ctg gat gcc cgc				1440
Gly Asn Ala Arg Ile Val Gln Glu Leu Pro Gln Leu Leu Asp Ala Arg				
465	470	475	480	
tcc gcc cca ctc att gca gac cag gca gtg ctg cag ctc ctc cca aag				1488
Ser Ala Pro Leu Ile Ala Asp Gln Ala Val Leu Gln Leu Leu Pro Lys				
481	486	491	496	
acc tac att ctg acg tgt gag cat gat gtc ctc aga gac gat ggc atc				1536
Thr Tyr Ile Leu Thr Cys Glu His Asp Val Leu Arg Asp Asp Gly Ile				
497	502	507	512	
atg tat gcc aag cgt ttg gag agt gcc ggt gtg gag gtg acc ctg gat				1584
Met Tyr Ala Lys Arg Leu Glu Ser Ala Gly Val Glu Val Thr Leu Asp				
513	518	523	528	
cac ttt gag gat ggc ttt cac gga tgt atg att ttc act agc tgg ccc				1632
His Phe Glu Asp Gly Phe His Gly Cys Met Ile Phe Thr Ser Trp Pro				
529	534	539	544	
acc aac ttc tca gtg gga atc cgg act agg aat agt tac atc aag tgg				1680
Thr Asn Phe Ser Val Gly Ile Arg Thr Arg Asn Ser Tyr Ile Lys Trp				
545	550	555	560	
cta gat caa aac ctg taa aggagc aaaacttcca gaagcctoga gccctcttg				1734
Leu Asp Gln Asn Leu *				
561	566			
acctcctaca cctgctttgg aaagacatgc acttttttagt tgactaatc ttcctccat				1794
ttccctctac ttgcgagtta tggaatttct attccataac tgaagtcttt atgataacct				1854
aatttttaaaa aatgaatttg actaacttaa gtgcaaaaca tgtaaatttg gttcccagag				1914
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aagcaggact aggaactgga aataactttg ggtcctgcct tcattaggac gttcttttta				2034
gaagcagttc ttccagctct ggatcataga gtgaccttta ataagttaaa aaaacgagga				2094
ctccttaatt ctgctagagt taaccttgag ttcagagcag tattaaatgc gtgcactttc				2154
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2232

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<220>
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<222> (355) .. (2223)

<400> 381

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tcctggaggg ggctgaggcc ccagcttctg gccaccacaa cgtatcaagc tatctccagg 300
gttgggctca ggactcagag ctgacgcagc tgggggtgcc cttgggtctg gagg atg 357
Met
1

agg ctc ctc cgc aga cgc cac atg ccc ctg cgc ctg gcc atg gtg ggc 405
Arg Leu Leu Arg Arg Arg His Met Pro Leu Arg Leu Ala Met Val Gly
2 7 12 17

tgc gcc ttt gtg ctc ttc ctc ttc ctc ctg cat agg gat gtg agc agc 453
Cys Ala Phe Val Leu Phe Leu Phe Leu Leu His Arg Asp Val Ser Ser
18 23 28 33

aga gag gag gcc aca gag aag ccg tgg ctg aag tcc ctg gtg agc cgg 501
Arg Glu Glu Ala Thr Glu Lys Pro Trp Leu Lys Ser Leu Val Ser Arg
34 39 44 49

aag gat cac gtc ctg gac ctc atg ctg gag gcc atg aac aac ctt aga 549
Lys Asp His Val Leu Asp Leu Met Leu Glu Ala Met Asn Asn Leu Arg
50 55 60 65

gat tca atg ccc aag ctc caa atc agg gct cca gaa gcc cag cag act 597
Asp Ser Met Pro Lys Leu Gln Ile Arg Ala Pro Glu Ala Gln Gln Thr
66 71 76 81

ctg ttc tcc ata aat cag tcc tgc ctc cct ggg ttc tat acc cca gct 645
Leu Phe Ser Ile Asn Gln Ser Cys Leu Pro Gly Phe Tyr Thr Pro Ala
82 87 92 97

gaa ctg aag ccc ttc tgg gaa cgg cca cca cag gac ccc aat gcc cct 693
Glu Leu Lys Pro Phe Trp Glu Arg Pro Pro Gln Asp Pro Asn Ala Pro
98 103 108 113

ggg gca gat gga aaa gca ttt cag aag agc aag tgg acc ccc ctg gag	741
Gly Ala Asp Gly Lys Ala Phe Gln Lys Ser Lys Trp Thr Pro Leu Glu	
114 119 124 129	
acc cag gaa aag gaa gaa ggc tat aag aag cac tgt ttc aat gcc ttt	789
Thr Gln Glu Lys Glu Glu Gly Tyr Lys Lys His Cys Phe Asn Ala Phe	
130 135 140 145	
gcc agc gac cgg atc tcc ctg cag agg tcc ctg ggg cca gac acc cga	837
Ala Ser Asp Arg Ile Ser Leu Gln Arg Ser Leu Gly Pro Asp Thr Arg	
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Pro Pro Glu Cys Val Asp Gln Lys Phe Arg Arg Cys Pro Pro Leu Ala	
162 167 172 177	
acc acc agc gtg atc att gtg ttc cac aac gaa gcc tgg tcc aca ctg	933
Thr Thr Ser Val Ile Ile Val Phe His Asn Glu Ala Trp Ser Thr Leu	
178 183 188 193	
ctg cga aca gtg tac agc gtc cta cac acc acc cct gcc atc ttg ctc	981
Leu Arg Thr Val Tyr Ser Val Leu His Thr Thr Pro Ala Ile Leu Leu	
194 199 204 209	
aag gag atc ata ctg gtg gat gat gcc agc aca gag gag cac cta aag	1029
Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Thr Glu Glu His Leu Lys	
210 215 220 225	
gag aag ctg gag cag tac gtg aag cag ctg cag gtg gtg agg gtg gtg	1077
Glu Lys Leu Glu Gln Tyr Val Lys Gln Leu Gln Val Val Arg Val Val	
226 231 236 241	
cgg cag gag gag cgg aag ggg ctg atc acc gcc cgg ctg ctg ggg gcc	1125
Arg Gln Glu Glu Arg Lys Gly Leu Ile Thr Ala Arg Leu Leu Gly Ala	
242 247 252 257	
agc gtg gca cag gcg gag gtg ctc acg ttc ctg gat gcc cac tgt gag	1173
Ser Val Ala Gln Ala Glu Val Leu Thr Phe Leu Asp Ala His Cys Glu	
258 263 268 273	
tgc ttc cac ggc tgg ctg gag ccc ctc ctg gct cga atc gct gag gac	1221
Cys Phe His Gly Trp Leu Glu Pro Leu Leu Ala Arg Ile Ala Glu Asp	
274 279 284 289	
aag aca gtg gtg gtg agc cca gac atc gtc acc atc gac ctt aat act	1269
Lys Thr Val Val Val Ser Pro Asp Ile Val Thr Ile Asp Leu Asn Thr	
290 295 300 305	
ttt gag ttc gcc aag ccc gtc cag agg ggc aga gtc cat agc cga ggc	1317
Phe Glu Phe Ala Lys Pro Val Gln Arg Gly Arg Val His Ser Arg Gly	
306 311 316 321	
aac ttt gac tgg agc ctg acc ttc ggc tgg gaa aca ctt cct cca cat	1365
Asn Phe Asp Trp Ser Leu Thr Phe Gly Trp Glu Thr Leu Pro Pro His	
322 327 332 337	

gag aag cag agg cgc aag gat gaa acc tac ccc atc aaa tcc ccg acg	1413
Glu Lys Gln Arg Arg Lys Asp Glu Thr Tyr Pro Ile Lys Ser Pro Thr	
338 343 348 353	
ttt gct ggt ggc ctc ttc tcc atc tcc aag tcc tac ttt gag cac atc	1461
Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Ser Tyr Phe Glu His Ile	
354 359 364 369	
ggt acc tat gat aat cag atg gag atc tgg gga ggg gag aac gtg gaa	1509
Gly Thr Tyr Asp Asn Gln Met Glu Ile Trp Gly Gly Glu Asn Val Glu	
370 375 380 385	
atg tcc ttc cgg gtg tgg cag tgt ggg ggc cag ctg gag atc atc ccc	1557
Met Ser Phe Arg Val Trp Gln Cys Gly Gly Gln Leu Glu Ile Ile Pro	
386 391 396 401	
tgc tct gtc gta ggc cat gtg ttc cgg acc aag agc ccc cac acc ttc	1605
Cys Ser Val Val Gly His Val Phe Arg Thr Lys Ser Pro His Thr Phe	
402 407 412 417	
ccc aag ggc act agt gtc att gct cgc aat caa gtg cgc ctg gca gag	1653
Pro Lys Gly Thr Ser Val Ile Ala Arg Asn Gln Val Arg Leu Ala Glu	
418 423 428 433	
gtc tgg atg gac agc tac aag aag att ttc tat agg aga aat ctg cag	1701
Val Trp Met Asp Ser Tyr Lys Lys Ile Phe Tyr Arg Arg Asn Leu Gln	
434 439 444 449	
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Ala Ala Lys Met Ala Gln Glu Lys Ser Phe Gly Asp Ile Ser Glu Arg	
450 455 460 465	
ctg cag ctg agg gaa caa ctg cac tgt cac aac ttt tcc tgg tac ctg	1797
Leu Gln Leu Arg Glu Gln Leu His Cys His Asn Phe Ser Trp Tyr Leu	
466 471 476 481	
cac aat gtc tac cca gag atg ttt gtt cct gac ctg acg ccc acc ttc	1845
His Asn Val Tyr Pro Glu Met Phe Val Pro Asp Leu Thr Pro Thr Phe	
482 487 492 497	
tat ggt gcc atc aag aac ctc ggc acc aac caa tgc ctg gat gtg ggt	1893
Tyr Gly Ala Ile Lys Asn Leu Gly Thr Asn Gln Cys Leu Asp Val Gly	
498 503 508 513	
gag aac aac cgc ggg ggg aag ccc ctc atc atg tac tcc tgc cac ggc	1941
Glu Asn Asn Arg Gly Gly Lys Pro Leu Ile Met Tyr Ser Cys His Gly	
514 519 524 529	
ctt ggc ggc aac cag tac ttt gag tac aca act cag agg gac ctt cgc	1989
Leu Gly Gly Asn Gln Tyr Phe Glu Tyr Thr Thr Gln Arg Asp Leu Arg	
530 535 540 545	
cac aac atc gca aag cag ctg tgt cta cat gtc agc aag ggt gct ctg	2037
His Asn Ile Ala Lys Gln Leu Cys Leu His Val Ser Lys Gly Ala Leu	
546 551 556 561	
ggc ctt ggg agc tgt cac ttc act ggc aag aat agc cag gtc ccc aag	2085

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Asp	Glu	Glu	Trp	Glu	Leu	Ala	Gln	Asp	Gln	Leu	Ile	Arg	Asn	Ser	Gly	
578					583					588					593	
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Ser	Gly	Thr	Cys	Leu	Thr	Ser	Gln	Asp	Lys	Lys	Pro	Ala	Met	Ala	Pro	
594					599					604					609	
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Cys	Asn	Pro	Ser	Asp	Pro	His	Gln	Leu	Trp	Leu	Phe	Val	*			
610					615					620						
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cctgaaagca tggataatta ttcacatttc caccagctga gggtcacgga agaggaaata																180
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aga agt gag gtc tca cag gtg aaa aga gaa aag gaa aat att cag act	1104
Arg Ser Glu Val Ser Gln Val Lys Arg Glu Lys Glu Asn Ile Gln Thr	
189 194 199 204	
ctc ttg aaa tcc aaa gag caa gaa gta aat gaa ctt ctg caa aaa ttc	1152
Leu Leu Lys Ser Lys Glu Gln Glu Val Asn Glu Leu Leu Gln Lys Phe	
205 210 215 220	
cag caa gct cag gaa gaa ctt gca gaa atg aaa aga tac tct gag agc	1200
Gln Gln Ala Gln Glu Glu Leu Ala Glu Met Lys Arg Tyr Ser Glu Ser	
221 226 231 236	
tct tca aaa ctg gag gaa gat aaa gat aaa aag ata aat gag atg tcg	1248
Ser Ser Lys Leu Glu Glu Asp Lys Asp Lys Lys Ile Asn Glu Met Ser	
237 242 247 252	
aag gaa gtc acc aaa ttg aag gag gcc ttg aac agc ctc tcc cag ctc	1296
Lys Glu Val Thr Lys Leu Lys Glu Ala Leu Asn Ser Leu Ser Gln Leu	
253 258 263 268	
tcc tac tca aca agc tca tcc aaa agg cag agt cag cag ctg gag gcg	1344
Ser Tyr Ser Thr Ser Ser Ser Lys Arg Gln Ser Gln Gln Leu Glu Ala	
269 274 279 284	
ctg cag cag caa gtc aaa cag ctc cag aac cag ctg gcg gaa tgc aag	1392
Leu Gln Gln Gln Val Lys Gln Leu Gln Asn Gln Leu Ala Glu Cys Lys	
285 290 295 300	
aaa caa cac cag gag gtc ata tca gtt tac aga atg cat ctt ctg tat	1440
Lys Gln His Gln Glu Val Ile Ser Val Tyr Arg Met His Leu Leu Tyr	
301 306 311 316	
gct gtg cag ggc cag atg gat gaa gat gtc cag aaa gta ctg aag caa	1488
Ala Val Gln Gly Gln Met Asp Glu Asp Val Gln Lys Val Leu Lys Gln	
317 322 327 332	
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Ile Leu Thr Met Cys Lys Asn Gln Ser Gln Lys Lys *	
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$\frac{1}{2}(\sigma_x + \sigma_y)$	$\begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix}$	$\frac{1}{2}(\sigma_x - \sigma_y)$	$\begin{pmatrix} 1 & -1 \\ -1 & 1 \end{pmatrix}$
$\frac{1}{2}(\sigma_x + i\sigma_z)$	$\begin{pmatrix} 1 & i \\ i & 1 \end{pmatrix}$	$\frac{1}{2}(\sigma_x - i\sigma_z)$	$\begin{pmatrix} 1 & -i \\ i & 1 \end{pmatrix}$
$\frac{1}{2}(\sigma_x + \sigma_z)$	$\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$	$\frac{1}{2}(\sigma_x - \sigma_z)$	$\begin{pmatrix} 1 & 0 \\ 0 & -1 \end{pmatrix}$
$\frac{1}{2}(\sigma_y + i\sigma_z)$	$\begin{pmatrix} i & 1 \\ 1 & i \end{pmatrix}$	$\frac{1}{2}(\sigma_y - i\sigma_z)$	$\begin{pmatrix} i & -1 \\ -1 & i \end{pmatrix}$
$\frac{1}{2}(\sigma_y + \sigma_z)$	$\begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$	$\frac{1}{2}(\sigma_y - \sigma_z)$	$\begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix}$
$\frac{1}{2}(\sigma_z + i\sigma_x)$	$\begin{pmatrix} i & 0 \\ 0 & i \end{pmatrix}$	$\frac{1}{2}(\sigma_z - i\sigma_x)$	$\begin{pmatrix} i & 0 \\ 0 & -i \end{pmatrix}$
$\frac{1}{2}(\sigma_z + \sigma_y)$	$\begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$	$\frac{1}{2}(\sigma_z - \sigma_y)$	$\begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix}$

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Tyr Leu Leu Val Thr Asp Gln Gly Phe Leu Gln Glu Glu Gln Val Val	
166 171 176 181	
tg g gag agc ctg cac aat gtg gat gga gac agc tgc ttt tgt gac tct	989
Trp Glu Ser Leu His Asn Val Asp Gly Asp Ser Cys Phe Cys Asp Ser	
182 187 192 197	
gac ttt cac ctg agt cat tcc ctg ggc aag ggg cct gga gca gaa ggt	1037
Asp Phe His Leu Ser His Ser Leu Gly Lys Gly Pro Gly Ala Glu Gly	
198 203 208 213	
ggg agt ggc tcc cca gaa aag cag ctg cag gta gac cag gac tac ctg	1085
Gly Ser Gly Ser Pro Glu Lys Gln Leu Gln Val Asp Gln Asp Tyr Leu	
214 219 224 229	
att gct ctg tcc ctg cag cag caa cag cca cga ggc ccg ctg ggg ctt	1133
Ile Ala Leu Ser Leu Gln Gln Gln Gln Pro Arg Gly Pro Leu Gly Leu	
230 235 240 245	
acc gac ttg gag ctg gcc cag cag ctt cag caa gag gag tat caa cag	1181
Thr Asp Leu Glu Leu Ala Gln Gln Leu Gln Gln Glu Glu Tyr Gln Gln	
246 251 256 261	
cag cag gca gcg cag cca gtg cgg atg cgg acg cgg gtc ctg tca ctg	1229
Gln Gln Ala Ala Gln Pro Val Arg Met Arg Thr Arg Val Leu Ser Leu	
262 267 272 277	
cag ggg aga gga gcc aca tct gga cgc cca gcc ggg gag cgt cgg cag	1277
Gln Gly Arg Gly Ala Thr Ser Gly Arg Pro Ala Gly Glu Arg Arg Gln	
278 283 288 293	
agg ccg aag cac gag tca gac tgc att ctg ctg tag ctct gccccagtgc	1327
Arg Pro Lys His Glu Ser Asp Cys Ile Leu Leu *	
294 299 304	
caggctggcc tgcccccttct tccagaggct atggctagtt ggcttgctcc cccgcctcca	1387
cccctgagat gtgctggata acttatttat ggactgttgg ggatgagagc aggcaacaaa	1447
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aaaacttctg gccgggcaaa aaaaaaa	1774

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<211> 1952

<212> DNA
<213> Homo sapiens

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<400> 384

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agc gta gct gag ggg gtg cgg cta agt cca gag cct ggc agg gag gga	96
Ser Val Ala Glu Gly Val Arg Leu Ser Pro Glu Pro Gly Arg Glu Gly	
17 22 27 32	
gta agg gac tta gca ggg gcg gag gag ttc ggc ggc gga gag gag ggg	144
Val Arg Asp Leu Ala Gly Ala Glu Glu Phe Gly Gly Gly Glu Glu Gly	
33 38 43 48	
aca ggg ctg aca ggg ata aag gag ata ggg gat gga gag gaa gga agt	192
Thr Gly Leu Thr Gly Ile Lys Glu Ile Gly Asp Gly Glu Glu Gly Ser	
49 54 59 64	
gga caa agg cca gag gaa ata ccg atg gac cta acg gta gtg aag cag	240
Gly Gln Arg Pro Glu Glu Ile Pro Met Asp Leu Thr Val Val Lys Gln	
65 70 75 80	
gaa att ata gac tgg cca ggt aca gaa ggc agg ttg gct ggc cag tgg	288
Glu Ile Ile Asp Trp Pro Gly Thr Glu Gly Arg Leu Ala Gly Gln Trp	
81 86 91 96	
gta gaa cag gag gtg gag gat agg cct gag gtg aag gat gag aac gca	336
Val Glu Gln Glu Val Glu Asp Arg Pro Glu Val Lys Asp Glu Asn Ala	
97 102 107 112	
ggc gta ttg gag gtg aag cag gag acg gat agt agt tta gtg gta aaa	384
Gly Val Leu Glu Val Lys Gln Glu Thr Asp Ser Ser Leu Val Val Lys	
113 118 123 128	
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Glu Ala Lys Val Gly Glu Pro Glu Val Lys Glu Glu Lys Val Lys Glu	
129 134 139 144	
gag gta atg gac tgg tca gaa gtg aag gaa gag aag gat aac ttg gag	480
Glu Val Met Asp Trp Ser Glu Val Lys Glu Glu Lys Asp Asn Leu Glu	
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Ile Lys Gln Glu Glu Lys Phe Val Gly Gln Cys Ile Lys Glu Glu Leu	
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Met His Gly Glu Cys Val Lys Glu Glu Lys Asp Phe Leu Lys Lys Glu	
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Ile Val Asp Asp Thr Lys Val Lys Glu Glu Pro Pro Ile Asn His Pro	
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Val Gly Cys Lys Arg Lys Leu Ala Met Ser Arg Cys Glu Thr Cys Gly	
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Thr Glu Glu Ala Lys Tyr Arg Cys Pro Arg Cys Met Arg Tyr Ser Cys	
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Ser Leu Pro Cys Val Lys Lys His Lys Ala Glu Leu Thr Cys Asn Gly	
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Val Arg Asp Lys Thr Ala Tyr Ile Ser Ile Gln Gln Phe Thr Glu Met	
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Asn Leu Leu Ser Asp Tyr Arg Phe Leu Glu Asp Val Ala Arg Thr Ala	
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Lys Leu Leu Pro Asn Gly Phe Thr Lys Arg Lys Glu Asn Ser Thr Phe	
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Tyr Tyr Glu Leu Asp Pro Tyr Lys Ser Leu Leu Asp Asn Leu Arg Asn	

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ccctgcccc ccgaaggcct ggagcaggat gtccctccagg ccattgaccg ggccatcgag	300
gctgtacaca acacagcc atg cgg gat ggt ggc aag tac agc ctg gaa cag	351
Met Arg Asp Gly Gly Lys Tyr Ser Leu Glu Gln	

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Arg Gly Val Leu Gln Lys Leu Ile His His Arg Lys Glu Thr Leu Ser	
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Ser Asp His His Leu Asp Ala Ala Ala Arg Gln Pro Asn Gly Val	
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Cys Arg Ala Gly Phe Glu Arg Gln His Ser Leu Pro Ser Ser Glu His	
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Ile Pro Pro Gln Pro Arg Arg Ala Ala Pro Thr Thr Pro Pro Pro	
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Val Lys Arg Arg Asp Arg Glu Ala Leu Met Ala Ser Gly Ser Gly Gly	
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His Asn Thr Met Pro Ser Gly Gly Asn Ser Val Ser Ser Gly Ser Ser	
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Val Ser Ser Thr Ser Leu Asp Thr Leu Tyr Thr Ser Ser Ser Pro Ser	
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Ser Ala Pro Glu Pro Pro Ala Glu Glu Glu Val Ala Thr Gly Thr Thr	
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Ser Ala Ser Asp Asp Leu Glu Ala Leu Gly Thr Leu Ser Leu Gly Thr	
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Ala Glu Leu Met Glu Leu Val Arg Arg Asn Thr Gly Leu Ser His Glu	
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Val Pro Ala Ser Ser Pro Val Met Glu Gln Val Leu Leu Ser Leu Val	
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Ile Ile Ser Thr Leu Val Ser Ser Val Leu Pro Val Glu Leu Ala Arg	
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Asp Met Gln Thr Asp Thr Gln Asp His Gln Lys Leu Cys Tyr Ser Ala	
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Val Glu Asp Gly Leu Pro Leu Asp Thr Thr Glu Gln Leu Pro Asp Leu	
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Cys Val Asn Leu Leu Leu Ala Leu Asn Leu His Leu Pro Ala Ala Asp	
476 481 486 491	
cag aat gtc atc atg gct gcc ctg agc aaa cac gcc aat gtc aag atc	1839
Gln Asn Val Ile Met Ala Ala Leu Ser Lys His Ala Asn Val Lys Ile	
492 497 502 507	
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Phe Ser Glu Lys Leu Leu Leu Leu Leu Asn Arg Gly Asp Asp Pro Val	
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Arg Ile Phe Lys His Glu Pro Gln Pro Pro His Ser Val Leu Lys Phe	
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Leu Ser Pro Gly Asp Lys Leu Arg Met Glu Tyr Leu Ser Leu Met His	
572 577 582 587	
gct ata gtc cgc acc aca ccc tac ctg cag cac cgc cac cgg cta ccc	2127
Ala Ile Val Arg Thr Thr Pro Tyr Leu Gln His Arg His Arg Leu Pro	
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Asp Leu Gln Ala Ile Leu Arg Arg Ile Leu Asn Glu Glu Glu Thr Ser	
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ccc cag tgc cag atg gac cgc atg att gtc cga gag atg tgc aag gaa	2223
Pro Gln Cys Gln Met Asp Arg Met Ile Val Arg Glu Met Cys Lys Glu	
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Phe Leu Val Leu Gly Glu Ala Pro Ser *	
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 Met Leu Lys Ser Met
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 Val Leu Trp Leu Gly Glu Gln Val Gln Ser Leu Gln Leu Gln Gln
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 Leu Arg His His Phe Asn His Ile His Ile Cys Val Thr Asn Ser Glu
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 Tyr Asn Gln Ser Glu Tyr Pro Trp Asp Leu Val Lys Ala His Leu Gln
 38 43 48 53
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 Gly Ala Phe Thr Ser Asn Ile Thr Phe Asp Ile Ser Glu Leu Gln Asn
 54 59 64 69
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 Lys Ile Leu Asp Leu Asn Arg His Thr Gln Glu Phe Gln Pro Ser Leu
 70 75 80 85
 gaa gac tgg act gaa ttc cag gaa ggc ctg gag agc ctc aac cct tgg 403
 Glu Asp Trp Thr Glu Phe Gln Glu Gly Leu Glu Ser Leu Asn Pro Trp
 86 91 96 101

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gaa atg atg gaa gga gaa aca aac ttc agc tct gaa ata gaa gat ctt				483
Glu Met Met Glu Gly Glu Thr Asn Phe Ser Ser Glu Ile Glu Asp Leu				
60	65	70	75	
gca agg gaa ggc gac atg cca att cat gaa ctt ctc agc ctt tat ggt				531
Ala Arg Glu Gly Asp Met Pro Ile His Glu Leu Leu Ser Leu Tyr Gly				
76	81	86	91	
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Tyr Gly Ser Thr Val Arg Leu Pro Glu Glu Asp Glu Glu Glu Glu				
92	97	102	107	
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Glu Glu Glu Glu Gly Glu Asp Asp Glu Asp Ala Asp Asn Asp Asp Asn				
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Asp Tyr Ile Pro Ser Glu Asp Trp Lys Lys Glu Ile Met Val Gly Ser				
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Met Phe Gln Ala Glu Ile Pro Val Gly Ile Cys Arg Tyr Lys Glu Asn				
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Pro Pro Thr Ala Ser Asn Ser Ser Asn Ser Gln Ser Glu Lys Glu Asp	
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Gly Thr Val Ser Thr Ala Asn Gln Asn Gly Lys Gln Pro Glu Lys His	
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37 42 47 52

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53 58 63 68

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69 74 79 84

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133 138 143 148

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cag gtg cca gtg ctg aag ccc atg gat ctg atg gtg gag gtg agc cct 716
Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val Glu Val Ser Pro

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149		154		159		164	
cgg agg atc ttt gcc aat ggc cac acc tac cac atc aac tcc atc tcc	764						
Arg Arg Ile Phe Ala Asn Gly His Thr Tyr His Ile Asn Ser Ile Ser							
165		170		175		180	
gtc aac agt gac tgc gag acc tac atg tgc ggc gat gac ctg cgc atc	812						
Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala Asp Asp Leu Arg Ile							
181		186		191		196	
aac ctc tgg cac ctg gcc atc acc gac agg agc ttc aac atc gtg gac	860						
Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe Asn Ile Val Asp							
197		202		207		212	
atc aag ccg gcc aac atg gag gac ctt acg gag gtg atc aca gca tct	908						
Ile Lys Pro Ala Asn Met Glu Asp Leu Thr Glu Val Ile Thr Ala Ser							
213		218		223		228	
gag ttc cat ccg cac cac tgc aac ctc ttc gtc tac agc agc agc aag	956						
Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr Ser Ser Ser Lys							
229		234		239		244	
ggc tcc ctg cgg ctc tgc gac atg cgg gca gct gcc ctg tgt gac aag	1004						
Gly Ser Leu Arg Leu Cys Asp Met Arg Ala Ala Leu Cys Asp Lys							
245		250		255		260	
cat tcc aag ctc ttt gaa gag cct gag gac ccc agt aac cgc tca ttc	1052						
His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser Asn Arg Ser Phe							
261		266		271		276	
ttc tgc gaa atc atc tcc tcc gtg tcc gac gtg aag ttc agc cac agc	1100						
Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys Phe Ser His Ser							
277		282		287		292	
ggc cgc tac atg ctc acc cgg gac tac ctt aca gtc aag gtc tgg gac	1148						
Gly Arg Tyr Met Leu Thr Arg Asp Tyr Leu Thr Val Lys Val Trp Asp							
293		298		303		308	
ctg aac atg gag gca aga ccc ata gag acc tac cag gtc cat gac tac	1196						
Leu Asn Met Glu Ala Arg Pro Ile Glu Thr Tyr Gln Val His Asp Tyr							
309		314		319		324	
ctt cgg agc aag ctc tgt tcc ctg tac gag aac gac tgc att ttc gac	1244						
Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp Cys Ile Phe Asp							
325		330		335		340	
aag ttt gaa tgt gcc tgg aac ggg agc gac agc gtc atc atg acc ggg	1292						
Lys Phe Glu Cys Ala Trp Asn Gly Ser Asp Ser Val Ile Met Thr Gly							
341		346		351		356	
acc tac aac aac ttc ttc cgc atg ttc gat cgg aac acc aag cgg gac	1340						
Thr Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asn Thr Lys Arg Asp							
357		362		367		372	
gtg acc ctg gag gcc tgc agg gaa agc agc aag ccc cgg gct gtg ctc	1388						
Val Thr Leu Glu Ala Ser Arg Glu Ser Ser Lys Pro Arg Ala Val Leu							
373		378		383		388	

aag cca cgg cgc gtg tgc gtg ggg ggc aag cgc cgg cgt gat gac atc	1436
Lys Pro Arg Arg Val Cys Val Gly Gly Lys Arg Arg Arg Asp Asp Ile	
389 394 399 404	
agt gtg gac agc ttg gac ttc acc aag aag atc ctg cac acg gcc tgg	1484
Ser Val Asp Ser Leu Asp Phe Thr Lys Lys Ile Leu His Thr Ala Trp	
405 410 415 420	
cac ccg gct gag aac atc att gcc att gcc gcc acc aac aac ctg tac	1532
His Pro Ala Glu Asn Ile Ile Ala Ile Ala Ala Thr Asn Asn Leu Tyr	
421 426 431 436	
atc ttc cag gac aag gta aac tct gac atg cac tag gtat gtgcagatcc	1582
Ile Phe Gln Asp Lys Val Asn Ser Asp Met His *	
437 442 447	
cgccccctgc caccagcct catgcaagtc atccccgaca tgaccttcac gaccgcaatg	1642
caaggagggg aagaaagtca cagcactgat gaggacagct gcagaggtgg cagtgtgtgg	1702
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gaatgtcttg aaacatccca ggtcccaggt ctggtgcggt ttcccagagag gagcggagtg	2242
gggtttgtct tctgtgtgcc tgtgtcctca tctgattcac ctgccatttg ctgagcctct	2302
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tgcacgattt tttggaatct tcctcctgac tgtgaggtgg gtgttcattc atttcctcca	2482
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ccaataaagc cagtgaagaaa ggagcttacc aaaggcagtg tacgaagaag gttcctggga	120
gactgtcaga a atg agt ttt tca ctg aac ttc acc ctg ccg gcg aac aca	170
Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr	
1 5 10	
acg tcc tct cct gtc aca ggt ggg aaa gaa acg gac tgt ggg ccc tct	218
Thr Ser Ser Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser	
14 19 24 29	
ctt gga tta gcg gcg ggc ata cca ttg ctg gtg gcc aca gcc ctg ctg	266
Leu Gly Leu Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu	
30 35 40 45	
gtg gct tta cta ttt act ttg att cac cga aga aga agc agc att gag	314
Val Ala Leu Leu Phe Thr Leu Ile His Arg Arg Arg Ser Ser Ile Glu	
46 51 56 61	
gcc atg gag gaa agt gac aga cca tgt gaa att tca gaa att gat gac	362
Ala Met Glu Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp	
62 67 72 77	
aat ccc aag ata tct gag aat cct agg aga tca ccc aca cat gag aag	410
Asn Pro Lys Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys	
78 83 88 93	
aat acg atg gga gca caa gag gcc cac ata tat gtg aag act gta gca	458
Asn Thr Met Gly Ala Gln Glu Ala His Ile Tyr Val Lys Thr Val Ala	
94 99 104 109	
gga agc gag gaa cct gtg cat gac cgt tac cgt cct act ata gaa atg	506
Gly Ser Glu Glu Pro Val His Asp Arg Tyr Arg Pro Thr Ile Glu Met	
110 115 120 125	
gaa aga agg agg gga ttg tgg tgg ctt gtg ccc aga ctg agc ctg gaa	554
Glu Arg Arg Arg Gly Leu Trp Trp Leu Val Pro Arg Leu Ser Leu Glu	
126 131 136 141	
tga tgca gctcagtcaa ggagcagcag acctggcact ggaacagggt tgaaaaccca	611
*	
142	
gggttttgta cttggagagg aaagatgcca agctgcttct taatcaatcc aaatttcatt	671
tacagctctg gaacactttg gggctgattt gtctcttttag gggacatccc caacatgggt	731
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gtaggaacca tgtggagcca cacattccct gaccacaggg aagcacctgg ctcaatcatg	1091
tcacacagca gtggaaagaa tacggactct taagtcacac ctaccactga gcagctgtac	1151
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aagttacaac ttcttttatt ttatttttta aaggcttcag attaaacaag agcccttaag	1811
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cagtaactcc tcttcccatt ttccaatcca tcccagcca tttttttttt tcttctgtac	2051
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                               Met Gly Ala His
                               1

ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg      164
Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
   5                10                15                20

cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag      212
Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
  21                26                31                36

cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg cag ctg agg      260
Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Gln Leu Arg
  37                42                47                52

ctc cag ctg cgg gac tac tgc gcc cac cac ctc atc cgg ctg ctc aag      308
Leu Gln Leu Arg Asp Tyr Cys Ala His His Leu Ile Arg Leu Leu Lys
  53                58                63                68

tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg      356
Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
  69                74                79                84

cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag      404
His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
  85                90                95                100

gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag      452
Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
 101                106                111                116

aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac      500
Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
 117                122                127                132

ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa      554
Pro Lys Val Ala Leu *
 133                138

aagccttcag gccctcaaa aaaaaaaaaa      583
  
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taggtgaccc tcggctgctg cagggatctg cagcgactgc agcc atg ggg gcg cac      116
                Met Gly Ala His
                        1

ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg      164
Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
    5                10                15                20

cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag      212
Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
    21                26                31                36

cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg ctg ctc aag      260
Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Leu Leu Lys
    37                42                47                52

tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg      308
Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
    53                58                63                68

cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag      356
His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
    69                74                79                84

gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag      404
Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
    85                90                95                100

aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac      452
Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
    101                106                111                116

ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa      506
Pro Lys Val Ala Leu *
    117                122

aagccttcag gcccctcaaa aaaaaaaaaa      535
  
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taagggaagc cgtg atg agg gcc gtg ttg acg tgg aga gat aaa gcc gag	110
Met Arg Ala Val Leu Thr Trp Arg Asp Lys Ala Glu	
1 5 10	
cac tgt ata aat gac atc gca ttt aag cct gat gga act caa ctg att	158
His Cys Ile Asn Asp Ile Ala Phe Lys Pro Asp Gly Thr Gln Leu Ile	
13 18 23 28	
ttg gct gcc gga agc aga tta ctg gtt tat gac acc tct gat ggc acc	206
Leu Ala Ala Gly Ser Arg Leu Leu Val Tyr Asp Thr Ser Asp Gly Thr	
29 34 39 44	
tta ctt cag ccc ctc aag gga cac aaa gac act gtg tac tgt gtg gca	254
Leu Leu Gln Pro Leu Lys Gly His Lys Asp Thr Val Tyr Cys Val Ala	
45 50 55 60	
tat gcg aag gat ggc aag cgc ttt gct tct gga tca gct gac aaa agc	302
Tyr Ala Lys Asp Gly Lys Arg Phe Ala Ser Gly Ser Ala Asp Lys Ser	
61 66 71 76	
gtt att atc tgg aca tca aaa ctg gaa ggc att ctg aag tac acg cac	350
Val Ile Ile Trp Thr Ser Lys Leu Glu Gly Ile Leu Lys Tyr Thr His	
77 82 87 92	
aat gat gct ata caa tgt gtc tcc tac aat cct att act cat caa ctg	398
Asn Asp Ala Ile Gln Cys Val Ser Tyr Asn Pro Ile Thr His Gln Leu	
93 98 103 108	
gca tct tgt tcc tcc agt gac ttt ggg ttg tgg tct cct gaa cag aag	446
Ala Ser Cys Ser Ser Ser Asp Phe Gly Leu Trp Ser Pro Glu Gln Lys	
109 114 119 124	
tct gtc tcc aaa cac aaa tca agc agc aag atc atc tgc tgc agc tgg	494
Ser Val Ser Lys His Lys Ser Ser Ser Lys Ile Ile Cys Cys Ser Trp	
125 130 135 140	
aca aat gat ggt cag tac ctg gcg ctg ggg atg ttc aat ggg atc atc	542
Thr Asn Asp Gly Gln Tyr Leu Ala Leu Gly Met Phe Asn Gly Ile Ile	
141 146 151 156	
agc ata cgg aac aaa aat ggc gag gag aaa gta aag atc gag cgg ccg	590
Ser Ile Arg Asn Lys Asn Gly Glu Glu Lys Val Lys Ile Glu Arg Pro	
157 162 167 172	
ggg ggc tcc ctc tcg cca ata tgg tcc atc tgc tgg aac cct tca agc	638
Gly Gly Ser Leu Ser Pro Ile Trp Ser Ile Cys Trp Asn Pro Ser Ser	
173 178 183 188	

cga tgg gag agt ttc tgg atg aac aga gag aat gag gat gcc gag gat	686
Arg Trp Glu Ser Phe Trp Met Asn Arg Glu Asn Glu Asp Ala Glu Asp	
189 194 199 204	
gtc att gtc aac aga tat att cag gaa atc cct tcc act ctg aag tca	734
Val Ile Val Asn Arg Tyr Ile Gln Glu Ile Pro Ser Thr Leu Lys Ser	
205 210 215 220	
gca gtg tac agt agt cag ggt agt gag gca gag gag gaa gaa cca gag	782
Ala Val Tyr Ser Ser Gln Gly Ser Glu Ala Glu Glu Glu Glu Pro Glu	
221 226 231 236	
gaa gag gac gac agt ccc agg gac gac aac tta gag gaa cgt aat gac	830
Glu Glu Asp Asp Ser Pro Arg Asp Asp Asn Leu Glu Glu Arg Asn Asp	
237 242 247 252	
atc ctg gct gtg gct gac tgg gga cag aaa gtt tcc ttc tac cag ctg	878
Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr Gln Leu	
253 258 263 268	
agt gga aaa cag att gga aag gat cgg gca ctg aac ttt gac ccc tgc	926
Ser Gly Lys Gln Ile Gly Lys Asp Arg Ala Leu Asn Phe Asp Pro Cys	
269 274 279 284	
tgc atc agc tac ttt act aaa ggc gag tac att ttg ctg ggg ggt tca	974
Cys Ile Ser Tyr Phe Thr Lys Gly Glu Tyr Ile Leu Leu Gly Gly Ser	
285 290 295 300	
gac aag caa gta tct ctt ttc acc aag gat gga gtg cgg ctt ggg act	1022
Asp Lys Gln Val Ser Leu Phe Thr Lys Asp Gly Val Arg Leu Gly Thr	
301 306 311 316	
gtt ggg gag cag aac tcc tgg gtg tgg acg tgt caa gcg aaa ccg gat	1070
Val Gly Glu Gln Asn Ser Trp Val Trp Thr Cys Gln Ala Lys Pro Asp	
317 322 327 332	
tcc aac tat gtg gtg gtc ggc tgc cag gac ggc acc att tcc ttc tac	1118
Ser Asn Tyr Val Val Val Gly Cys Gln Asp Gly Thr Ile Ser Phe Tyr	
333 338 343 348	
cag ctt att ttc agc aca gtc cat ggg ctt tac aag gac cgc tat gcc	1166
Gln Leu Ile Phe Ser Thr Val His Gly Leu Tyr Lys Asp Arg Tyr Ala	
349 354 359 364	
tac agg gat agc atg act gac gtc att gtg cag cac ctg atc act gag	1214
Tyr Arg Asp Ser Met Thr Asp Val Ile Val Gln His Leu Ile Thr Glu	
365 370 375 380	
cag aaa gtt cgg att aaa tgc aaa gag ctt gtc aag aag att gcc atc	1262
Gln Lys Val Arg Ile Lys Cys Lys Glu Leu Val Lys Lys Ile Ala Ile	
381 386 391 396	
tac aga aat cga ttg gct atc caa ctg cca gag aaa atc ctc atc tat	1310
Tyr Arg Asn Arg Leu Ala Ile Gln Leu Pro Glu Lys Ile Leu Ile Tyr	
397 402 407 412	

gag ttg tat tca gag gac tta tca gac atg cat tac cgg gta aag gag	1358
Glu Leu Tyr Ser Glu Asp Leu Ser Asp Met His Tyr Arg Val Lys Glu	
413 418 423 428	
aag att atc aag aag ttt gag tgc aac ctc ctg gtg gtg tgt gcc aat	1406
Lys Ile Ile Lys Lys Phe Glu Cys Asn Leu Leu Val Val Cys Ala Asn	
429 434 439 444	
cac atc atc ctg tgc cag gag aaa cgg ctg cag tgc ctg tcc ttc agc	1454
His Ile Ile Leu Cys Gln Glu Lys Arg Leu Gln Cys Leu Ser Phe Ser	
445 450 455 460	
gga gtg aag gag cgg gag tgg cag atg gag tct ctc att cgt tac atc	1502
Gly Val Lys Glu Arg Glu Trp Gln Met Glu Ser Leu Ile Arg Tyr Ile	
461 466 471 476	
aag gtg atc ggt ggc cct cct gga aga gaa ggc ctc tta gtg ggg ctg	1550
Lys Val Ile Gly Gly Pro Pro Gly Arg Glu Gly Leu Leu Val Gly Leu	
477 482 487 492	
aag aat gga cag atc ctg aag atc ttc gtg gac aat ctc ttt gct atc	1598
Lys Asn Gly Gln Ile Leu Lys Ile Phe Val Asp Asn Leu Phe Ala Ile	
493 498 503 508	
gtc ctg ctg aag cag gcc aca gct gtg cgc tgc ttg gac atg agt gcc	1646
Val Leu Leu Lys Gln Ala Thr Ala Val Arg Cys Leu Asp Met Ser Ala	
509 514 519 524	
tcc cgt aag aag ctg gcc gtg gta gat gaa aat gac act tgc ctg gtg	1694
Ser Arg Lys Lys Leu Ala Val Val Asp Glu Asn Asp Thr Cys Leu Val	
525 530 535 540	
tat gac atc gac acc aag gag ctg ctt ttt cag gaa cca aac gcc aac	1742
Tyr Asp Ile Asp Thr Lys Glu Leu Leu Phe Gln Glu Pro Asn Ala Asn	
541 546 551 556	
agt gta gct tgg aac acc cag tgt gag gac atg ctc tgc ttc tcg gga	1790
Ser Val Ala Trp Asn Thr Gln Cys Glu Asp Met Leu Cys Phe Ser Gly	
557 562 567 572	
gga ggc tac ctc aac atc aaa gcc agc acc ttc cct gtg cac cgg cag	1838
Gly Gly Tyr Leu Asn Ile Lys Ala Ser Thr Phe Pro Val His Arg Gln	
573 578 583 588	
aag ctg cag ggc ttt gtg gtc ggc tac aat ggc tcc aag atc ttc tgc	1886
Lys Leu Gln Gly Phe Val Val Gly Tyr Asn Gly Ser Lys Ile Phe Cys	
589 594 599 604	
ctc cat gtc ttc tcc att tct gcc gtg gag gtg ccg cag tcc gct ccc	1934
Leu His Val Phe Ser Ile Ser Ala Val Glu Val Pro Gln Ser Ala Pro	
605 610 615 620	
atg tac cag tac ctg gat agg aaa ctg ttc aag gaa gcc tac cag att	1982
Met Tyr Gln Tyr Leu Asp Arg Lys Leu Phe Lys Glu Ala Tyr Gln Ile	
621 626 631 636	
gct tgc ttg ggt gtc aca gac act gat tgg cgt gaa ctg gcc atg gaa	2030

Ala Cys Leu Gly Val Thr Asp Thr Asp Trp Arg Glu Leu Ala Met Glu	
637 642 647 652	
gcg cta gaa ggt tta gat ttt gaa aca gca aag aag gcc ttc atc aga	2078
Ala Leu Glu Gly Leu Asp Phe Glu Thr Ala Lys Lys Ala Phe Ile Arg	
653 658 663 668	
gta caa gac ctc cga tat tta gag ctc atc agc agc att gag gag agg	2126
Val Gln Asp Leu Arg Tyr Leu Glu Leu Ile Ser Ser Ile Glu Glu Arg	
669 674 679 684	
aag aag cgg gga gag acc aac aat gac ctg ttt ctg gca gat gtg ttt	2174
Lys Lys Arg Gly Glu Thr Asn Asn Asp Leu Phe Leu Ala Asp Val Phe	
685 690 695 700	
tcc tac cag ggg aag ttc cat gag gcc gcc aaa ctg tac aag agg agt	2222
Ser Tyr Gln Gly Lys Phe His Glu Ala Ala Lys Leu Tyr Lys Arg Ser	
701 706 711 716	
ggg cac gag aac ctc gcg ctt gaa atg tac acc gac ctc tgc atg ttt	2270
Gly His Glu Asn Leu Ala Leu Glu Met Tyr Thr Asp Leu Cys Met Phe	
717 722 727 732	
gag tat gcc aag gat ttc ctt gga tct gga gac ccc aaa gaa aca aag	2318
Glu Tyr Ala Lys Asp Phe Leu Gly Ser Gly Asp Pro Lys Glu Thr Lys	
733 738 743 748	
atg cta atc acc aaa cag gct gac tgg gcc aga aat atc aag gag ccc	2366
Met Leu Ile Thr Lys Gln Ala Asp Trp Ala Arg Asn Ile Lys Glu Pro	
749 754 759 764	
aaa gcc gcc gtg gag atg tac atc tca gca gga gag cac gtc aag gcc	2414
Lys Ala Ala Val Glu Met Tyr Ile Ser Ala Gly Glu His Val Lys Ala	
765 770 775 780	
atc gag atc tgt ggt gac cat ggc tgg gtt gac atg ttg atc gac atc	2462
Ile Glu Ile Cys Gly Asp His Gly Trp Val Asp Met Leu Ile Asp Ile	
781 786 791 796	
gcc cgc aaa ctg gac aag gct gag cgc gag ccc ctg ctg ctg tgc gct	2510
Ala Arg Lys Leu Asp Lys Ala Glu Arg Glu Pro Leu Leu Leu Cys Ala	
797 802 807 812	
acc tac ctc aag aag ctg gac agc cct ggc tat gct gct gag acc tac	2558
Thr Tyr Leu Lys Lys Leu Asp Ser Pro Gly Tyr Ala Ala Glu Thr Tyr	
813 818 823 828	
ctg aag atg ggt gac ctc aag tcc ctg gtg cag ctg cac gtg gag acc	2606
Leu Lys Met Gly Asp Leu Lys Ser Leu Val Gln Leu His Val Glu Thr	
829 834 839 844	
cag cgc tgg gat gag gcc ttt gct ttg ggt gag aag cat cct gag ttt	2654
Gln Arg Trp Asp Glu Ala Phe Ala Leu Gly Glu Lys His Pro Glu Phe	
845 850 855 860	
aag gat gac atc tac atg ccg tat gct cag tgg cta gca gag aac gat	2702
Lys Asp Asp Ile Tyr Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp	

861	866	871	876	
cgc ttt gag gaa gcc cag aaa gcg ttc cac aag gct ggg cga cag aga				2750
Arg Phe Glu Glu Ala Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg				
877	882	887	892	
gaa gcg gtc cag gtg ctg gag cag ctc aca aac aat gcc gtg gcg gag				2798
Glu Ala Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu				
893	898	903	908	
agc agg ttt aat gat gct gcc tat tat tac tgg atg ctg tcc atg cag				2846
Ser Arg Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln				
909	914	919	924	
tgc ctc gat ata gct caa gat cct gcc cag aag gac aca atg ctt ggc				2894
Cys Leu Asp Ile Ala Gln Asp Pro Ala Gln Lys Asp Thr Met Leu Gly				
925	930	935	940	
aag ttc tac cac ttc cag cgt ttg gca gag ctg tac cat ggt tac cat				2942
Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His Gly Tyr His				
941	946	951	956	
gcc atc cat cgc cac acg gaa gat ccg ttc agt gtc cat cgt cct gaa				2990
Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His Arg Pro Glu				
957	962	967	972	
act ctt ttc aac atc tcc agg ttc ctg ctg cac agc ctg ccc aag gac				3038
Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu Pro Lys Asp				
973	978	983	988	
acc ccc tcg ggc atc tct aaa gtg aaa ata ctc ttc acc ttg gcc aag				3086
Thr Pro Ser Gly Ile Ser Lys Val Lys Ile Leu Phe Thr Leu Ala Lys				
989	994	999	1004	
cag agc aag gcc ctc ggt gcc tac agg ctg gcc cgg cac gcc tat gac				3134
Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His Ala Tyr Asp				
1005	1010	1015	1020	
aag ctg cgt ggc ctg tac atc cct gcc aga ttc caa aag tcc att gag				3182
Lys Leu Arg Gly Leu Tyr Ile Pro Ala Arg Phe Gln Lys Ser Ile Glu				
1021	1026	1031	1036	
ctg ggt acc ctg acc atc cgc gcc aag ccc ttc cac gac agt gag gag				3230
Leu Gly Thr Leu Thr Ile Arg Ala Lys Pro Phe His Asp Ser Glu Glu				
1037	1042	1047	1052	
ttg gtg ccc ttg tgc tac cgc tgc tcc acc aac aac ccg ctg ctc aac				3278
Leu Val Pro Leu Cys Tyr Arg Cys Ser Thr Asn Asn Pro Leu Leu Asn				
1053	1058	1063	1068	
aac ctg ggc aac gtc tgc atc aac tgc cgc cag ccc ttc atc ttc tcc				3326
Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro Phe Ile Phe Ser				
1069	1074	1079	1084	
gcc tct tcc tac gac gtg cta cac ctg gtt gag ttc tac ctg gag gaa				3374
Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe Tyr Leu Glu Glu				
1085	1090	1095	1100	

ggg atc act gat gaa gaa gcc atc tcc ctc atc gac ctg gag gtg ctg	3422
Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp Leu Glu Val Leu	
1101 1106 1111 1116	
aga ccc aag cgg gat gac aga cag cta gag att gca aac aac agc tcc	3470
Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Ala Asn Asn Ser Ser	
1117 1122 1127 1132	
cag att ctg cgg cta gtg gag acc aag gac tcc atc gga gat gag gac	3518
Gln Ile Leu Arg Leu Val Glu Thr Lys Asp Ser Ile Gly Asp Glu Asp	
1133 1138 1143 1148	
ccg ttc aca gct aag ctg agc ttt gag caa ggt ggc tca gag ttc gtg	3566
Pro Phe Thr Ala Lys Leu Ser Phe Glu Gln Gly Gly Ser Glu Phe Val	
1149 1154 1159 1164	
cca gtg gtg gtg agc cgg ctg gtg ctg cgc tcc atg agc cgc cgg gat	3614
Pro Val Val Val Ser Arg Leu Val Leu Arg Ser Met Ser Arg Arg Asp	
1165 1170 1175 1180	
gtc ctc atc aag cga tgg ccc cca ccc ctg agg tgg caa tac ttc cgc	3662
Val Leu Ile Lys Arg Trp Pro Pro Pro Leu Arg Trp Gln Tyr Phe Arg	
1181 1186 1191 1196	
tca ctg ctg cct gac gcc tcc att acc atg tgc ccc tcc tgc ttc cag	3710
Ser Leu Leu Pro Asp Ala Ser Ile Thr Met Cys Pro Ser Cys Phe Gln	
1197 1202 1207 1212	
atg ttc cat tct gag gac tat gag ttg ctg gtg ctt cag cat ggc tgc	3758
Met Phe His Ser Glu Asp Tyr Glu Leu Leu Val Leu Gln His Gly Cys	
1213 1218 1223 1228	
tgc ccc tac tgc cgc agg tgc aag gat gac cct ggc cca tga ccagcat	3807
Cys Pro Tyr Cys Arg Arg Cys Lys Asp Asp Pro Gly Pro *	
1229 1234 1239	
cctggggacg gcctgcaccc tctgcccgcc ttggggtctg ctgggctgtg aaggagaata	3867
aagagttaaa ctgtcaaaaa aaaaaaaaaa	3897

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (87)..(1139)

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ccggcaggca agcgtttgcc tccgcc atg aac ccc agg ggc ctg ttc cag gac	113

Met Asn Pro Arg Gly Leu Phe Gln Asp
1 5

ttc aac ccc agt aag gtt ctc atc tac acc tgc ctg ctg ctc ttc tcg	161
Phe Asn Pro Ser Lys Val Leu Ile Tyr Thr Cys Leu Leu Leu Phe Ser	
10 15 20 25	
ggg ctg ctg ccc ctc cgc ctg gac ggc atc atc caa tgg agc tac tgg	209
Gly Leu Leu Pro Leu Arg Leu Asp Gly Ile Ile Gln Trp Ser Tyr Trp	
26 31 36 41	
gcc gtc ttt gcc ccc ata tgg ctg agg aag ctt cta gtc gtc gca ggc	257
Ala Val Phe Ala Pro Ile Trp Leu Arg Lys Leu Leu Val Val Ala Gly	
42 47 52 57	
gcc tcc gtg ggc gcg ggc gtt tgg gcc cgc aac cct cgc tac cgc acc	305
Ala Ser Val Gly Ala Gly Val Trp Ala Arg Asn Pro Arg Tyr Arg Thr	
58 63 68 73	
gag gga gag gcc tgt gtg gag atc aaa gcc atg ctg atc gct gtg ggc	353
Glu Gly Glu Ala Cys Val Glu Ile Lys Ala Met Leu Ile Ala Val Gly	
74 79 84 89	
atc cac ctg ctg ctg ctc atg ttc gaa gtc ctg gtc tgc gac agg gtg	401
Ile His Leu Leu Leu Leu Met Phe Glu Val Leu Val Cys Asp Arg Val	
90 95 100 105	
gag agg ggc acc cac ttc tgg ctg ctg gtc ttc atg cct ctc ttc ttc	449
Glu Arg Gly Thr His Phe Trp Leu Leu Val Phe Met Pro Leu Phe Phe	
106 111 116 121	
gtg tcc ccc gtg tcc gtg gct gcc tgc gtc tgg ggc ttt cga cac gat	497
Val Ser Pro Val Ser Val Ala Ala Cys Val Trp Gly Phe Arg His Asp	
122 127 132 137	
agg tcg ctg gag ctg gag atc ctg tgc tcg gtc aac atc ctg cag ttc	545
Arg Ser Leu Glu Leu Glu Ile Leu Cys Ser Val Asn Ile Leu Gln Phe	
138 143 148 153	
atc ttc atc gcc cta aag ctg gac agg att att cac tgg ccg tgg ctg	593
Ile Phe Ile Ala Leu Lys Leu Asp Arg Ile Ile His Trp Pro Trp Leu	
154 159 164 169	
gtg gtg ttt gtg ccc ctg tgg atc ctc atg tcg ttc ctt tgc ctg gtc	641
Val Val Phe Val Pro Leu Trp Ile Leu Met Ser Phe Leu Cys Leu Val	
170 175 180 185	
gtc ctc tat tac atc gtc tgg tcc ctc ctg ttc ctg cgg tcc ctg gat	689
Val Leu Tyr Tyr Ile Val Trp Ser Leu Leu Phe Leu Arg Ser Leu Asp	
186 191 196 201	
gtg gtt gcc gag cag cgg aga aca cac gtg acc atg gct atc agt tgg	737
Val Val Ala Glu Gln Arg Arg Thr His Val Thr Met Ala Ile Ser Trp	
202 207 212 217	
ata acg att gtc gtg cct ctg ctc act ttt gag gtc ctg ctg gtt cac	785
Ile Thr Ile Val Val Pro Leu Leu Thr Phe Glu Val Leu Leu Val His	

218	223	228	233	
aga ttg gat ggc cac	aat aca ttc tcc tac	gtc tcc ata ttt gtc	ccc	833
Arg Leu Asp Gly His	Asn Thr Phe Ser Tyr	Val Ser Ile Phe Val	Pro	
234	239	244	249	
ctt tgg ctt tcc tta	cta act tta atg gcc	aca aca ttt agg cga	aag	881
Leu Trp Leu Ser Leu	Leu Thr Leu Met Ala	Thr Thr Phe Arg Arg	Lys	
250	255	260	265	
ggg ggc aat cat tgg	tgg ttt ggc att cgc	aga gac ttc tgt cag	ttt	929
Gly Gly Asn His Trp	Trp Phe Gly Ile Arg	Arg Asp Phe Cys Gln	Phe	
266	271	276	281	
ctg ctt gaa att ttc	cca ttt tta aga gaa	tat ggg aac att tca	tat	977
Leu Leu Glu Ile Phe	Pro Phe Leu Arg Glu	Tyr Gly Asn Ile Ser	Tyr	
282	287	292	297	
gat ctc cat cac gaa	gat agt gaa gat gct	gaa gaa aca tca gtt	cca	1025
Asp Leu His His Glu	Asp Ser Glu Asp Ala	Glu Glu Thr Ser Val	Pro	
298	303	308	313	
gaa gct ccg aaa att	gct cca ata ttt gga	aag aag gcc aga gta	gtt	1073
Glu Ala Pro Lys Ile	Ala Pro Ile Phe Gly	Lys Lys Ala Arg Val	Val	
314	319	324	329	
ata acc cag agc cct	ggg aaa tac gtt ccc	ccc cct ccc aag tta	aat	1121
Ile Thr Gln Ser Pro	Gly Lys Tyr Val Pro	Pro Pro Pro Lys Leu	Asn	
330	335	340	345	
att gat atg cca gat	taa actcct agagaggacc	caggcacaca cagactccac		1175
Ile Asp Met Pro Asp	*			
346	351			
ttggccttcg cctcttggtc	attcatccca aacctggaaa	tggaacagg cttcaaacac		1235
tcgtctcacg ccgtgtttga	gatcaccgcc tcatcagtat	gcacataga tggaggtggt		1295
ttcagtatgt ggggtgtgtg	ggtgtgtacc tgggtaagag	acttgctttc caggttcgca		1355
ctttcaggtg tagctggggg	cagtaagtcg aattgtttta	gtaggtcctc aaaaggaata		1415
accacacagc tgtttgttta	aatgctactg tacctatcaa	aactattggt taaaaagtat		1475
ttttatacac tgctaactta	aaattgtatt tcagattgtg	cctgtcataa caatagcaaa		1535
tgtaaaaagt tctctttccc	accacttggt tataaacctc	atagttgata tttttagtgt		1595
tcctactggt aaaatactct	ctccttgggc tttgctgata	ctggtcttta atattctgat		1655
aggtgaattt ttctaattga	atgaacccat gcatatatag	tatttatatg aatattttag		1715
cagtgaata tgttgaattc	tagttctctg cattaccatt	attacgttaa agtatttttt		1775
aaagcttagg tgtgaaaaaa	aaaaaaa			1802

<210> 395
 <211> 1413
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (21)..(740)

<400> 395

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	Met Thr Cys Phe Gly Pro Tyr Pro Ile Gly	
	1 5	
act gga ctt cag gga ata acc ttg tgt tat agt tgt ttt ccc tcc ttc	98	
Thr Gly Leu Gln Gly Ile Thr Leu Cys Tyr Ser Cys Phe Pro Ser Phe		
11 16 21 26		
tgc aag atg aaa agc agg atg tgc atg gct atc agc att tgt cag acg	146	
Cys Lys Met Lys Ser Arg Met Cys Met Ala Ile Ser Ile Cys Gln Thr		
27 32 37 42		
ctt tcc atg ttg agt ttt gtg gtc tgt gct ttc agg tac agg cat atg	194	
Leu Ser Met Leu Ser Phe Val Val Cys Ala Phe Arg Tyr Arg His Met		
43 48 53 58		
ttc aaa agg ggt tgg cca atg ggt aca tgt tgt ttg ttt ctg ccc aca	242	
Phe Lys Arg Gly Trp Pro Met Gly Thr Cys Cys Leu Phe Leu Pro Thr		
59 64 69 74		
gct gcc cca gtg ctc agc tgt gaa gct gca aca cag act gaa agg aga	290	
Ala Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu Arg Arg		
75 80 85 90		
ctg gat ctg gct gca gtg act ctg agg aga ggc ttg aga tct aga gct	338	
Leu Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser Arg Ala		
91 96 101 106		
tcg cga tgc aga ccg cgg tct ttg ata gat tac aaa tcc tac atg gac	386	
Ser Arg Cys Arg Pro Arg Ser Leu Ile Asp Tyr Lys Ser Tyr Met Asp		
107 112 117 122		
acc aag ctg ctg gtg gcg agg ttc ctg gag cag tcc tct tgt acc atg	434	
Thr Lys Leu Leu Val Ala Arg Phe Leu Glu Gln Ser Ser Cys Thr Met		
123 128 133 138		
acc cca gac atc cat gaa ctt gta gaa aac att aaa tct gtt ttg aaa	482	
Thr Pro Asp Ile His Glu Leu Val Glu Asn Ile Lys Ser Val Leu Lys		
139 144 149 154		
tct gat gag gag cac atg gag gaa gcc atc aca agt gcc agt ttt cta	530	
Ser Asp Glu Glu His Met Glu Glu Ala Ile Thr Ser Ala Ser Phe Leu		
155 160 165 170		
gaa cag ata atg gcc cca ttg cag ccc agc aca tcc agg gcc cac aag	578	

Glu Gln Ile Met Ala Pro Leu Gln Pro Ser Thr Ser Arg Ala His Lys	
171 176 181 186	
ctg ccc ttg cgg aga cag cct ggc ctg ctg cac ctc cag agc tgc ggc	626
Leu Pro Leu Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser Cys Gly	
187 192 197 202	
gac ctt cac acc atc aca cca gcg ggg agg ccc cga gcc gag agg agg	674
Asp Leu His Thr Ile Thr Pro Ala Gly Arg Pro Arg Ala Glu Arg Arg	
203 208 213 218	
ccc cgg cga gtg gag gct gag cgg tca cac agc ctc att ggg gtc atc	722
Pro Arg Arg Val Glu Ala Glu Arg Ser His Ser Leu Ile Gly Val Ile	
219 224 229 234	
cga gag act gtc ctg tga accctg gaagacagaa ggtcactcca aggggaagga	776
Arg Glu Thr Val Leu *	
235 240	
tccctctcct ctctgtcatg tcttgatgg gagctgtggc ccacctcaaa aaaaaaggag	836
cactctggac acgtgttccc acctgttggg tcccggtgtc gctgactgag ggcattcagg	896
agtaaagcga caggctcggc caggcccgtc tgggtttggg atgcactgag ttggagggtta	956
tgaaagcttt gatcctcttc ttcctctgct gggcctcgca gcattcccaa gggtcacatg	1016
ccctggcatg ggcagaaact gggctaataa ttctttgccc acttcacccc tcgtgtctct	1076
ctttgttgct aagttctttc cctcttgga ggacagatct gccgggctgc tatttatagt	1136
tgcccttggc ctttctactgc tctgcgattt ggcaggaaat aaggcgatta accctatgtg	1196
tccacaagcc tcaagccttg tttcagggtc ccctcaaata acactctctt taggcaaaac	1256
aggaaacttc ttaagtgaca aattttaatg ccagacattt aaggagagga ttattgttga	1316
ttccatttac tcatgcttgc aaaactagag acccctaagg cagaactgag aataaacatg	1376
tttacttttg gccactgggc ttgatgtgta aaaaaaa	1413

<210> 396
 <211> 1711
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (338) .. (1051)

<400> 396	
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tgaggacgtt tgggacaaag gtatagtcaa agtgatcaga gcattacatt catctgacaa	120

gtcttgtctc tcttcagccc ctctctctct taattgacta cttcatcctc gctccttgga 180
acatcctttc attggtcagc cacatttttc ctgcttggcc catccatccc catctatttg 240
tcatacccca tgaaacttaa cctcattatg gtttgcattc tggattctcc tctccacat 300
ctggctttac cttgggggtg gtgtcgtaca tgacaca atg acg tgt ttc ggg cca 355
Met Thr Cys Phe Gly Pro
1

tat cct att gga act gga ctt cag gga ata acc ttg tgt tgt ttt ccc 403
Tyr Pro Ile Gly Thr Gly Leu Gln Gly Ile Thr Leu Cys Cys Phe Pro
7 12 17 22

tcc ttc tgc aag atg aaa agc agg atg tgc atg gct atc agc att tgt 451
Ser Phe Cys Lys Met Lys Ser Arg Met Cys Met Ala Ile Ser Ile Cys
23 28 33 38

cag atg ctt tcc atg ttg agt ttt gtg gtc tgt gct ttc agg tac agg 499
Gln Met Leu Ser Met Leu Ser Phe Val Val Cys Ala Phe Arg Tyr Arg
39 44 49 54

cat atg ttc aaa agg ggc tgg cca atg ggt aca tgt tgt ttg ttt ctg 547
His Met Phe Lys Arg Gly Trp Pro Met Gly Thr Cys Cys Leu Phe Leu
55 60 65 70

ccc aca gct gcc cca gtg ctc agc tgt gaa gct gca aca cag act gaa 595
Pro Thr Ala Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu
71 76 81 86

agg aga ctg gat ctg gct gca gtg act ctg agg aga ggc ttg aga tct 643
Arg Arg Leu Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser
87 92 97 102

aga gct tcg cga tgc aga ccg cgg tct ttg ata gat tac aaa tcc tac 691
Arg Ala Ser Arg Cys Arg Pro Arg Ser Leu Ile Asp Tyr Lys Ser Tyr
103 108 113 118

atg gac acc aag ctg ctg gtg gcg agg ttc ctg gag cag tcc tct tgt 739
Met Asp Thr Lys Leu Leu Val Ala Arg Phe Leu Glu Gln Ser Ser Cys
119 124 129 134

acc atg acc cca gac atc cat gaa ctt gta gaa aac att aaa tct gtt 787
Thr Met Thr Pro Asp Ile His Glu Leu Val Glu Asn Ile Lys Ser Val
135 140 145 150

ttg aaa tct gat gag gag cac atg gag gaa gcc atc aca agt gcc agt 835
Leu Lys Ser Asp Glu Glu His Met Glu Glu Ala Ile Thr Ser Ala Ser
151 156 161 166

ttt cta gaa cag ata atg gcc cca ttg cag ccc agc aca tcc agg gcc 883
Phe Leu Glu Gln Ile Met Ala Pro Leu Gln Pro Ser Thr Ser Arg Ala
167 172 177 182

cac aag ctg ccc tcg cgg aga cag cct ggc ctg ctg cac ctc cag agc 931
His Lys Leu Pro Ser Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser

183	188	193	198	
tgc ggc gac ctt cac acc ttc aca cca gcg ggg agg ccc cga gcc gag				979
Cys Gly Asp Leu His Thr Phe Thr Pro Ala Gly Arg Pro Arg Ala Glu				
199	204	209	214	
agg agg ccc cgg cga gtg gag gct gag cgg cca cac agc ctc att ggg				1027
Arg Arg Pro Arg Arg Val Glu Ala Glu Arg Pro His Ser Leu Ile Gly				
215	220	225	230	
gtc atc cga gag act gtc ctg tga accctggaag acagaaggcc actccaagg				1081
Val Ile Arg Glu Thr Val Leu *				
231	236			
gaaggatccc tctcctctct gccatttctt ggctgggagc tgtgggtccac ctcaaaaaa				1141
aggagcactc tggaggacac gttttcccac ctgttggtctc ccgtgtctgc tgactgaggg				1201
cattcaggag taaatgcaca ggctcggcca ggcccgtctg ggtttgggat gcactgagtt				1261
ggaggttatg aaagctttga tcctcttctt cctctgctgg gcctcgcagc attccaagg				1321
gtcacatgcc ctggcatggg cagaaactgg gctaattgatt ctttgccac ttcaccctc				1381
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cctatgtgtc cacaagcctc aagccttggt tcaggtcacc ctcaaatac actctcttta				1561
ggcaaaacag gaaacttctt aagtgacaaa ttttaatgcc agacatttaa ggagaggatt				1621
attgttgatt ccatttactc atgcttgcaa aactagagac ccctaaggca gaactgagaa				1681
taaacatggt tactttgggc caaaaaaaaa				1711

<210> 397
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (90)..(407)

<400> 397		
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gcagtgtttt gccttcaccc caagtgacc atg aga ggt gcc acg cga gtc tca		113
Met Arg Gly Ala Thr Arg Val Ser		
1 5		
atc atg ctc ctc cta gta act gtg tct gac tgt gct gtg atc aca ggg		161
Ile Met Leu Leu Leu Val Thr Val Ser Asp Cys Ala Val Ile Thr Gly		

9	14	19	24	
gcc tgt gag cgg gat gtc cag tgt ggg gca ggc acc tgc tgt gcc atc				209
Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile				
25	30	35	40	
agc ctg tgg ctt cga ggg ctg cgg atg tgc acc ccg ctg ggg cgg gaa				257
Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu				
41	46	51	56	
ggc gag gag tgc cac ccc ggc agc cac aag atc ccc ttc ttc agg aaa				305
Gly Glu Glu Cys His Pro Gly Ser His Lys Ile Pro Phe Phe Arg Lys				
57	62	67	72	
cgc aag cac cac acc tgt cct tgc ttg ccc aac ctg ctg tgc tcc agg				353
Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg				
73	78	83	88	
ttc ccg gac ggc agg tac cgc tgc tcc atg gac ttg aag aac atc aat				401
Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn				
89	94	99	104	
ttt tag gcgcttgccct ggtctcagga taccacccat tcttttctg agcaca				453
Phe *				
105				

<210> 398
 <211> 1735
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (473) .. (1201)

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ccccctcccc cctccggcgc ggaccccgcg tgcgccttgc tcgcccgcag ccccgagacc	180
gcaggcgtca caatgtagca gggaccccgag gcgtcgtgct cagaaaatgg aaaaagagcc	240
agggccggaa ggagggtgca gaagcgagtc cgcgtgcgga gccaggaggc agcgtcgcgt	300
gggagtgtctg gcctgaagcc tccatgcccc ggcagaggga cggacacgcg gacgtctagc	360
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gaggagaagg ggaggatttg actttggaag tctctgtgac cagaagccaa ag atg	475
	Met
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Leu Thr Arg Lys Ile Lys Leu Trp Asp Ile Asn Ala His Ile Thr Cys	
2 7 12 17	
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Arg Leu Cys Ser Gly Tyr Leu Ile Asp Ala Thr Thr Val Thr Glu Cys	
18 23 28 33	
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Leu His Thr Phe Cys Arg Ser Cys Leu Val Lys Tyr Leu Glu Glu Asn	
34 39 44 49	
atc acc tgc ccc acc tgc agg att gtg atc cac cag agc cac ccc ctg	667
Ile Thr Cys Pro Thr Cys Arg Ile Val Ile His Gln Ser His Pro Leu	
50 55 60 65	
cag tac atc ggt cat gac aga acc atg caa gat att gtt tac aaa ttg	715
Gln Tyr Ile Gly His Asp Arg Thr Met Gln Asp Ile Val Tyr Lys Leu	
66 71 76 81	
gta cca ggc ctc caa gaa gcg gaa atg aga aag cag agg gag ttc tat	763
Val Pro Gly Leu Gln Glu Ala Glu Met Arg Lys Gln Arg Glu Phe Tyr	
82 87 92 97	
cac aaa ttg ggc atg gag gtg ccg gga gac atc aag ggg gag acc tgc	811
His Lys Leu Gly Met Glu Val Pro Gly Asp Ile Lys Gly Glu Thr Cys	
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Ser Ala Lys Gln His Leu Asp Ser His Arg Asn Gly Glu Thr Lys Ala	
114 119 124 129	
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Asp Asp Ser Ser Asn Lys Glu Ala Ala Glu Glu Lys Pro Glu Glu Asp	
130 135 140 145	
aac gac tac cac cgc agc gac gag cag gtg agc atc tgc ctg gag tgt	955
Asn Asp Tyr His Arg Ser Asp Glu Gln Val Ser Ile Cys Leu Glu Cys	
146 151 156 161	
aac agc agc aaa ctg cgc ggg ctg aag cgg aag tgg atc cgc tgc tca	1003
Asn Ser Ser Lys Leu Arg Gly Leu Lys Arg Lys Trp Ile Arg Cys Ser	
162 167 172 177	
gcc cag gcg acc gtc ttg cat ctg aag aag ttc atc gcc aaa aaa ctc	1051
Ala Gln Ala Thr Val Leu His Leu Lys Lys Phe Ile Ala Lys Lys Leu	
178 183 188 193	
aac ctt tca tcc ttt aac gag ctg gac att tta tgc aac gag gag atc	1099
Asn Leu Ser Ser Phe Asn Glu Leu Asp Ile Leu Cys Asn Glu Glu Ile	
194 199 204 209	
ctg ggc aag gac cac aca ctc aag ttc gtg gtt gtc act agg tgg aga	1147
Leu Gly Lys Asp His Thr Leu Lys Phe Val Val Val Thr Arg Trp Arg	
210 215 220 225	


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Phe Lys Lys Ala Pro Leu Leu Leu His Tyr Arg Pro Lys Met Asp Leu
226                231                236                241

ctg tga atggtgccac acagcgccca cagactgggc cctcgacccc ttgggtgctc      1251
Leu *
242

ccggccgccg cgcttaagaa cattgcctct ggggtgcatg tggaccagac ttctgaatag      1311

agaatattta taacttttgt atgagagaga attcacactc aacaagacac taccagcacc      1371

acgtttacag aggatgaaaa cacttcacag tctcccagag ccgatcgtcc tctccccgc      1431

cccaccccggt gcttcagcct tgcagggaga gtgatgctcc aggcaacacg gttctgagtc      1491

accttctgac acgagctccc tctgcttgct ttccaggtct tgaaaatctg aattcacttc      1551

agtttagttt atgaatttta ggtttcatga taagcctcaa ttgtagttgg acttttattg      1611

aatccttcct aagttattga aaaaatgtct tttcatggtg aatgacaata tttatgttgc      1671

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Ala Glu Val Ser Arg Leu Leu Leu Ala Thr Gly His Trp Lys Arg Leu
15              20              25              30

cgg cga gac aac ccc aga ttc aac ctg atg ctg gga gag agg aat cgg      143
Arg Arg Asp Asn Pro Arg Phe Asn Leu Met Leu Gly Glu Arg Asn Arg
31              36              41              46

ctg ccc ttc ggg aga ctg ggt cac gag ccc ggg ctg gta cag ttg gtg      191
Leu Pro Phe Gly Arg Leu Gly His Glu Pro Gly Leu Val Gln Leu Val
47              52              57              62

aat tac tac agg ggt gct gac aaa ctg tgt cgc aaa gct tct tta gtg      239
Asn Tyr Tyr Arg Gly Ala Asp Lys Leu Cys Arg Lys Ala Ser Leu Val

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aag cta atc aag aca agc cct gaa ctg gct gag tcc tgc aca tgg ttc				287
Lys Leu Ile Lys Thr Ser Pro Glu Leu Ala Glu Ser Cys Thr Trp Phe				
79	84	89	94	
cct gaa tct tat gtg att tat cca acc aat ctc aag act cca gtt gct				335
Pro Glu Ser Tyr Val Ile Tyr Pro Thr Asn Leu Lys Thr Pro Val Ala				
95	100	105	110	
cca gca cag aat gga att cag cca cca atc agt aac tca agg aca gat				383
Pro Ala Gln Asn Gly Ile Gln Pro Pro Ile Ser Asn Ser Arg Thr Asp				
111	116	121	126	
gaa aga gaa ttc ttt ctc gcc tct tat aac aga aag aaa gag gat gga				431
Glu Arg Glu Phe Phe Leu Ala Ser Tyr Asn Arg Lys Lys Glu Asp Gly				
127	132	137	142	
gag ggc aac gtt tgg att gca aag tca tca gcc ggt gcc aaa ggt gaa				479
Glu Gly Asn Val Trp Ile Ala Lys Ser Ser Ala Gly Ala Lys Gly Glu				
143	148	153	158	
ggc att ctc atc tcc tca gag gct tca gag ctt ctc gat ttc ata gac				527
Gly Ile Leu Ile Ser Ser Glu Ala Ser Glu Leu Leu Asp Phe Ile Asp				
159	164	169	174	
aac cag ggc caa gtg cac gtg atc cag aaa tat ctt gag cac cct ctg				575
Asn Gln Gly Gln Val His Val Ile Gln Lys Tyr Leu Glu His Pro Leu				
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ctg ctt gag cca ggt cat cgc aag ttt gac atc cga agc tgg gtc ttg				623
Leu Leu Glu Pro Gly His Arg Lys Phe Asp Ile Arg Ser Trp Val Leu				
191	196	201	206	
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Val Asp His Gln Tyr Asn Ile Tyr Leu Tyr Arg Glu Gly Val Leu Arg				
207	212	217	222	
act gct tca gaa cca tat cat gtt gat aat ttc caa gac aaa acc tgc				719
Thr Ala Ser Glu Pro Tyr His Val Asp Asn Phe Gln Asp Lys Thr Cys				
223	228	233	238	
cat ttg acc aat cac tgc att caa aaa gag tat tca aag aac tac ggg				767
His Leu Thr Asn His Cys Ile Gln Lys Glu Tyr Ser Lys Asn Tyr Gly				
239	244	249	254	
aag tat gaa gaa gga aat gaa atg ttc ttc aag gag ttc aat cag tac				815
Lys Tyr Glu Glu Gly Asn Glu Met Phe Phe Lys Glu Phe Asn Gln Tyr				
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cta aca agt gct ttg aac att acc cta gaa agt agt atc tta cta caa				863
Leu Thr Ser Ala Leu Asn Ile Thr Leu Glu Ser Ser Ile Leu Leu Gln				
271	276	281	286	
atc aaa cat ata ata agg aac tgc ctc ctg agc gtg gag cct gcc att				911
Ile Lys His Ile Ile Arg Asn Cys Leu Leu Ser Val Glu Pro Ala Ile				
287	292	297	302	

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Ser Thr Lys His Leu Pro Tyr Gln Ser Phe Gln Leu Phe Gly Phe Asp	
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Phe Met Val Asp Glu Glu Leu Lys Val Trp Leu Ile Glu Val Asn Gly	
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Ala Pro Ala Cys Ala Gln Lys Leu Tyr Ala Glu Leu Cys Gln Gly Ile	
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Val Asp Ile Ala Ile Ser Ser Val Phe Pro Pro Pro Asp Val Glu Gln	
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cct cag acc cag cca gct gcc ttc atc aag ctg tga caga gggcactccc	1153
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caagccgtag cggccgcgcc cttcagcta gctcgctcgc tcgctctgct tccctgctgc	240
cggtcgcgcc atg gcg ttg gcg ttg gcg gcg ctg gcg gcg gtc gag ccg	289
Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro	
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gcc tgc ggc agc cgg tac cag cag ttg cag aat gaa gaa gag tct gga	337
Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly	
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gaa cct gaa cag gct gca ggt gat gct cct cca cct tac agc agc att	385
Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile	
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Ser	Ala	Glu	Ser	Ala	Ala	Tyr	Phe	Asp	Tyr	Lys	Asp	Glu	Ser	Gly	Phe	
46					51					56					61	
cca	aag	ccc	cca	tct	tac	aat	gta	gct	aca	aca	ctg	ccc	agt	tat	gat	481
Pro	Lys	Pro	Pro	Ser	Tyr	Asn	Val	Ala	Thr	Thr	Leu	Pro	Ser	Tyr	Asp	
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gaa	gcg	gag	agg	acc	aag	gct	gaa	gct	act	atc	cct	ttg	gtt	cct	ggg	529
Glu	Ala	Glu	Arg	Thr	Lys	Ala	Glu	Ala	Thr	Ile	Pro	Leu	Val	Pro	Gly	
78					83					88					93	
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Arg	Asp	Glu	Asp	Phe	Val	Gly	Arg	Asp	Asp	Phe	Asp	Asp	Ala	Asp	Gln	
94					99					104					109	
ctg	agg	ata	gga	aat	gat	ggg	att	ttc	atg	tta	act	ttt	ttc	atg	gca	625
Leu	Arg	Ile	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Thr	Phe	Phe	Met	Ala	
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Phe	Leu	Phe	Asn	Trp	Ile	Gly	Phe	Phe	Leu	Ser	Phe	Cys	Leu	Thr	Thr	
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Ser	Ala	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Ser	Gly	Phe	Gly	Leu	Ser	Leu	
142					147					152					157	
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Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Thr	Tyr	Phe	Pro	Gly	Tyr	
158					163					168					173	
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Phe	Asp	Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Val	Phe	Leu	Val	Leu	Gly	Phe	
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 Met Ala Leu Ala
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 Ser Gly Pro Ala Arg Arg Ala Leu Ala Gly Ser Gly Gln Leu Gly Leu
 5 10 15 20

ggg ggc ttc ggg gcc ccg aga cgc ggg gcg tat gag tgg ggc gtg cgc 210
 Gly Gly Phe Gly Ala Pro Arg Arg Gly Ala Tyr Glu Trp Gly Val Arg
 21 26 31 36

tcc acg cgg aag tcg gag cct cct ccc ctg gat agg gtg tac gag atc 258
 Ser Thr Arg Lys Ser Glu Pro Pro Pro Leu Asp Arg Val Tyr Glu Ile
 37 42 47 52

cct gga ctg gag ccc atc acc ttt gcg ggg aag atg cac ttc gtg ccc 306
 Pro Gly Leu Glu Pro Ile Thr Phe Ala Gly Lys Met His Phe Val Pro

53	58	63	68	
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Trp Leu Ala Arg Pro Ile Phe Pro Pro Trp Asp Arg Gly Tyr Lys Asp				
69	74	79	84	
cca agg ttc tac cgc tgc ccc cct ctt cac gag cat ccg ctg tac aaa				402
Pro Arg Phe Tyr Arg Ser Pro Pro Leu His Glu His Pro Leu Tyr Lys				
85	90	95	100	
gac cag gcc tgc tat atc ttt cac cac cgt tgc cgc ctt ctc gag ggt				450
Asp Gln Ala Cys Tyr Ile Phe His His Arg Cys Arg Leu Leu Glu Gly				
101	106	111	116	
gta aag cag gcc ctc tgg ctc acc aag acc aag tta ata gaa ggc ctt				498
Val Lys Gln Ala Leu Trp Leu Thr Lys Thr Lys Leu Ile Glu Gly Leu				
117	122	127	132	
ccc gag aaa gtg ctt agc ctt gtt gat gat cca agg aac cac ata gag				546
Pro Glu Lys Val Leu Ser Leu Val Asp Asp Pro Arg Asn His Ile Glu				
133	138	143	148	
aac caa gac gag tgc gtt ctg aat gtg atc tct cac gcc cgt ctc tgg				594
Asn Gln Asp Glu Cys Val Leu Asn Val Ile Ser His Ala Arg Leu Trp				
149	154	159	164	
cag acc act gag gaa atc ccc aag aga gag acc tac tgc ccg gtc atc				642
Gln Thr Thr Glu Glu Ile Pro Lys Arg Glu Thr Tyr Cys Pro Val Ile				
165	170	175	180	
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Val Asp Asn Leu Ile Gln Leu Cys Lys Ser Gln Ile Leu Lys His Pro				
181	186	191	196	
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Ser Leu Ala Arg Arg Ile Cys Val Gln Asn Ser Thr Phe Ser Ala Thr				
197	202	207	212	
tgg aac cga gag tct ctt ctc ctt caa gtc cgt ggt tct ggt gga gcc				786
Trp Asn Arg Glu Ser Leu Leu Leu Gln Val Arg Gly Ser Gly Gly Ala				
213	218	223	228	
cga ctg agc act aag gat cct ctg ccc acc atc gcc tcc aga gag gag				834
Arg Leu Ser Thr Lys Asp Pro Leu Pro Thr Ile Ala Ser Arg Glu Glu				
229	234	239	244	
att gaa gct act aag aat cat gtt cta gag acc ttc tac ccc ata tca				882
Ile Glu Ala Thr Lys Asn His Val Leu Glu Thr Phe Tyr Pro Ile Ser				
245	250	255	260	
ccc atc atc gat ctt cat gaa tgc aat att tat gat gtg aaa aat gac				930
Pro Ile Ile Asp Leu His Glu Cys Asn Ile Tyr Asp Val Lys Asn Asp				
261	266	271	276	
aca gga ttc cag gaa ggc tat cct tac ccc tat ccc cat acc ctg tac				978
Thr Gly Phe Gln Glu Gly Tyr Pro Tyr Pro Tyr Pro His Thr Leu Tyr				
277	282	287	292	

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Leu Leu Asp Lys Ala Asn Leu Arg Pro His Arg Leu Gln Pro Asp Gln	
293 298 303 308	
ctg cgg gcc aag atg atc ctg ttt gct ttt ggc agt gcc ctg gct cag	1074
Leu Arg Ala Lys Met Ile Leu Phe Ala Phe Gly Ser Ala Leu Ala Gln	
309 314 319 324	
gcc cgg ctc ctc tat ggg aat gat gcc aag gtc ttg gag cag ccc gtg	1122
Ala Arg Leu Leu Tyr Gly Asn Asp Ala Lys Val Leu Glu Gln Pro Val	
325 330 335 340	
gtg gtg cag agc gtg ggc acg gat gga cgt gtc ttc cat ttc cta gtg	1170
Val Val Gln Ser Val Gly Thr Asp Gly Arg Val Phe His Phe Leu Val	
341 346 351 356	
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Phe Gln Leu Asn Thr Thr Asp Leu Asp Cys Asn Glu Gly Val Lys Asn	
357 362 367 372	
ttg gcc tgg gtg gac tca gac cag ctc ctc tat cag cat ttt tgg tgt	1266
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373 378 383 388	
ctc cca gtg atc aaa aag aga gtg gtt gtg gaa cct gtt ggg cca gtt	1314
Leu Pro Val Ile Lys Lys Arg Val Val Val Glu Pro Val Gly Pro Val	
389 394 399 404	
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Gly Phe Lys Pro Glu Thr Phe Arg Lys Phe Leu Ala Leu Tyr Leu His	
405 410 415 420	
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Gly Ala Ala *	
421	
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Met Val Gly Tyr Asp Pro Lys Pro Asp	
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Gly Arg Asn Asn Thr Lys Phe Gln Val Ala Val Ala Gly Ser Val Ser	
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Gly Leu Val Thr Arg Ala Leu Ile Ser Pro Phe Asp Val Ile Lys Ile	
26 31 36 41	
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Arg Phe Gln Leu Gln His Glu Arg Leu Ser Arg Ser Asp Pro Ser Ala	
42 47 52 57	
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Lys Tyr His Gly Ile Leu Gln Ala Ser Arg Gln Ile Leu Gln Glu Glu	
58 63 68 73	
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Gly Pro Thr Ala Phe Trp Lys Gly His Val Pro Ala Gln Ile Leu Ser	
74 79 84 89	
ata ggc tat gga gct gtc caa ttc ttg tca ttt gaa atg ctg acg gag	461
Ile Gly Tyr Gly Ala Val Gln Phe Leu Ser Phe Glu Met Leu Thr Glu	
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Leu Val His Arg Gly Ser Val Tyr Asp Ala Arg Glu Phe Ser Val His	
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Phe Val Cys Gly Gly Leu Ala Ala Cys Met Ala Thr Leu Thr Val His	
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Pro Val Asp Val Leu Arg Thr Arg Phe Ala Ala Gln Gly Glu Pro Lys	
138 143 148 153	
gtc tat aat acg ctg cgc cac gcc gtg ggg acc atg tat agg agc gaa	653
Val Tyr Asn Thr Leu Arg His Ala Val Gly Thr Met Tyr Arg Ser Glu	
154 159 164 169	
ggc ccc cag gtt ttc tac aaa ggc ttg gct ccc acc ttg atc gcc atc	701
Gly Pro Gln Val Phe Tyr Lys Gly Leu Ala Pro Thr Leu Ile Ala Ile	
170 175 180 185	
ttc ccc tac gcc ggg ctg cag ttc tct tgc tac agc tcc ttg aag cac	749
Phe Pro Tyr Ala Gly Leu Gln Phe Ser Cys Tyr Ser Ser Leu Lys His	
186 191 196 201	
ctg tac aag tgg gcc ata cca gcc gaa gga aag aaa aat gag aac ctc	797
Leu Tyr Lys Trp Ala Ile Pro Ala Glu Gly Lys Lys Asn Glu Asn Leu	
202 207 212 217	

caa aac ctg ctt tgt ggc agt gga gct ggt gtc atc agc aag acc ctg	845
Gln Asn Leu Leu Cys Gly Ser Gly Ala Gly Val Ile Ser Lys Thr Leu	
218 223 228 233	
aca tat ccg ctg gac ctc ttc aag aag cgg cta cag gtt gga ggg ttt	893
Thr Tyr Pro Leu Asp Leu Phe Lys Lys Arg Leu Gln Val Gly Gly Phe	
234 239 244 249	
gag cat gcc aga gct gcc ttt ggc cag gta cgg aga tac aag ggc ctc	941
Glu His Ala Arg Ala Ala Phe Gly Gln Val Arg Arg Tyr Lys Gly Leu	
250 255 260 265	
atg gac tgt gcc aag cag gtg cta caa aag gaa ggc gcc ctg ggc ttc	989
Met Asp Cys Ala Lys Gln Val Leu Gln Lys Glu Gly Ala Leu Gly Phe	
266 271 276 281	
ttc aag ggc ctg tcc ccc agc ttg ctg aag gct gcc ctc tcc aca ggc	1037
Phe Lys Gly Leu Ser Pro Ser Leu Leu Lys Ala Ala Leu Ser Thr Gly	
282 287 292 297	
ttc atg ttc ttc tcg tat gaa ttc ttc tgt aat gtc ttc cac tgc atg	1085
Phe Met Phe Phe Ser Tyr Glu Phe Phe Cys Asn Val Phe His Cys Met	
298 303 308 313	
aac agg aca gcc agc cag cgc tga gcgcaggaag gacccaggt cttccctgga	1139
Asn Arg Thr Ala Ser Gln Arg *	
314 319	
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ctgcaggcca gctgccccaa gcggggtagc agccttgaac ccacccagct gggacaccac	1259
cagaaggtcc agggctctcc ccatgagaga atcagaggga atgcaggacg tggctctatgg	1319
tgagccaacg acacagttag aaggagcagg aagttgctgt ttctcctctg accagcccac	1379
actgcaaagg aaacagacgc catcctacac ctatcagccc tgccctgccag gagaacagaa	1439
cacactcctg gtctggatgg ggctgctgct tgagtgcaga gggctgcggt aggccctttg	1499
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<400> 403

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cggagatgtc gctcggccgc cttctaccag gagcctgac cgtgccgccc gccgcccgga	180
tgggaccacc agagtgtctt aaagtctcca gtgaatattg aattgctgag gattttggga	240
aaagacaaat caaagttccc attcc atg gat ccc tta ggt gca cct tcc cag	292
Met Asp Pro Leu Gly Ala Pro Ser Gln	
1 5	
ttt gtg gat gtg gat aca cta cca agc tgg ggt gac tca tgc caa gat	340
Phe Val Asp Val Asp Thr Leu Pro Ser Trp Gly Asp Ser Cys Gln Asp	
10 15 20 25	
gaa tta aat tcc tct gat act aca gct gaa ata ttt cag gaa gac act	388
Glu Leu Asn Ser Ser Asp Thr Thr Ala Glu Ile Phe Gln Glu Asp Thr	
26 31 36 41	
gtt cga tca cct ttt ctt tat aat aag gac gtc aat gga aaa gtg gtt	436
Val Arg Ser Pro Phe Leu Tyr Asn Lys Asp Val Asn Gly Lys Val Val	
42 47 52 57	
ctt tgg aaa gga gat gtg gca tta ctg aac tgt aca gcc att gtg aat	484
Leu Trp Lys Gly Asp Val Ala Leu Leu Asn Cys Thr Ala Ile Val Asn	
58 63 68 73	
acc agc aat gaa agt ctc aca gat aag aat cct gtg tca gaa agt atc	532
Thr Ser Asn Glu Ser Leu Thr Asp Lys Asn Pro Val Ser Glu Ser Ile	
74 79 84 89	
ttc atg ctt gca ggg cct gat ttg aag gaa gat ctc cag aaa ctt aaa	580
Phe Met Leu Ala Gly Pro Asp Leu Lys Glu Asp Leu Gln Lys Leu Lys	
90 95 100 105	
ggg tgc cga aca ggt gaa gca aaa ttg aca aaa gga ttc aat cta gct	628
Gly Cys Arg Thr Gly Glu Ala Lys Leu Thr Lys Gly Phe Asn Leu Ala	
106 111 116 121	
gcc cgg ttc atc att cac aca gtg gga cct aaa tat aaa agc cgc tat	676
Ala Arg Phe Ile Ile His Thr Val Gly Pro Lys Tyr Lys Ser Arg Tyr	
122 127 132 137	
cgc aca gca gct gag agt tcc ctt tat agc tgc tac aga aac gta ctt	724
Arg Thr Ala Ala Glu Ser Ser Leu Tyr Ser Cys Tyr Arg Asn Val Leu	
138 143 148 153	
caa cta gca aaa gag cag tca atg tct tct gtt ggc ttc tgt gtc atc	772
Gln Leu Ala Lys Glu Gln Ser Met Ser Ser Val Gly Phe Cys Val Ile	
154 159 164 169	
aat tct gca aaa cgt ggt tat cct tta gag gat gca aca cac ata gca	820
Asn Ser Ala Lys Arg Gly Tyr Pro Leu Glu Asp Ala Thr His Ile Ala	
170 175 180 185	
ctt cgc act gta aga aga ttc cta gag att cat ggg gaa acc att gaa	868

Leu	Arg	Thr	Val	Arg	Arg	Phe	Leu	Glu	Ile	His	Gly	Glu	Thr	Ile	Glu	
186					191					196					201	
aaa	gta	gta	ttt	gct	gtc	tct	gat	ctt	gaa	gag	ggg	act	tac	caa	aag	916
Lys	Val	Val	Phe	Ala	Val	Ser	Asp	Leu	Glu	Glu	Gly	Thr	Tyr	Gln	Lys	
202					207					212					217	
ctg	cta	cct	ctc	tac	ttc	cca	agg	tca	tta	aaa	gag	gag	aat	cga	tca	964
Leu	Leu	Pro	Leu	Tyr	Phe	Pro	Arg	Ser	Leu	Lys	Glu	Glu	Asn	Arg	Ser	
218					223					228					233	
ttg	ccc	tac	cta	cct	gca	gat	att	gga	aat	gca	gaa	ggg	gag	cct	gtg	1012
Leu	Pro	Tyr	Leu	Pro	Ala	Asp	Ile	Gly	Asn	Ala	Glu	Gly	Glu	Pro	Val	
234					239					244					249	
gta	cct	gaa	cga	cag	att	aga	ata	agt	gag	aaa	cct	ggg	gct	cca	gaa	1060
Val	Pro	Glu	Arg	Gln	Ile	Arg	Ile	Ser	Glu	Lys	Pro	Gly	Ala	Pro	Glu	
250					255					260					265	
gat	aac	caa	gaa	gag	gag	gat	gaa	ggc	ttg	gga	gtt	gat	ctc	tct	ttc	1108
Asp	Asn	Gln	Glu	Glu	Glu	Asp	Glu	Gly	Leu	Gly	Val	Asp	Leu	Ser	Phe	
266					271					276					281	
att	ggc	tct	cat	gct	ttt	gct	cga	atg	gaa	gga	gat	att	gac	aag	caa	1156
Ile	Gly	Ser	His	Ala	Phe	Ala	Arg	Met	Glu	Gly	Asp	Ile	Asp	Lys	Gln	
282					287					292					297	
aga	aaa	ctg	atc	ctt	cag	gga	caa	tta	tca	gag	gca	gct	ctg	cag	aag	1204
Arg	Lys	Leu	Ile	Leu	Gln	Gly	Gln	Leu	Ser	Glu	Ala	Ala	Leu	Gln	Lys	
298					303					308					313	
cag	cat	caa	aga	aat	tat	aat	cgc	tgg	tta	tgt	caa	gca	cga	gct	gag	1252
Gln	His	Gln	Arg	Asn	Tyr	Asn	Arg	Trp	Leu	Cys	Gln	Ala	Arg	Ala	Glu	
314					319					324					329	
gat	ctg	tct	gat	att	gct	tct	cta	aaa	gcc	tta	tac	caa	aca	ggg	gtt	1300
Asp	Leu	Ser	Asp	Ile	Ala	Ser	Leu	Lys	Ala	Leu	Tyr	Gln	Thr	Gly	Val	
330					335					340					345	
gat	aac	tgt	ggg	cga	aca	gtg	atg	gtg	gta	gtt	gga	aga	aac	att	cct	1348
Asp	Asn	Cys	Gly	Arg	Thr	Val	Met	Val	Val	Val	Gly	Arg	Asn	Ile	Pro	
346					351					356					361	
gta	aca	tta	ata	gat	atg	gac	aag	gct	ctc	tta	tat	ttc	att	cat	gta	1396
Val	Thr	Leu	Ile	Asp	Met	Asp	Lys	Ala	Leu	Leu	Tyr	Phe	Ile	His	Val	
362					367					372					377	
atg	gat	cac	att	gct	gtg	aag	gag	tat	gta	tta	gtg	tat	ttt	cac	acc	1444
Met	Asp	His	Ile	Ala	Val	Lys	Glu	Tyr	Val	Leu	Val	Tyr	Phe	His	Thr	
378					383					388					393	
ctg	acc	agc	gaa	tac	aat	cac	ctg	gac	tcc	gac	ttc	ctg	aag	aaa	ctc	1492
Leu	Thr	Ser	Glu	Tyr	Asn	His	Leu	Asp	Ser	Asp	Phe	Leu	Lys	Lys	Leu	
394					399					404					409	
tac	gat	gtt	gtt	gat	gtc	aag	tac	aag	agg	aat	ttg	aag	gct	gtt	tat	1540
Tyr	Asp	Val	Val	Asp	Val	Lys	Tyr	Lys	Arg	Asn	Leu	Lys	Ala	Val	Tyr	

410	415	420	425	
ttt gta cat ccc aca ttt cgt tca aag gtg tca aca tgg ttt ttt acc				1588
Phe Val His Pro Thr Phe Arg Ser Lys Val Ser Thr Trp Phe Phe Thr				
426	431	436	441	
acc ttt tct gtc tca gga ctg aag gac aaa atc cac cat gtg gac agc				1636
Thr Phe Ser Val Ser Gly Leu Lys Asp Lys Ile His His Val Asp Ser				
442	447	452	457	
ctc cac cag ctg ttt tct gcc ata tca cca gaa cag att gac ttt cct				1684
Leu His Gln Leu Phe Ser Ala Ile Ser Pro Glu Gln Ile Asp Phe Pro				
458	463	468	473	
cct ttt gtc ctt gaa tat gat gcc agg gaa aac ggg cct tac tat aca				1732
Pro Phe Val Leu Glu Tyr Asp Ala Arg Glu Asn Gly Pro Tyr Tyr Thr				
474	479	484	489	
tca tat ccc cca tca cca gat ttg tga cctgc catctttcag tgcttcttg				1784
Ser Tyr Pro Pro Ser Pro Asp Leu *				
490	495			
ttcccaggat gccacttcct ccacgaatag ctacctgttg aagtgatatt cattgttgct				1844
gtacagatcc agagagcctt ttgtccccac ctctctggta tttttttatt gactgtatat				1904
tttctggcac ataagcaatc taaaaatggt aggccattct gaactgcaca cattttaaat				1964
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aacttttgag tatcttttagt ttcttgaagg acaccgaatt ctccattaga taaaccacca				2084
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ccttcaggcc tcaggcagag tcacggtggc agcattgaga gttggacacc cgggtccttg	180
aagtgatctc taggccccag ccccaaatec gccaccattc cgtgctgcgg ggacacc	237
atg gct cca gaa gag gac gct gga ggg gag gcc tta ggg ggc agt ttc	285

Met	Ala	Pro	Glu	Glu	Asp	Ala	Gly	Gly	Glu	Ala	Leu	Gly	Gly	Ser	Phe	
1				5					10					15		
tgg	gag	gct	ggc	aac	tac	agg	cgc	acg	gta	cag	cgg	gtg	gag	gac	ggg	333
Trp	Glu	Ala	Gly	Asn	Tyr	Arg	Arg	Thr	Val	Gln	Arg	Val	Glu	Asp	Gly	
17					22					27					32	
cac	cgg	ctg	tgc	ggg	gac	ctg	gtc	agc	tgc	ttc	cag	gag	cgc	gcc	cgc	381
His	Arg	Leu	Cys	Gly	Asp	Leu	Val	Ser	Cys	Phe	Gln	Glu	Arg	Ala	Arg	
33					38					43					48	
atc	gag	aag	gct	tat	gcc	cag	cag	ttg	gct	gac	tgg	gcc	cga	aag	tgg	429
Ile	Glu	Lys	Ala	Tyr	Ala	Gln	Gln	Leu	Ala	Asp	Trp	Ala	Arg	Lys	Trp	
49					54					59					64	
agg	ggg	acc	gtg	gag	aag	ggc	ccc	cag	tat	ggc	aca	ctg	gag	aag	gcc	477
Arg	Gly	Thr	Val	Glu	Lys	Gly	Pro	Gln	Tyr	Gly	Thr	Leu	Glu	Lys	Ala	
65					70					75					80	
tgg	cat	gcc	ttt	ttc	acg	gcg	gct	gag	cgg	ctg	agc	gcg	ctg	cac	ctg	525
Trp	His	Ala	Phe	Phe	Thr	Ala	Ala	Glu	Arg	Leu	Ser	Ala	Leu	His	Leu	
81					86					91					96	
gag	gtg	cgg	gag	aag	ctg	caa	ggg	cag	gac	agt	gag	cgg	gtg	cgc	gcc	573
Glu	Val	Arg	Glu	Lys	Leu	Gln	Gly	Gln	Asp	Ser	Glu	Arg	Val	Arg	Ala	
97					102					107					112	
tgg	cag	cgg	ggg	gct	ttc	cac	cgg	cct	gtg	ctg	ggc	ggc	ttc	cgc	gag	621
Trp	Gln	Arg	Gly	Ala	Phe	His	Arg	Pro	Val	Leu	Gly	Gly	Phe	Arg	Glu	
113					118					123					128	
agc	cgg	gcg	gcc	gag	gac	ggc	ttc	cgc	aag	gcc	cag	aag	ccc	tgg	ctg	669
Ser	Arg	Ala	Ala	Glu	Asp	Gly	Phe	Arg	Lys	Ala	Gln	Lys	Pro	Trp	Leu	
129					134					139					144	
aag	agg	ctg	aag	gag	gtt	gag	gct	tcc	aag	aaa	agc	tac	cac	gca	gcc	717
Lys	Arg	Leu	Lys	Glu	Val	Glu	Ala	Ser	Lys	Lys	Ser	Tyr	His	Ala	Ala	
145					150					155					160	
cgg	aag	gat	gag	aag	acc	gcc	cag	acg	agg	gag	agc	cac	gca	aag	gca	765
Arg	Lys	Asp	Glu	Lys	Thr	Ala	Gln	Thr	Arg	Glu	Ser	His	Ala	Lys	Ala	
161					166					171					176	
gac	agc	gcc	gtc	tcc	cag	gag	cag	ctg	cgc	aaa	ctg	cag	gaa	cgg	gtg	813
Asp	Ser	Ala	Val	Ser	Gln	Glu	Gln	Leu	Arg	Lys	Leu	Gln	Glu	Arg	Val	
177					182					187					192	
gaa	cgc	tgt	gcc	aag	gag	gcc	gag	aag	aca	aaa	gct	cag	tat	gag	cag	861
Glu	Arg	Cys	Ala	Lys	Glu	Ala	Glu	Lys	Thr	Lys	Ala	Gln	Tyr	Glu	Gln	
193					198					203					208	
acg	ctg	gca	gag	ctg	cat	cgc	tac	act	cca	cgc	tac	atg	gag	gac	atg	909
Thr	Leu	Ala	Glu	Leu	His	Arg	Tyr	Thr	Pro	Arg	Tyr	Met	Glu	Asp	Met	
209					214					219					224	
gaa	cag	gcc	ttt	gag	acc	tgc	cag	gcc	gcc	gag	cgc	cag	cgg	ctt	ctt	957
Glu	Gln	Ala	Phe	Glu	Thr	Cys	Gln	Ala	Ala	Glu	Arg	Gln	Arg	Leu	Leu	

225	230	235	240	
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Phe Phe Lys Asp Met Leu Leu Thr Leu His	Gln His Leu Asp Leu Ser			
241	246 251 256			
agc agt gag aag ttc cat gaa ctc cac cgt	gac ttg cac cag ggc att	1053		
Ser Ser Glu Lys Phe His Glu Leu His Arg	Asp Leu His Gln Gly Ile			
257	262 267 272			
gag gca gcc agt gac gaa gag gat ctg cgc	tgg tgg cgc agc acc cac	1101		
Glu Ala Ala Ser Asp Glu Glu Asp Leu Arg	Trp Trp Arg Ser Thr His			
273	278 283 288			
ggg cca ggc atg gcc atg aac tgg cca cag	ttc gag gag tgg tcc ttg	1149		
Gly Pro Gly Met Ala Met Asn Trp Pro Gln	Phe Glu Glu Trp Ser Leu			
289	294 299 304			
gac aca cag agg aca atc agc cgg aaa gag	aag ggt ggc cgg agc cct	1197		
Asp Thr Gln Arg Thr Ile Ser Arg Lys Glu	Lys Gly Gly Arg Ser Pro			
305	310 315 320			
gat gag gtt acc ctg acc agc att gtg cct	aca aga gat ggc acc gca	1245		
Asp Glu Val Thr Leu Thr Ser Ile Val Pro	Thr Arg Asp Gly Thr Ala			
321	326 331 336			
ccc cca ccc cag tcc ccg ggg tcc cca ggc	acg ggg cag gat gag gag	1293		
Pro Pro Pro Gln Ser Pro Gly Ser Pro Gly	Thr Gly Gln Asp Glu Glu			
337	342 347 352			
tgg tca gat gaa gag agt ccc cgg aag gct	gcc acc ggg gtt cgg gtg	1341		
Trp Ser Asp Glu Glu Ser Pro Arg Lys Ala	Ala Thr Gly Val Arg Val			
353	358 363 368			
agg gca ctc tat gac tac gct ggc cag gaa	gct gat gag ctg agc ttc	1389		
Arg Ala Leu Tyr Asp Tyr Ala Gly Gln Glu	Ala Asp Glu Leu Ser Phe			
369	374 379 384			
cga gca ggg gag gag ctg ctg aag atg agt	gag gag gac gag cag ggc	1437		
Arg Ala Gly Glu Glu Leu Leu Lys Met Ser	Glu Glu Asp Glu Gln Gly			
385	390 395 400			
tgg tgc caa ggc cag ttg cag agt ggc cgc	att ggc ctg tac cct gcc	1485		
Trp Cys Gln Gly Gln Leu Gln Ser Gly Arg	Ile Gly Leu Tyr Pro Ala			
401	406 411 416			
aac tac gtg gag tgt gtg ggc gcc tga	gtgtc ctgacagccc ttctgcaacg	1537		
Asn Tyr Val Glu Cys Val Gly Ala *				
417	422			
tttaccacc ctggttcaga gcccagcttc tccctggagag	ccggaccctc agggccctga	1597		
accgtcgctc tctggctgct cctctgtccc ttgagggagg	aagtcctggg acccagggag	1657		
gggaggggcc tttgtctagg gaagggactg gtagggaagg	gacgagtcta ggctgagggc	1717		
aagatgggag gtcagaggtg acagaagcgt tcaggggtgc	ctgggcctcc ccaggagctg	1777		

tggactcagt tcctgacctc tgctttgggg ttcttggggg gggcttgggg tgagtgtagt 1837
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 ccacacacaa aaacaaaaaac accaaaaaaa aaa 1930

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 gggaaggagc ctggacacag tgacacattc tcaaaggccc tgcaggacca cc atg 175
 Met
 1
 gct tat gat gac tcc gtg aag aaa gaa gat tgt ttt gat ggt gat cat 223
 Ala Tyr Asp Asp Ser Val Lys Lys Glu Asp Cys Phe Asp Gly Asp His
 2 7 12 17
 acc ttt gag gac ata gga ctt gca gct ggc cga agc caa cga gag aaa 271
 Thr Phe Glu Asp Ile Gly Leu Ala Ala Gly Arg Ser Gln Arg Glu Lys
 18 23 28 33
 aaa cgt tct tac aaa gat ttt tta agg gaa gag gaa gaa att gct gct 319
 Lys Arg Ser Tyr Lys Asp Phe Leu Arg Glu Glu Glu Glu Ile Ala Ala
 34 39 44 49
 cag gtc agg aat tct tcc aag aag aag ttg aag gat agt gaa ctt tac 367
 Gln Val Arg Asn Ser Ser Lys Lys Lys Leu Lys Asp Ser Glu Leu Tyr
 50 55 60 65
 ttc ttg ggg acg gac aca cac aag aag aag agg aag cac tcc tct gat 415
 Phe Leu Gly Thr Asp Thr His Lys Lys Lys Arg Lys His Ser Ser Asp
 66 71 76 81
 gat tac tac tat gga gac att tcg tct ttg gaa tcg tca cag aag aaa 463
 Asp Tyr Tyr Tyr Gly Asp Ile Ser Ser Leu Glu Ser Ser Gln Lys Lys
 82 87 92 97
 aag aaa aag tcc agc cca cag tct act gat aca gct atg gac ctg ttg 511
 Lys Lys Lys Ser Ser Pro Gln Ser Thr Asp Thr Ala Met Asp Leu Leu
 98 103 108 113
 aaa gct atc act tcc cca ctg gca gca ggc tcc aag ccc tcc aaa aag 559

Lys	Ala	Ile	Thr	Ser	Pro	Leu	Ala	Ala	Gly	Ser	Lys	Pro	Ser	Lys	Lys	
114					119					124					129	
act	ggg	gag	aaa	tcc	tct	ggc	tct	tca	agc	cat	tcg	gag	agt	aaa	aag	607
Thr	Gly	Glu	Lys	Ser	Ser	Gly	Ser	Ser	Ser	His	Ser	Glu	Ser	Lys	Lys	
130					135					140					145	
gag	cac	cac	agg	aag	aaa	gtc	agt	gga	agc	agt	ggg	gaa	cta	ccc	cta	655
Glu	His	His	Arg	Lys	Lys	Val	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Pro	Leu	
146					151					156					161	
gag	gat	ggt	ggc	tcc	cac	aaa	tcg	aaa	aaa	atg	aaa	cct	ctc	tat	gtg	703
Glu	Asp	Gly	Gly	Ser	His	Lys	Ser	Lys	Lys	Met	Lys	Pro	Leu	Tyr	Val	
162					167					172					177	
aac	aca	gag	aca	ctg	acc	ctt	cgg	gag	cct	gat	ggt	tta	aaa	atg	aaa	751
Asn	Thr	Glu	Thr	Leu	Thr	Leu	Arg	Glu	Pro	Asp	Gly	Leu	Lys	Met	Lys	
178					183					188					193	
ctt	att	ctg	tca	cca	aag	gag	aag	gga	agc	agc	tct	gtt	gat	gag	gag	799
Leu	Ile	Leu	Ser	Pro	Lys	Glu	Lys	Gly	Ser	Ser	Ser	Val	Asp	Glu	Glu	
194					199					204					209	
tct	ttt	caa	tat	ccc	tcc	caa	caa	gcg	act	gtg	aaa	aaa	tcc	tca	aag	847
Ser	Phe	Gln	Tyr	Pro	Ser	Gln	Gln	Ala	Thr	Val	Lys	Lys	Ser	Ser	Lys	
210					215					220					225	
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cag	agc	ttt	ctg	aaa	aca	gcc	cgg	aaa	aag	cac	aag	tca	tcc	tca	gac	943
Gln	Ser	Phe	Leu	Lys	Thr	Ala	Arg	Lys	Lys	His	Lys	Ser	Ser	Ser	Asp	
242					247					252					257	
gca	cat	tca	tct	cct	ggc	cct	gaa	ggc	tgt	ggg	tct	gac	gcc	tcc	cag	991
Ala	His	Ser	Ser	Pro	Gly	Pro	Glu	Gly	Cys	Gly	Ser	Asp	Ala	Ser	Gln	
258					263					268					273	
ttc	gca	gag	tcc	cac	agt	gct	aac	ctt	gat	ctt	tca	ggg	ctt	gaa	cct	1039
Phe	Ala	Glu	Ser	His	Ser	Ala	Asn	Leu	Asp	Leu	Ser	Gly	Leu	Glu	Pro	
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Ile	Leu	Val	Glu	Ser	Asp	Ser	Ser	Ser	Gly	Gly	Glu	Leu	Glu	Ala	Gly	
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gag	tta	gtg	ata	gat	gat	tct	tac	cga	gaa	atc	aag	aag	aaa	aag	aag	1135
Glu	Leu	Val	Ile	Asp	Asp	Ser	Tyr	Arg	Glu	Ile	Lys	Lys	Lys	Lys	Lys	
306					311					316					321	
tca	aag	aag	agc	aaa	aag	aag	aaa	gac	aag	gag	aag	cat	aaa	gag	aag	1183
Ser	Lys	Lys	Ser	Lys	Lys	Lys	Lys	Asp	Lys	Glu	Lys	His	Lys	Glu	Lys	
322					327					332					337	
cga	cac	tcc	aag	tcc	aag	aga	agt	tta	gga	ctt	tct	gcc	gtg	cca	gtg	1231
Arg	His	Ser	Lys	Ser	Lys	Arg	Ser	Leu	Gly	Leu	Ser	Ala	Val	Pro	Val	

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Gly Glu Val Thr Val	Thr Ser Gly Pro Pro	Pro Ser Ile Pro Tyr Ala					
354	359	364	369				
gga gca gca gca cct	ccc ctg cca ctt cct	ggc ctc cac aca gat ggg	1327				
Gly Ala Ala Ala Pro	Pro Leu Pro Leu Pro	Gly Leu His Thr Asp Gly					
370	375	380	385				
cat agt gaa aaa aaa	aaa aaa aaa gag aag	gac aaa gag aga gag	1375				
His Ser Glu Lys Lys	Lys Lys Lys Glu Lys	Asp Lys Glu Arg Glu					
386	391	396	401				
aga gga gaa aag cca	aaa aag aag aac atg	tcg gcc tac cag gtg ttc	1423				
Arg Gly Glu Lys Pro	Lys Lys Lys Asn Met	Ser Ala Tyr Gln Val Phe					
402	407	412	417				
tgt aaa gag tat cgc	gtg acc att gtg gct	gac cat cca ggt ata gat	1471				
Cys Lys Glu Tyr Arg	Val Thr Ile Val Ala	Asp His Pro Gly Ile Asp					
418	423	428	433				
ttt ggg gaa ctt agt	aaa aaa ctg gct gag	gtg tgg aag caa tta cca	1519				
Phe Gly Glu Leu Ser	Lys Lys Leu Ala Glu	Val Trp Lys Gln Leu Pro					
434	439	444	449				
gaa aaa gac aaa ctg	att tgg aag caa aaa	gct cag tat ctg cag cac	1567				
Glu Lys Asp Lys Leu	Ile Trp Lys Gln Lys	Ala Gln Tyr Leu Gln His					
450	455	460	465				
aaa cag aac aaa gca	gaa gcc aca act gtg	aaa agg aaa gca tcc agc	1615				
Lys Gln Asn Lys Ala	Glu Ala Thr Thr Val	Lys Arg Lys Ala Ser Ser					
466	471	476	481				
tca gaa ggt tcc atg	aaa gtc aaa gcc tct	tct gta gga gta ctg tca	1663				
Ser Glu Gly Ser Met	Lys Val Lys Ala Ser	Ser Val Gly Val Leu Ser					
482	487	492	497				
ccc cag aag aag tcc	cca ccc acc acc atg	ctg tta cca gcc tca cca	1711				
Pro Gln Lys Lys Ser	Pro Pro Thr Thr Met	Leu Leu Pro Ala Ser Pro					
498	503	508	513				
gcc aaa gcc cct gag	aca gag ccc att gat	gtt gct gct cat ctt cag	1759				
Ala Lys Ala Pro Glu	Thr Glu Pro Ile Asp	Val Ala Ala His Leu Gln					
514	519	524	529				
ctg ttg gga gag tcc	cta agc ctc att gga	cac cgt ctg cag gaa act	1807				
Leu Leu Gly Glu Ser	Leu Ser Leu Ile Gly	His Arg Leu Gln Glu Thr					
530	535	540	545				
gag ggt atg gtg gct	gtg tct ggc agt ttg	tca gtg ctt ctg gat tcc	1855				
Glu Gly Met Val Ala	Val Ser Gly Ser Leu	Ser Val Leu Leu Asp Ser					
546	551	556	561				
att atc tgt gcc ctt	ggc ccc ttg gca tgt	ctc acc aca caa cta cct	1903				
Ile Ile Cys Ala Leu	Gly Pro Leu Ala Cys	Leu Thr Thr Gln Leu Pro					
562	567	572	577				

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Val Ala Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly				
42	47	52	57	
gcc cag ggc ttc cgc tcc ggc cgg cac tac tgg gag gta gag gtg ggc				425
Ala Gln Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly				
58	63	68	73	
ggg cgg cgg ggc tgg gcg gtg ggt gct gcc cgt gaa tca acc cat cat				473
Gly Arg Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His				
74	79	84	89	
aag gaa aag gtg ggc cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc				521
Lys Glu Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala				
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agc tcc tgc cgc cat cac cat cgc cgc cgc cgg ctc cac ctg ccc cag				569
Ser Ser Ser Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln				
106	111	116	121	
cag ccc ctg ctc cag cgg gaa gtg tgg tgc gtg ggc acc aac ggc aaa				617
Gln Pro Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys				
122	127	132	137	
cgc tat cag gcc cag agc tcc aca gaa cag acg ctg ctg agc ccc agt				665
Arg Tyr Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser				
138	143	148	153	
gag aaa cca agg cgc ttt ggt gtg tac ctg gac tat gaa gct ggg cgc				713
Glu Lys Pro Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg				
154	159	164	169	
ctg ggc ttc tac aac gca gag act cta gcc cac gtg cac acc ttc tgc				761
Leu Gly Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser				
170	175	180	185	
gct gcc ttc ctg ggc gag cgt gtc ttt cct ttc ttc cgg gtg ctc tcc				809
Ala Ala Phe Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser				
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Lys Gly Thr Arg Ile Lys Leu Cys Pro *				
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ccgcgccccg agcatctccc tggaggaacg gagacaaagg aggattc atg tcc aaa	176
	Met Ser Lys
	1
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Gly Leu Pro Glu Thr Arg Thr Asp Ala Ala Met Ser Glu Leu Val Pro	
4 9 14 19	
gag ccc agg cct aag cca gcg gtg ccc atg aag ccc atg agc atc aac	272
Glu Pro Arg Pro Lys Pro Ala Val Pro Met Lys Pro Met Ser Ile Asn	
20 25 30 35	
tcc aac ctg ctg ggc tac atc ggc atc gac acc atc atc gag cag atg	320
Ser Asn Leu Leu Gly Tyr Ile Gly Ile Asp Thr Ile Ile Glu Gln Met	
36 41 46 51	
cgc aag aag acc atg aag acc ggt ttc gac ttc aac atc atg gtc gtt	368

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ggc	cag	agt	gga	ctg	ggc	aaa	tca	acg	ctg	gtc	aac	acg	ctc	ttc	aaa	416
Gly	Gln	Ser	Gly	Leu	Gly	Lys	Ser	Thr	Leu	Val	Asn	Thr	Leu	Phe	Lys	
68					73					78					83	
tcc	caa	gtg	agc	cgc	aag	gcc	tcc	agc	tgg	aac	cgg	gag	gag	aag	atc	464
Ser	Gln	Val	Ser	Arg	Lys	Ala	Ser	Ser	Trp	Asn	Arg	Glu	Glu	Lys	Ile	
84					89					94					99	
ccc	aag	aca	gtg	gag	atc	aaa	gct	atc	ggg	cat	gtg	ata	gag	gaa	ggc	512
Pro	Lys	Thr	Val	Glu	Ile	Lys	Ala	Ile	Gly	His	Val	Ile	Glu	Glu	Gly	
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Gln	Ile	Asn	Asn	Glu	Asn	Cys	Trp	Glu	Pro	Ile	Glu	Lys	Tyr	Ile	Asn	
132					137					142					147	
gag	cag	tac	gag	aag	ttc	ctg	aag	gag	gag	gtc	aac	atc	gcc	agg	aag	656
Glu	Gln	Tyr	Glu	Lys	Phe	Leu	Lys	Glu	Glu	Val	Asn	Ile	Ala	Arg	Lys	
148					153					158					163	
aaa	cgc	atc	cct	gac	act	cgt	gtc	cac	tgc	tgc	ctt	tac	ttc	atc	tct	704
Lys	Arg	Ile	Pro	Asp	Thr	Arg	Val	His	Cys	Cys	Leu	Tyr	Phe	Ile	Ser	
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ccc	aca	gga	cac	tcc	ttg	cga	cct	ctg	gat	ctt	gag	ttc	atg	aaa	cac	752
Pro	Thr	Gly	His	Ser	Leu	Arg	Pro	Leu	Asp	Leu	Glu	Phe	Met	Lys	His	
180					185					190					195	
ctc	agc	aag	gtt	gtg	aac	atc	atc	cct	gtc	att	gct	aag	gct	gac	acc	800
Leu	Ser	Lys	Val	Val	Asn	Ile	Ile	Pro	Val	Ile	Ala	Lys	Ala	Asp	Thr	
196					201					206					211	
atg	acc	ctg	gag	gag	aag	tct	gaa	ttc	aag	caa	agg	gtt	cgc	aag	gag	848
Met	Thr	Leu	Glu	Glu	Lys	Ser	Glu	Phe	Lys	Gln	Arg	Val	Arg	Lys	Glu	
212					217					222					227	
ctt	gaa	gta	aat	ggc	att	gaa	ttc	tac	ccc	cag	aag	gaa	ttt	gat	gag	896
Leu	Glu	Val	Asn	Gly	Ile	Glu	Phe	Tyr	Pro	Gln	Lys	Glu	Phe	Asp	Glu	
228					233					238					243	
gat	ttg	gag	gat	aag	acg	gag	aat	gac	aaa	atc	agg	cag	gag	agc	atg	944
Asp	Leu	Glu	Asp	Lys	Thr	Glu	Asn	Asp	Lys	Ile	Arg	Gln	Glu	Ser	Met	
244					249					254					259	
cct	ttt	gct	gtg	gtg	gga	agt	gac	aag	gag	tac	caa	gtg	aat	ggc	aag	992
Pro	Phe	Ala	Val	Val	Gly	Ser	Asp	Lys	Glu	Tyr	Gln	Val	Asn	Gly	Lys	
260					265					270					275	
agg	gtc	ctc	ggc	cga	aaa	act	cca	tgg	ggg	atc	atc	gaa	gtg	gaa	aac	1040
Arg	Val	Leu	Gly	Arg	Lys	Thr	Pro	Trp	Gly	Ile	Ile	Glu	Val	Glu	Asn	

276	281	286	291	
ctc aac cac tgt gag ttt gcc ctg ctt cga gac ttt gtc atc agg acc				1088
Leu Asn His Cys Glu Phe Ala Leu Leu Arg Asp Phe Val Ile Arg Thr				
292	297	302	307	
cac ctc cag gac ctc aag gaa gtg aca cac aac atc cac tat gag act				1136
His Leu Gln Asp Leu Lys Glu Val Thr His Asn Ile His Tyr Glu Thr				
308	313	318	323	
tac agg gcc aag cgg ctc aat gac aat gga ggc ctc cct ccg gtg agc				1184
Tyr Arg Ala Lys Arg Leu Asn Asp Asn Gly Gly Leu Pro Pro Val Ser				
324	329	334	339	
gtg gac aca gag gaa agc cac gac agt aac cca tga cgac cactttctctg				1234
Val Asp Thr Glu Glu Ser His Asp Ser Asn Pro *				
340	345	350		
tgatcatcaca catacccact tcacacacac acatcccaaa taccaccacc aaccaccttc				1294
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			Met	
			1	
ttg cgc tgg ctg cgg gac ttc gtg ctg ccc acc gcg gcc tgc cag gac				163
Leu Arg Trp Leu Arg Asp Phe Val Leu Pro Thr Ala Ala Cys Gln Asp				
2	7	12	17	
gcg gag cag ccg atg cgc tac gag acc ctc ttc cag gca ctg gac cgc				211
Ala Glu Gln Pro Met Arg Tyr Glu Thr Leu Phe Gln Ala Leu Asp Arg				

18	23	28	33	
aat ggg gac gga gtg gtg gac atc ggc gag ctg cag gag ggg ctc agg				259
Asn Gly Asp Gly Val Val Asp Ile Gly Glu Leu Gln Glu Gly Leu Arg				
34	39	44	49	
aac ctg ggc atc cct ctg ggc cag gac gcc gag gag aaa att ttt act				307
Asn Leu Gly Ile Pro Leu Gly Gln Asp Ala Glu Glu Lys Ile Phe Thr				
50	55	60	65	
act gga gat gtc aac aaa gat ggg aag ctg gat ttt gaa gaa ttt atg				355
Thr Gly Asp Val Asn Lys Asp Gly Lys Leu Asp Phe Glu Glu Phe Met				
66	71	76	81	
aag tac ctt aaa gac cat gag aag aaa atg aaa ttg gca ttt aag agt				403
Lys Tyr Leu Lys Asp His Glu Lys Lys Met Lys Leu Ala Phe Lys Ser				
82	87	92	97	
tta gac aaa aat aat gat gga aaa att gag gct tca gaa att gtc cag				451
Leu Asp Lys Asn Asn Asp Gly Lys Ile Glu Ala Ser Glu Ile Val Gln				
98	103	108	113	
tct ctc cag aca ctg ggt ctg act att tct gaa caa caa gca gag ttg				499
Ser Leu Gln Thr Leu Gly Leu Thr Ile Ser Glu Gln Gln Ala Glu Leu				
114	119	124	129	
att ctt caa agc att gat gtt gat ggg aca atg aca gtg gac tgg aat				547
Ile Leu Gln Ser Ile Asp Val Asp Gly Thr Met Thr Val Asp Trp Asn				
130	135	140	145	
gaa tgg aga gac tac ttc tta ttt aat cct gtt aca gac att gag gaa				595
Glu Trp Arg Asp Tyr Phe Leu Phe Asn Pro Val Thr Asp Ile Glu Glu				
146	151	156	161	
att atc cgt ttc tgg aaa cat tct aca gga att gac ata ggg gat agc				643
Ile Ile Arg Phe Trp Lys His Ser Thr Gly Ile Asp Ile Gly Asp Ser				
162	167	172	177	
tta act att cca gat gaa ttc acg gaa gac gaa aaa aaa tcc gga caa				691
Leu Thr Ile Pro Asp Glu Phe Thr Glu Asp Glu Lys Lys Ser Gly Gln				
178	183	188	193	
tgg tgg agg cag ctt ttg gca gga ggc att gct ggt gct gtc tct cga				739
Trp Trp Arg Gln Leu Leu Ala Gly Gly Ile Ala Gly Ala Val Ser Arg				
194	199	204	209	
aca agc act gcc cct ttg gac cgt ctg aaa atc atg atg cag gtt cac				787
Thr Ser Thr Ala Pro Leu Asp Arg Leu Lys Ile Met Met Gln Val His				
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Gly Ser Lys Ser Asp Lys Met Asn Ile Phe Gly Gly Phe Arg Gln Met				
226	231	236	241	
gta aaa gaa gga ggt atc cgc tcg ctt tgg agg gga aat ggt aca aac				883
Val Lys Glu Gly Gly Ile Arg Ser Leu Trp Arg Gly Asn Gly Thr Asn				
242	247	252	257	

gtc atc aaa att gct cct gag aca gct gtt aaa ttc tgg gca tat gaa	931
Val Ile Lys Ile Ala Pro Glu Thr Ala Val Lys Phe Trp Ala Tyr Glu	
258 263 268 273	
cag tac aag aag tta ctt act gaa gaa gga caa aaa ata gga aca ttt	979
Gln Tyr Lys Lys Leu Leu Thr Glu Glu Gly Gln Lys Ile Gly Thr Phe	
274 279 284 289	
gag aga ttt att tct ggt tcc atg gct gga gca act gca cag act ttt	1027
Glu Arg Phe Ile Ser Gly Ser Met Ala Gly Ala Thr Ala Gln Thr Phe	
290 295 300 305	
ata tat cca atg gag gtt atg aaa acc agg ctg gct gta ggc aaa act	1075
Ile Tyr Pro Met Glu Val Met Lys Thr Arg Leu Ala Val Gly Lys Thr	
306 311 316 321	
ggg cag tac tct gga ata tat gat tgt gcc aag aag att ttg aaa cat	1123
Gly Gln Tyr Ser Gly Ile Tyr Asp Cys Ala Lys Lys Ile Leu Lys His	
322 327 332 337	
gaa ggc ttg gga gct ttt tac aaa ggc tat gtt ccc aat tta tta ggt	1171
Glu Gly Leu Gly Ala Phe Tyr Lys Gly Tyr Val Pro Asn Leu Leu Gly	
338 343 348 353	
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Ile Ile Pro Tyr Ala Gly Ile Asp Leu Ala Val Tyr Glu Leu Leu Lys	
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Ser Tyr Trp Leu Asp Asn Phe Ala Lys Asp Ser Val Asn Pro Gly Val	
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Met Val Leu Leu Gly Cys Gly Ala Leu Ser Ser Thr Cys Gly Gln Leu	
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Gln Ser Leu Phe Thr Asn Lys Glu Asn Glu Ser Gln Thr Val Phe Gln
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46 51 56 61	
act gga ctt aaa aaa act aca cag tgc ccc aaa cta gaa gac tca gaa	481
Thr Gly Leu Lys Lys Thr Thr Gln Cys Pro Lys Leu Glu Asp Ser Glu	
62 67 72 77	
aaa gaa tat gtt ctt gat ccc aaa ccg ccg ccg ttg act ttg gca cag	529
Lys Glu Tyr Val Leu Asp Pro Lys Pro Pro Pro Leu Thr Leu Ala Gln	
78 83 88 93	
aag ttg ggc ctc att ggg cct cca cca cct cca ctg tca tca gat gaa	577
Lys Leu Gly Leu Ile Gly Pro Pro Pro Pro Pro Leu Ser Ser Asp Glu	
94 99 104 109	
tgg gag aag gtg aaa cag cgc tct ctc ctg caa ggg gac tcc gtg caa	625
Trp Glu Lys Val Lys Gln Arg Ser Leu Leu Gln Gly Asp Ser Val Gln	
110 115 120 125	
cca tgc ccc atc tgt aaa gaa gaa ttc gag ctt cgt cct cag gtg ttt	673
Pro Cys Pro Ile Cys Lys Glu Glu Phe Glu Leu Arg Pro Gln Val Phe	
126 131 136 141	
agc ata cga ggg tgc tgc ttt cat gct ccc atg tgt tcc aca aag cat	721
Ser Ile Arg Gly Cys Cys Phe His Ala Pro Met Cys Ser Thr Lys His	
142 147 152 157	
gtc ttc agg ctt ttg aaa agt tca caa ata aga aaa cct gtc ctc tct	769
Val Phe Arg Leu Leu Lys Ser Ser Gln Ile Arg Lys Pro Val Leu Ser	
158 163 168 173	
gta gaa aga acc agt atc aaa ccc gag tga t acacgatggg gcccgctgt	820
Val Glu Arg Thr Ser Ile Lys Pro Glu *	
174 179	
tcagaatcaa gtgtgtgacc agaatccaag cctactggag aggatgtgtt gttagaaagt	880
ggtacagaaa cctgaggaaa acagtacctc ccacagatgc caagttaaga aaaaaattct	940
ttgaaaaaaaa gttcacagaa atcagccacc gcatcctgtg ctcatacaac accaacattg	1000
aagagctctt tgcagaaatc gatcagtgtt tggccataaa tcgaagtgtt cttcagcagt	1060
tggaagaaaa atgtggccat gagatcacag aagaggaatg ggagaaaaatc caagtgcagg	1120
ctctgcgccg ggagaccac gagtgcttca ttctgcctgg cccctctctc cgctgctggc	1180
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tttccatgcc tgtcctctct gccgacctg gttccagaat agcattcacg agtgcgtaag	1360
tcatagtcaa gtagagcgag gtcagtctga ggtataaagt tcgccaatcg ttcggtagtg	1420
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<400> 412

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1 5 10	
gag gac agc ata agc agt act ata atg gat gta gac agc aca att tcc	98
Glu Asp Ser Ile Ser Ser Thr Ile Met Asp Val Asp Ser Thr Ile Ser	
14 19 24 29	
agt ggg cgt tca act cca gca atg atg aat gga caa gga agc act act	146
Ser Gly Arg Ser Thr Pro Ala Met Met Asn Gly Gln Gly Ser Thr Thr	
30 35 40 45	
tct tca agc aaa aat att gcc tat aat tgt tgt tgg gac cag tgc cag	194
Ser Ser Ser Lys Asn Ile Ala Tyr Asn Cys Cys Trp Asp Gln Cys Gln	
46 51 56 61	
gct tgc ttc aac tct agc cca gat ctg gca gat cac atc cgt tcc ata	242
Ala Cys Phe Asn Ser Ser Pro Asp Leu Ala Asp His Ile Arg Ser Ile	
62 67 72 77	
cat gta gat ggt cag cga gga ggg gta ttt gtt tgc tta tgg aaa ggt	290
His Val Asp Gly Gln Arg Gly Gly Val Phe Val Cys Leu Trp Lys Gly	
78 83 88 93	
tgt aaa gta tat aac act cca tct acc agt caa agt tgg tta caa agg	338
Cys Lys Val Tyr Asn Thr Pro Ser Thr Ser Gln Ser Trp Leu Gln Arg	
94 99 104 109	
cat atg ctg aca cac agt gga gac aaa cct ttc aag tgt gtt gtt ggt	386
His Met Leu Thr His Ser Gly Asp Lys Pro Phe Lys Cys Val Val Gly	
110 115 120 125	
ggc tgc aat gcc agc ttt gct tct cag gga ggg cta gct cgt cat gta	434
Gly Cys Asn Ala Ser Phe Ala Ser Gln Gly Gly Leu Ala Arg His Val	
126 131 136 141	
ccc aca cac ttc agt cag cag aac tcc tca aaa gtt tct agc cag cca	482
Pro Thr His Phe Ser Gln Gln Asn Ser Ser Lys Val Ser Ser Gln Pro	
142 147 152 157	
aag gcc aaa gaa gaa tct cct tct aaa gct gga atg aac aaa agg agg	530
Lys Ala Lys Glu Glu Ser Pro Ser Lys Ala Gly Met Asn Lys Arg Arg	
158 163 168 173	

aaa tta aag aac aaa aga cga cgc tca tta cca cgg cca cat gat ttc	578
Lys Leu Lys Asn Lys Arg Arg Arg Ser Leu Pro Arg Pro His Asp Phe	
174 179 184 189	
ttc gat gca caa aca ctg gat gcg ata aga cat cga gcc ata tgc ttt	626
Phe Asp Ala Gln Thr Leu Asp Ala Ile Arg His Arg Ala Ile Cys Phe	
190 195 200 205	
aac ctc tca gct cat ata gaa agt tta ggg aag gga cac agt gtt gtt	674
Asn Leu Ser Ala His Ile Glu Ser Leu Gly Lys Gly His Ser Val Val	
206 211 216 221	
ttt cat agt cct gta ata gct aag aga aaa gaa gat tct ggg aag atc	722
Phe His Ser Pro Val Ile Ala Lys Arg Lys Glu Asp Ser Gly Lys Ile	
222 227 232 237	
aaa ctt ttg ctt cat tgg atg cct gaa gac att ctg cat gat gtg tgg	770
Lys Leu Leu Leu His Trp Met Pro Glu Asp Ile Leu His Asp Val Trp	
238 243 248 253	
gtg aat gaa agt gaa cga cat cag tta aaa act aaa gta gtt cat tta	818
Val Asn Glu Ser Glu Arg His Gln Leu Lys Thr Lys Val Val His Leu	
254 259 264 269	
tca aag cta ccc aaa gat act gcc ttg ctt ttg gac cca aac ata tac	866
Ser Lys Leu Pro Lys Asp Thr Ala Leu Leu Leu Asp Pro Asn Ile Tyr	
270 275 280 285	
aga aca atg ccg cag aag agg ttg aag agg taa aaaaaaaaaa aaaaa	914
Arg Thr Met Pro Gln Lys Arg Leu Lys Arg *	
286 291 296	

<210> 413

<211> 913

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(662)

<400> 413

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	1 5	
cag ctg atg gcg gag gcc gag aag cga gtc aag gcc tcc cac tcc ttc	98	
Gln Leu Met Ala Glu Ala Glu Lys Arg Val Lys Ala Ser His Ser Phe		
12 17 22 27		
ctc cga ggg ctg ttt gga gga aac aca aga ata gaa gag gct tgt gaa	146	
Leu Arg Gly Leu Phe Gly Gly Asn Thr Arg Ile Glu Glu Ala Cys Glu		

28	33	38	43	
atg tat acc aga gct gca aat atg ttc aag atg gct aaa aat tgg agt				194
Met Tyr Thr Arg Ala Ala Asn Met Phe Lys Met Ala Lys Asn Trp Ser				
44	49	54	59	
gct gca gga aac gca ttt tgt cag gca gcc aag ctc cac atg cag ctt				242
Ala Ala Gly Asn Ala Phe Cys Gln Ala Ala Lys Leu His Met Gln Leu				
60	65	70	75	
cag agc aaa cat gac tct gct acc agc ttt gtg gat gct gga aat gct				290
Gln Ser Lys His Asp Ser Ala Thr Ser Phe Val Asp Ala Gly Asn Ala				
76	81	86	91	
tac aaa aag gca gat ccc caa gag gct atc aac tgc tta aat gca gcc				338
Tyr Lys Lys Ala Asp Pro Gln Glu Ala Ile Asn Cys Leu Asn Ala Ala				
92	97	102	107	
atc gac att tac aca gac atg gga agg ttt aca att gca gcc aag cac				386
Ile Asp Ile Tyr Thr Asp Met Gly Arg Phe Thr Ile Ala Ala Lys His				
108	113	118	123	
cac att act att gca gag atc tat gag act gaa ctt gta gac att gag				434
His Ile Thr Ile Ala Glu Ile Tyr Glu Thr Glu Leu Val Asp Ile Glu				
124	129	134	139	
aag gct att gca cat tat gaa caa tct gct gat tat tac aaa gga gaa				482
Lys Ala Ile Ala His Tyr Glu Gln Ser Ala Asp Tyr Tyr Lys Gly Glu				
140	145	150	155	
gaa tcc aac agc tca gca aac aag tgt ctg ctg aag gtg gca gca tat				530
Glu Ser Asn Ser Ser Ala Asn Lys Cys Leu Leu Lys Val Ala Ala Tyr				
156	161	166	171	
gct gcc cag ctt gag cag tac cag aaa gcc att gag atc tat gag cag				578
Ala Ala Gln Leu Glu Gln Tyr Gln Lys Ala Ile Glu Ile Tyr Glu Gln				
172	177	182	187	
gtt ggg gcc aac aca atg gaa tat ccc ttt gtg gaa tac agg cca aag				626
Val Gly Ala Asn Thr Met Glu Tyr Pro Phe Val Glu Tyr Arg Pro Lys				
188	193	198	203	
gat act tct tca aag ctg cct ttt gcc act cta tag agac gagttgaagg				676
Asp Thr Ser Ser Lys Leu Pro Phe Ala Thr Leu *				
204	209	214		
ccagcttgct cttgagaata tgaggaaatgt tccagcatta ctgattcaga gatgtaaatt				736
attgaaaaac tctagagctc atgacgacag acaggggaact tacctgagca gtgaggattg				796
gctcatatct gcttgacaga gttgacacat gtggtcgatac aaagccttcc agggatgaga				856
cgaatgggac taatgaaggt ttgtttggca gcatacacct tatttggttag caaggac				913

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 <211> 2047
 <212> DNA
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<220>
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 <222> (369) .. (860)

<400> 414

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ccgcctctct ctcaccgcgc cgctcccgcc tctcgtcctt gcgctgcggg ctcaggcgga      180
acccggaacg gccgtcctct tcccccgccc tccgcgcgct cctccttctc ctctcctctc      240
tctcctcctt ccttctcggc ttctcctca gccccgggccc ggagcggggg gtcggcgggc      300
gccggttcgg gcggcgactc gcgcttcttt gggcgggcggc gcttggccat gtcgtgtcgg      360
ggaaggta atg agc cgc aga gcc ccg ggg tct cgg ctg agc agc ggc ggc      410
      Met Ser Arg Arg Ala Pro Gly Ser Arg Leu Ser Ser Gly Gly
              1              5              10

ggc ggc ggc ggc acc aag tat ccg cgg agc tgg aat gac tgg caa ccc      458
Gly Gly Gly Gly Thr Lys Tyr Pro Arg Ser Trp Asn Asp Trp Gln Pro
      15              20              25              30

aga act gat agt gca tca gcc gac cca gat aat tta aaa tat tct tca      506
Arg Thr Asp Ser Ala Ser Ala Asp Pro Asp Asn Leu Lys Tyr Ser Ser
      31              36              41              46

tcc aga gat aga ggt ggt tct tcc tct tat gga ctg caa cct tca aat      554
Ser Arg Asp Arg Gly Gly Ser Ser Ser Tyr Gly Leu Gln Pro Ser Asn
      47              52              57              62

tca gct gtg gtg tct cgg caa agg cac gat gat acc aga gtc cac gct      602
Ser Ala Val Val Ser Arg Gln Arg His Asp Asp Thr Arg Val His Ala
      63              68              73              78

gac ata cag aat gac gaa aag ggt ggc tac agt gtc aat gga gga tct      650
Asp Ile Gln Asn Asp Glu Lys Gly Gly Tyr Ser Val Asn Gly Gly Ser
      79              84              89              94

ggg gaa aat act tat ggt cgg aag tcg ttg ggg caa gag ctg agg gtt      698
Gly Glu Asn Thr Tyr Gly Arg Lys Ser Leu Gly Gln Glu Leu Arg Val
      95              100              105              110

aac aat gtg acc agc cct gag ttc aca agt gtt cag cat ggc agt cgt      746
Asn Asn Val Thr Ser Pro Glu Phe Thr Ser Val Gln His Gly Ser Arg
      111              116              121              126

gct tta gcc acc aaa gac atg agg aaa tca cag gag aga tcg atg tct      794
Ala Leu Ala Thr Lys Asp Met Arg Lys Ser Gln Glu Arg Ser Met Ser
      127              132              137              142

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 <222> (295) .. (465)

<400> 415

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tccttgaaca taccaagtat attctcttgc ctcagggact ttgcttctgc ccttctccat	180
tcttgggata ctcttctccc agttattctg catgcctttc tcccacacct cttttaaata	240
tttgctttga agtcaccttc ttatcttttg ccttggttga ctctgaagg caaa atg	297
Met	
1	
gat cac aag cag ctc tgc tgg agc cac oca caa aaa tct ggc cag agt	345
Asp His Lys Gln Leu Cys Trp Ser His Pro Gln Lys Ser Gly Gln Ser	
2 7 12 17	
tct cgc tct tgt tgc atc tgc tca aac cag cat ggt ctg atc tgg aaa	393
Ser Arg Ser Cys Cys Ile Cys Ser Asn Gln His Gly Leu Ile Trp Lys	
18 23 28 33	
tat agc ctc aat atg tgc ctc cag tgt tgc cat cag tac gtg aag gat	441
Tyr Ser Leu Asn Met Cys Leu Gln Cys Cys His Gln Tyr Val Lys Asp	
34 39 44 49	
ata ggt ttc att aaa ttg gac taa gtgatcttcc ttgaatggat tatccaaggc	495
Ile Gly Phe Ile Lys Leu Asp *	
50 55	
atccacacaa tgaaaaatca tattagctgt ttgtacataa aataaaaatg aagaaaatga	555
agtcaaacga ca	567

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 <211> 888
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 <213> Homo sapiens

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 <222> (589) .. (858)

<400> 416

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tatctagcac ttttgtgtct ctggctttgc gcaaggttgg ggattggccc ctcaagtggcc	120
gcagagagaa gggactgaac caggagcccc aaggcagggg tctggccctc cagaagatgg	180
gtcaagagga agagagccct ccaagagagg agaggcccca gcagagtcca aaggtacagt	240

gtggagccgc ctgacaagga ctgccatcca cc	atg gtg aag ctg ggc tgc agc	173
	Met Val Lys Leu Gly Cys Ser	
	1 5	
ttc tct ggg aag cca ggt aaa gac cct ggg gac cag gat ggg gct gcc	221	
Phe Ser Gly Lys Pro Gly Lys Asp Pro Gly Asp Gln Asp Gly Ala Ala		
8 13 18 23		
atg gac agt gtg cct ctg atc agc ccc ttg gac atc agc cag ctc cag	269	
Met Asp Ser Val Pro Leu Ile Ser Pro Leu Asp Ile Ser Gln Leu Gln		
24 29 34 39		
ccg cca ctc cct gac cag gtg gtc atc aag aca cag aca gaa tac cag	317	
Pro Pro Leu Pro Asp Gln Val Val Ile Lys Thr Gln Thr Glu Tyr Gln		
40 45 50 55		
ctg tcc tcc cca gac cag cag aat ttc cct gac ctg gag ggc cag agg	365	
Leu Ser Ser Pro Asp Gln Gln Asn Phe Pro Asp Leu Glu Gly Gln Arg		
56 61 66 71		
ctg aac tgc agc cac cca gag gaa ggg cgc agg ctg ccc acc gca cgg	413	
Leu Asn Cys Ser His Pro Glu Glu Gly Arg Arg Leu Pro Thr Ala Arg		
72 77 82 87		
atg atc gcc ttc gcc atg gcg cta ctg ggc tgc gtg ctg atc atg tac	461	
Met Ile Ala Phe Ala Met Ala Leu Leu Gly Cys Val Leu Ile Met Tyr		
88 93 98 103		
aag gcc atc tgg tac gac cag ttc acc tgc ccc gac ggc ttc ctg ctg	509	
Lys Ala Ile Trp Tyr Asp Gln Phe Thr Cys Pro Asp Gly Phe Leu Leu		
104 109 114 119		
cgg cac aag atc tgc acg ccg ctg acc ctg gag atg tac tac acg gag	557	
Arg His Lys Ile Cys Thr Pro Leu Thr Leu Glu Met Tyr Tyr Thr Glu		
120 125 130 135		
atg gac ccc gag cgc cac cgc agc atc ctg gcg gcc atc ggg gcc tac	605	
Met Asp Pro Glu Arg His Arg Ser Ile Leu Ala Ala Ile Gly Ala Tyr		
136 141 146 151		
ccg ctg agc cgc aag cac ggc acg gag acg ccg gcg gcc tgg ggg gac	653	
Pro Leu Ser Arg Lys His Gly Thr Glu Thr Pro Ala Ala Trp Gly Asp		
152 157 162 167		
ggc tac cgc gca gcc aag gag gag cgc aag ggg ccc acc cag gct ggg	701	
Gly Tyr Arg Ala Ala Lys Glu Glu Arg Lys Gly Pro Thr Gln Ala Gly		
168 173 178 183		
gcg gcg gcg gcg gcc acc gaa ccc ccc ggg aag ccg tcg gcc aag gcg	749	
Ala Ala Ala Ala Ala Thr Glu Pro Pro Gly Lys Pro Ser Ala Lys Ala		
184 189 194 199		
gag aag gag gcg gcg cgg aag gcg gcc ggg agc gcg gcg ccc ccg ccc	797	
Glu Lys Glu Ala Ala Arg Lys Ala Ala Gly Ser Ala Ala Pro Pro Pro		
200 205 210 215		
gcg cag tga cgtctcc agccccgcag cccggccccgg gcgtctctccg ccagctctcg	853	

Ala Gln *

216

tgaccagcgc gtctcccgat gctctccgcc gtgttcgtgt ccccaggcgc cctcgtgca 913

gccccgcccc cgtgggtctc tgactctgtc gcttttctct aagtaaagat ttcacgtcca 973

aaaaaaaaa a 984

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<212> DNA

<213> Homo sapiens

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<222> (237) .. (1451)

<400> 418

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ggaaggcagc ggcgagggtgc ctccccacgt acccctcgcg ggcccagccg agcaacgtgg 180

ggcgaaggcg gcggcgaagg cccgggctgg gaggcttggc ggccggagtc ccagcc 236

atg gcg gag tct gtg gag cgc ctg cag cag cgg gtc cag gag ctg gag 284

Met Ala Glu Ser Val Glu Arg Leu Gln Gln Arg Val Gln Glu Leu Glu

1

5

10

15

cgg gaa ctt gcc cag gag agg agt ctg cag gtc ccg agg agc ggc gac 332

Arg Glu Leu Ala Gln Glu Arg Ser Leu Gln Val Pro Arg Ser Gly Asp

17

22

27

32

gga ggg ggc ggc cgg gtc cgc atc gag aag atg agc tca gag gtg gtg 380

Gly Gly Gly Gly Arg Val Arg Ile Glu Lys Met Ser Ser Glu Val Val

33

38

43

48

gat tcg aat ccc tac agc cgc ttg atg gca ttg aaa cga atg gga att 428

Asp Ser Asn Pro Tyr Ser Arg Leu Met Ala Leu Lys Arg Met Gly Ile

49

54

59

64

gta agc gac tat gag aaa atc cgt acc ttt gcc gta gca ata gta ggt 476

Val Ser Asp Tyr Glu Lys Ile Arg Thr Phe Ala Val Ala Ile Val Gly

65

70

75

80

gtt ggt gga gta ggt agt gtg act gct gaa atg ctg aca aga tgt ggc 524

Val Gly Gly Val Gly Ser Val Thr Ala Glu Met Leu Thr Arg Cys Gly

81

86

91

96

att ggt aag ttg cta ctc ttt gat tat gac aag gtg gaa cta gcc aat 572

Ile Gly Lys Leu Leu Phe Asp Tyr Asp Lys Val Glu Leu Ala Asn

97

102

107

112

atg aat aga ctt ttc ttc caa cct cat caa gca gga tta agt aaa gtt	620
Met Asn Arg Leu Phe Phe Gln Pro His Gln Ala Gly Leu Ser Lys Val	
113 118 123 128	
caa gca gca gaa cat act ctg agg aac att aat cct gat gtt ctt ttt	668
Gln Ala Ala Glu His Thr Leu Arg Asn Ile Asn Pro Asp Val Leu Phe	
129 134 139 144	
gaa gta cac aac tat aat ata acc aca gtg gaa aac ttt caa cat ttc	716
Glu Val His Asn Tyr Asn Ile Thr Thr Val Glu Asn Phe Gln His Phe	
145 150 155 160	
atg gat aga ata agt aat ggt ggg tta gaa gaa gga aaa cct gtt gat	764
Met Asp Arg Ile Ser Asn Gly Gly Leu Glu Glu Gly Lys Pro Val Asp	
161 166 171 176	
cta gtt ctt agc tgt gtg gac aat ttt gaa gct cga atg aca ata aat	812
Leu Val Leu Ser Cys Val Asp Asn Phe Glu Ala Arg Met Thr Ile Asn	
177 182 187 192	
aca gct tgt aat gaa ctt gga caa aca tgg atg gaa tct ggg gtc agt	860
Thr Ala Cys Asn Glu Leu Gly Gln Thr Trp Met Glu Ser Gly Val Ser	
193 198 203 208	
gaa aat gca gtt tca ggg cat ata cag ctt ata att cct gga gaa tct	908
Glu Asn Ala Val Ser Gly His Ile Gln Leu Ile Ile Pro Gly Glu Ser	
209 214 219 224	
gct tgt ttt gcg tgt gct cca cca ctt gta gtt gct gca aat att gat	956
Ala Cys Phe Ala Cys Ala Pro Pro Leu Val Val Ala Ala Asn Ile Asp	
225 230 235 240	
gaa aag act ctg aaa cga gaa ggt gtt tgt gca gcc agt ctt cct acc	1004
Glu Lys Thr Leu Lys Arg Glu Gly Val Cys Ala Ala Ser Leu Pro Thr	
241 246 251 256	
act atg ggt gtg gtt gct ggg atc tta gta caa aac gtg tta aag ttt	1052
Thr Met Gly Val Val Ala Gly Ile Leu Val Gln Asn Val Leu Lys Phe	
257 262 267 272	
ctg tta aat ttt ggt act gtt agt ttt tac ctt gga tac aat gca atg	1100
Leu Leu Asn Phe Gly Thr Val Ser Phe Tyr Leu Gly Tyr Asn Ala Met	
273 278 283 288	
cag gat ttt ttt cct act atg tcc atg aag cca aat cct cag tgt gat	1148
Gln Asp Phe Phe Pro Thr Met Ser Met Lys Pro Asn Pro Gln Cys Asp	
289 294 299 304	
gac aga aat tgc agg aag cag cag gag gaa tat aag aaa aag gta gca	1196
Asp Arg Asn Cys Arg Lys Gln Gln Glu Glu Tyr Lys Lys Lys Val Ala	
305 310 315 320	
gca ctg cct aaa caa gag gtt ata caa gaa gag gaa gag ata atc cat	1244
Ala Leu Pro Lys Gln Glu Val Ile Gln Glu Glu Glu Glu Ile Ile His	
321 326 331 336	
gaa gat aat gaa tgg ggt att gag ctg gta tct gag gtt tca gaa gag	1292

ggt ctc tac gtg gcc gag cag ttt ggg gaa gag aac gtg aac acc tac	344
Gly Leu Tyr Val Ala Glu Gln Phe Gly Glu Glu Asn Val Asn Thr Tyr	
83 88 93 98	
ttc gtg ctg tcc agc tgg tgg gcc aag gcc ctg ttt gtc ttc tgc ggc	392
Phe Val Leu Ser Ser Trp Trp Ala Lys Ala Leu Phe Val Phe Cys Gly	
99 104 109 114	
ctc ctc acg tgc tgc tac tgc tgc tgc tgt ctg tgc tgc tgc ttc aac	440
Leu Leu Thr Cys Cys Tyr Cys Cys Cys Cys Leu Cys Cys Cys Phe Asn	
115 120 125 130	
tgc tgc tgc ggg aag tgt aag ccc aag gcg cct gaa ggc gag gag acg	488
Cys Cys Cys Gly Lys Cys Lys Pro Lys Ala Pro Glu Gly Glu Glu Thr	
131 136 141 146	
gag ttc tac gtg tcc ccc gag gat ctg gag gca cag ctg cag tct gac	536
Glu Phe Tyr Val Ser Pro Glu Asp Leu Glu Ala Gln Leu Gln Ser Asp	
147 152 157 162	
gag agg gag gcc aca gac acg ccg atc gtc ata cag ccg gca tcc gcc	584
Glu Arg Glu Ala Thr Asp Thr Pro Ile Val Ile Gln Pro Ala Ser Ala	
163 168 173 178	
acc gag acc acc cag ctc aca gcc gac tcc cac ccc agc tac cac act	632
Thr Glu Thr Thr Gln Leu Thr Ala Asp Ser His Pro Ser Tyr His Thr	
179 184 189 194	
gac ggg ttc aac taa atccaggagg agctgtggtc agaggaggag ccggcgccctg	687
Asp Gly Phe Asn *	
195	
gccacgccaa ccttagaatc atgaactgta gtcacagaga tgggaaggca gcctcctgcc	747
tgccctggcc ttgctggggc cctcctgcc tccacgcccc cccagcgctcg acccttgacc	807
cacgaagtgc gtagcatgca gtatttaaag cagtgtagct acggtcttct gtttttttcc	867
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